

DE AA505075-derived oligonucleotide SEQ ID 4947.
XX
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cycostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Myce JM, Li Y, Sandraseagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI; 2003-093058/08.
XX
PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
XX Claim 15; SEQ ID NO 4947; 763pp; English.
XX
CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cycostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hyperextension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query March 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAAGTAA 1537

Db ||||| ||||
1 AAAAAAAAAAAAAAAAAA 18
RESULT 752
ABD25936
ID ABD25936 standard; DNA, 20 BP.
XX
AC ABD25936;
XX
DT 29-JUL-2004 (first entry)
XX
XX AA505075-derived oligonucleotide SEQ ID 4948.
DE
XX
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cycostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
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XX Homo sapiens.
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PD 31-OCT-2002.
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PF 23-APR-2002; 2002WO-US013143.
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CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
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CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
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CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to

CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it

SO Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAAGTAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 753

ABD32081/C
ID ABD32081 standard; DNA; 20 BP.

XX AC ABD32081;

XX DT 29-JUL-2004 (first entry)

DE Human PDE4C-derived oligonucleotide SEQ ID 14292.

XX Human; antisease; bronchoconstriction; allergy; hyposecretion; pain;
KM respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KM surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KM analgesic; hypotensive; immunosuppressive; cyclostatic; cystic fibrosis;
KM beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KM respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KM emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KM pulmonary transplantation rejection; ss; primer.

XX Homo sapiens.

XX WO200285309-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013143.

XX PR 24-APR-2001; 2001US-0286036P.

XX PA (EPIG-) EPIGENESIS PHARM INC.

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PI Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-093058/08.

XX Pharmaceutical composition for treating asthma, has antisease
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.

PS Claim 15; SEQ ID NO 14292; 763pp; English.

XX This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
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CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
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CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
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CC transplantation rejection, pulmonary infections, bronchitis or cancer.
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CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
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CC prevent any unwanted effects due to it

SO Sequence 20 BP; 0 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAAGTAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 754

ABD21541/C
ID ABD21541 standard; DNA; 20 BP.

XX AC ABD21541;

XX DT 29-JUL-2004 (first entry)

DE S100 calcium binding protein A2-derived oligo SEQ ID 553.

XX Human; antisease; bronchoconstriction; allergy; hyposecretion; pain;
KM respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KM surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KM analgesic; hypotensive; immunosuppressive; cyclostatic; cystic fibrosis;
KM beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KM respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KM emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KM pulmonary transplantation rejection; ss; primer.

XX Homo sapiens.

XX WO200285309-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013143.

XX PR 24-APR-2001; 2001US-0286036P.

XX PA (EPIG-) EPIGENESIS PHARM INC.

XX NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-093058/08.

XX Pharmaceutical composition for treating asthma, has antisease
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.

PS Claim 15; SEQ ID NO 553; 763pp; English.

XX This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating

CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
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CC or availability, or to increase the degradation of the target mRNA or to
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CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
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CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
CC
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 20;

Best Local Similarity 88.9%; Pred. No. 4.4e+02; Mismatches 2; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1520 AAAAAAAAAAGTAAAA 1537

Db 20 AAAAAAAAAAAAAAAAAA 3

RESULT 755
ABD25671

ID ABD25671 standard; DNA; 20 BP.

XX ABD25671;

DT 29-JUL-2004 (first entry)

DE A1024215-derived oligonucleotide SEQ ID 4683.

XX Human; antisease; bronchoconstriction; allergy; hyposecretion; pain;
XX respiratory tract inflammation; adenosine sensitivity; lung; cancer;
XX surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
XX analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
XX beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
XX respiratory distress syndrome; allergic rhinitis; pulmonary hyperextension;
XX emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
XX pulmonary transplantation rejection; ss; primer.

OS Homo sapiens.

XX WO200285309-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002MO-US013143.

XX 24-APR-2001; 2001US-0286036P.

XX (EPIC-) EPIGENESIS PHARM INC.

XX Nye JW, Li Y, Sandrasegara A, Katz E, Pabalan J, Aguilar D;
XX Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-093058/08.
XX
XX pharmaceutical composition for treating asthma, has antisease
XX oligonucleotide containing less percentage of adenosine, targeted to
XX nucleic acids associated with lung airway or lung dysfunction, and
XX bronchodilating agent.

PS Claim 15; SEQ ID NO 4683; 763pp; English.

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XX comprising oligonucleotides, effective for alleviating
XX bronchoconstriction, respiratory tract inflammation, allergies and
XX reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
XX surfactant depletion or hyposecretion, when administered to a mammal. The
XX oligonucleotides are derived from a gene encoding or regulating
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XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 20;

Best Local Similarity 88.9%; Pred. No. 4.4e+02; Mismatches 2; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1520 AAAAAAAAAAGTAAAA 1537

Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 756
ABD21765

ID ABD21765 standard; DNA; 20 BP.

XX ABD21765;

DT 29-JUL-2004 (first entry)

DE Human etanocalcin-derived oligo SEQ ID 777.

XX Human; antisease; bronchoconstriction; allergy; hyposecretion; pain;
XX respiratory tract inflammation; adenosine sensitivity; lung; cancer;
XX surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
XX analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
XX beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
XX respiratory distress syndrome; allergic rhinitis; pulmonary hyperextension;
XX emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
XX pulmonary transplantation rejection; ss; primer.

OS Homo sapiens.

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PN WO200285309-A2.
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XX 31-OCT-2002.
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PF 23-APR-2002; 2002WO-US013143.
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XX 24-APR-2001; 2001US-0286036P.
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XX (EPiG-) EPIGENESIS PHARM INC.
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PI NYce JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
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XX WPI; 2003-093058/08.
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DR
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PT Pharmaceutical composition for treating asthma, has antisense
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PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
XX Claim 15; SEQ ID NO 777; 763bp; English.
XX
XX This invention describes a novel composition (a) a first active agent,
XX comprising oligonucleotides, effective for alleviating
XX bronchoconstriction, respiratory tract inflammation, allergies and
XX reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
XX surfactant depletion or hyposecretion, when administered to a mammal. The
XX oligonucleotides are derived from a gene encoding or regulating
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XX
XX Sequence 20 BP; 18 A; 0 C; 2 G; 0 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAGTAAAA 1537
Db 2 AAAAAAAAAAGTAAAA 19
RESULT 757
ABD24675
ID ABD24675 standard; DNA; 20 BP.
XX
XX ABD24675;
AC
XX
XX 29-JUL-2004 (first entry)
DT
XX
DE AA281534-derived oligonucleotide SEQ ID 3687.
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XX
XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
XX respiratory tract inflammation; adenosine sensitivity; lung; cancer;
XX surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
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XX WO200285309-A2.
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XX Sequence 20 BP; 1 A; 3 C; 6 G; 10 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 716 TTCTGTTTGTGCTGTG 733
|||||
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Db 2 TTCTCTGTTCCGCTGTG 19

RESULT 758
ABD26880
ID ABD26880 standard; DNA; 20 BP.
XX
AC ABD26880;
XX
DT 29-JUL-2004 (first entry)
XX
DE AA278764-derived oligonucleotide SEQ ID 5892.
XX
XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KM respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KM surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
KM analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
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KM emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
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OS Homo sapiens.
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PN WO200285309-A2.
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PD 31-OCT-2002.
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PR 24-APR-2001; 2001US-0286036P.
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PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shanabuddin S;
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DR WPI; 2003-093058/08.
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SQ	Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
	Query Match 1.1%; Score 14.8; DB 1; Length 20;
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	Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0
Oy	1520 AAAAAAAAAAGTAAAA 1537 Db 1 AAAAAAAAAAAAAAAAAA 18
RESULT 759	
ABD24850	
ID	ABD24850 standard; DNA; 20 BP.
AC	
XX	ABD24850;
XX	
DT	29-JUL-2004 (first entry)
DE	
XX	AI092623-derived oligonucleotide SEQ ID 3862.
KM	Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KM	respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KM	surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KM	analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KM	beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KM	respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KM	emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KM	pulmonary transplantation rejection; ss; primer.
XX	
OS	Homo sapiens.
FN	WO200285309-A2.
PD	31-OCT-2002.
PE	23-APR-2002; 2002MO-US013143.
PR	24-APR-2001; 2001US-0286036P.
PA	(EPIG-) EPIGENESIS PHARM INC.
P1	Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
P1	Miller S, Tang L, Shahabuddin S;
DR	WPI; 2003-093058/08.
PT	Pharmaceutical composition for treating asthma, has antisease
PT	oligonucleotide containing less percentage of adenosine, targeted to
PT	nucleic acids associated with lung airway or lung dysfunction, and
PT	bronchodilating agent.
PS	Claim 15; SEQ ID NO 3862; 763bp; English.
XX	
CC	This invention describes a novel composition (a) a first active agent,
CC	comprising oligonucleotides, effective for alleviating
CC	bronchoconstriction, respiratory tract inflammation, allergies and
CC	reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC	surfactant depletion or hyposecretion, when administered to a mammal. The
CC	oligonucleotides are derived from a gene encoding or regulating
CC	expression of a target polypeptide associated with lung airway or lung
CC	dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC	The invention also describes a kit, that comprises: (a) a delivery
CC	device, in separate containers, (b) the oligonucleotides, (c)
CC	instructions for adding a carrier and for use of the kit. The composition
CC	of the invention has antiallergic, antiinflammatory, antiasthmatic,
CC	analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC	beta-adrenergic agonist. The composition is useful for preventing or
CC	treating a respiratory, lung or malignant disease. The administered

CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
CC
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query March 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 18
RESULT 760
ABD22850
ID ABD22850 standard; DNA; 20 BP.
AC ABD22850;
XX
DT 29-JUL-2004 (first entry)
DE Human myosin X-derived oligonucleotide SEQ ID 1862.
XX
XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytosstatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX
XX Homo sapiens.
OS
PN WO200285309-A2.
XX
XX 31-OCT-2002.
PD
XX 23-APR-2002; 2002WO-US013143.
PF
XX 24-APR-2001; 2001US-0286036P.
PR
XX (EPIG-) EPIGENESIS PHARM INC.
PA
XX NYCE JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-093058/08.
XX
XX Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
XX Claim 15; SEQ ID NO 1862; 763pp; English.
PS
XX This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and

CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytosstatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
CC
SQ Sequence 20 BP; 1 A; 4 C; 10 G; 5 T; 0 U; 0 Other;
Query March 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 486 GGCTGGGCGCGGCGTG 503
Db 2 GGCTGGCGCGGCGTG 19
RESULT 761
ABD24496
ID ABD24496 standard; DNA; 20 BP.
AC ABD24496;
XX
XX 29-JUL-2004 (first entry)
DT
XX
XX A1652901-derived oligonucleotide SEQ ID 3508.
DE
XX
XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytosstatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX
XX Homo sapiens.
OS
PN WO200285309-A2.
XX
XX 31-OCT-2002.
PD
XX 23-APR-2002; 2002WO-US013143.
PF
XX 24-APR-2001; 2001US-0286036P.
PR
XX (EPIG-) EPIGENESIS PHARM INC.
PA
XX NYCE JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX

DR WPI; 2003-093058/08.
XX
XX Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
XX Claim 15; SEQ ID NO 3508; 763bp; English.
XX
XX This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, antispasmodic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability of or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hyperextension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc. tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
XX Sequence 20 BP; 17 A; 1 C; 1 G; 1 T; 0 U; 0 Other;
SQ
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1519 TAAAAAAGTAA 1536
Db 3 TAAAAAAGTAA 20
XX
XX RESULT 762
ABD25532
ID ABD25532 standard; DNA; 20 BP.
XX
XX ABD25532;
XX
XX 29-JUN-2004 (first entry)
XX
XX A1125651-derived oligonucleotide SEQ ID 4544.
XX
XX Human, antisense; bronchoconstriction; allergy; hyposecretion; pain;
XX respiratory tract inflammation; adenosine sensitivity; lung; cancer;
XX surfactant depletion; anti-allergic; anti-inflammatory; antispasmodic;
XX analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
XX beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
XX respiratory distress syndrome; allergic rhinitis; pulmonary hyperextension;
XX emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
XX pulmonary transplantation rejection; pain; primer.
XX
XX Homo sapiens.
XX
XX WO200285309-A2.

XX
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013143.
XX
XX 24-APR-2001; 2001US-0286036P.
XX
XX (EPIC-) EPICGENESIS PHARM INC.
XX
XX Nye JM, Li Y, Sandrasegura A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI; 2003-093058/08.
XX
XX Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
XX Claim 15; SEQ ID NO 4544; 763bp; English.
XX
XX This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, antispasmodic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability of or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hyperextension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc. tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
SQ
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAGTAA 1537
Db 1 AAAAAAAGTAA 18
XX
XX RESULT 763
ABD25046
ID ABD25046 standard; DNA; 20 BP.
XX
XX ABD25046;
XX
XX 29-JUN-2004 (first entry)
XX
XX A1128305-derived oligonucleotide SEQ ID 4058.
XX

Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
respiratory tract inflammation; adenosine sensitivity; lung; cancer;
surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
pulmonary transplantation rejection; ss; primer.
Homo sapiens.
WO200285309-A2.
31-OCT-2002.
23-APR-2002; 2002WO-US013143.
24-APR-2001; 2001US-0286036P.
(EPIG-) EPIGENESIS PHARM INC.
Nyce JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
Miller S, Tang L, Shahbuddin S;
WPI; 2003-093058/08.
Pharmaceutical composition for treating asthma, has antisense
oligonucleotide containing less percentage of adenosine, targeted to
nucleic acids associated with lung airway or lung dysfunction, and
bronchodilating agent.
Claim 15; SEQ ID NO 4058; 763pp; English.
This invention describes a novel composition (a) a first active agent,
comprising oligonucleotides, effective for alleviating
bronchoconstriction, respiratory tract inflammation, allergies and
reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
surfactant depletion or hyposecretion, when administered to a mammal. The
oligonucleotides are derived from a gene encoding or regulating
expression of a target polypeptide associated with lung airway or lung
dysfunction or cancer and can be anti-sense to the corresponding mRNA.
The invention also describes a kit, that comprises: (a) a delivery
device, in separate containers, (b) the oligonucleotides, (c)
instructions for adding a carrier and for use of the kit. The composition
of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
beta-adrenergic agonist. The composition is useful for preventing or
treating a respiratory, lung or malignant disease. The administered
composition comprises oligo and is administered to reduce the production
or availability, or to increase the degradation of the target mRNA or to
reduce the amount of target polypeptide present in the lungs. The
oligonucleotides are derived from a gene encoding or regulating
expression of a target polypeptide associated with lung airway or lung
dysfunction or cancer and/or bronchoconstriction and/or lung
inflammation, allergies and/or surfactant hypoproduction are associated
with a disease or condition such as pulmonary vasoconstriction,
inflammation, allergies, asthma, impeded respiration, respiratory
distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
transplantation rejection, pulmonary infections, bronchitis or cancer.
The reduced adenosine content of the anti-sense oligos corresponding to
thymidines present in the target RNA serves to prevent the breakdown of
the oligonucleotides into products that free adenosine into the system
e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
prevent any unwanted effects due to it
Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
1520 AAAAAAAAAAAGTAAA 1537
1 AAAAAAAAAAAAAAAAAA 18

RESULT 764
ABD29094
ID ABD29094 standard; DNA; 20 BP.
AC ABD29094;
XX 29-JUL-2004 (first entry)
XX AA679352-derived oligonucleotide SEQ ID 8106.
XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
XX respiratory tract inflammation; adenosine sensitivity; lung; cancer;
XX surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
XX analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
XX beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
XX respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
XX emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
XX pulmonary transplantation rejection; ss; primer.
XX Homo sapiens.
XX WO200285309-A2.
XX 31-OCT-2002.
XX 23-APR-2002; 2002WO-US013143.
XX 24-APR-2001; 2001US-0286036P.
XX (EPIG-) EPIGENESIS PHARM INC.
XX Nyce JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX Miller S, Tang L, Shahbuddin S;
XX WPI; 2003-093058/08.
XX Pharmaceutical composition for treating asthma, has antisense
XX oligonucleotide containing less percentage of adenosine, targeted to
XX nucleic acids associated with lung airway or lung dysfunction, and
XX bronchodilating agent.
XX Claim 15; SEQ ID NO 8106; 763pp; English.
XX This invention describes a novel composition (a) a first active agent,
XX comprising oligonucleotides, effective for alleviating
XX bronchoconstriction, respiratory tract inflammation, allergies and
XX reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
XX surfactant depletion or hyposecretion, when administered to a mammal. The
XX oligonucleotides are derived from a gene encoding or regulating
XX expression of a target polypeptide associated with lung airway or lung
XX dysfunction or cancer and can be anti-sense to the corresponding mRNA.
XX The invention also describes a kit, that comprises: (a) a delivery
XX device, in separate containers, (b) the oligonucleotides, (c)
XX instructions for adding a carrier and for use of the kit. The composition
XX of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
XX analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
XX beta-adrenergic agonist. The composition is useful for preventing or
XX treating a respiratory, lung or malignant disease. The administered
XX composition comprises oligo and is administered to reduce the production
XX or availability, or to increase the degradation of the target mRNA or to
XX reduce the amount of target polypeptide present in the lungs. The
XX oligonucleotides are derived from a gene encoding or regulating
XX expression of a target polypeptide associated with lung airway or lung
XX dysfunction or cancer and/or bronchoconstriction and/or lung
XX inflammation, allergies and/or surfactant hypoproduction are associated
XX with a disease or condition such as pulmonary vasoconstriction,
XX inflammation, allergies, asthma, impeded respiration, respiratory
XX distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
XX hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
XX transplantation rejection, pulmonary infections, bronchitis or cancer.
XX The reduced adenosine content of the anti-sense oligos corresponding to
XX thymidines present in the target RNA serves to prevent the breakdown of
XX the oligonucleotides into products that free adenosine into the system

CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
SQ Sequence 20 BP; 12 A; 1 C; 2 G; 5 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1512 TGTATTATTAATAAAAAA 1529
Dd 3 TGTCAAGTAAAAAATAA 20
RESULT 765
ABD21825
ID ABD21825 standard; DNA; 20 BP.
XX
AC ABD21825;
XX
DT 29-JUL-2004 (first entry)
DE Human stannocalcin-derived oligo SEQ ID 837.
XX
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIC-) EPIGENESIS PHARM INC.
PI Nyce JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI, 2003-093058/08.
XX
PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 837; 763pp; English.
XX
XX This invention describes a novel composition (a) a first active agent,
XX comprising oligonucleotides, effective for alleviating
XX bronchoconstriction, respiratory tract inflammation, allergies and
XX reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
XX surfactant depletion or hyposecretion, when administered to a mammal. The
XX oligonucleotides are derived from a gene encoding or regulating
XX expression of a target polypeptide associated with lung airway or lung
XX dysfunction or cancer and can be anti-sense to the corresponding mRNA.
XX The invention also describes a kit, that comprises: (a) a delivery
XX device, in separate containers, (b) the oligonucleotides, (c)
XX instructions for adding a carrier and for use of the kit. The composition
XX of the invention has antiallergic, antiinflammatory, antiasthmatic,
XX analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
XX beta-adrenergic agonist. The composition is useful for preventing or
XX treating a respiratory, lung or malignant disease. The administered
XX composition comprises oligo and is administered to reduce the production

CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
SQ Sequence 20 BP; 0 A; 5 C; 7 G; 8 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 723 TTTTGCTGTGCTGCTGC 740
Dd 1 TTGTCGTGCTGCTGCTGC 18
RESULT 766
ABD23911/C
ID ABD23911 standard; DNA; 20 BP.
XX
AC ABD23911;
XX
DT 29-JUL-2004 (first entry)
DE Human calmodulin 2-derived oligonucleotide SEQ ID 2923.
XX
XX
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIC-) EPIGENESIS PHARM INC.
PI Nyce JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI, 2003-093058/08.
XX
PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 2923; 763pp; English.
XX
XX This invention describes a novel composition (a) a first active agent,
XX comprising oligonucleotides, effective for alleviating
XX bronchoconstriction, respiratory tract inflammation, allergies and
XX reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,

CC surfactant depletion or hyposecretion, when administered to a mammal. The
 CC oligonucleotides are derived from a gene encoding or regulating
 CC expression of a target polypeptide associated with lung airway or lung
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
 CC The invention also describes a kit, that comprises: (a) a delivery
 CC device, in separate containers, (b) the oligonucleotides, (c)
 CC instructions for adding a carrier and for use of the kit. The composition
 CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
 CC beta-adrenergic agonist. The composition is useful for preventing or
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 CC or availability, or to increase the degradation of the target mRNA or to
 CC reduce the amount of target polypeptide present in the lungs. The
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 CC inflammation, allergies and/or surfactant hypoproduction are associated
 CC with a disease or condition such as pulmonary vasoconstriction,
 CC inflammation, allergies, asthma, impeded respiration, respiratory
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
 CC hyperextension, emphysema, chronic obstructive pulmonary disease, pulmonary
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.
 CC The reduced adenosine content of the anti-sense oligos corresponding to
 CC thymidines present in the target RNA serves to prevent the breakdown of
 CC the oligonucleotides into products that free adenosine into the system
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
 CC prevent any unwanted effects due to it

XX Sequence 20 BP; 0 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 4.4e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
 Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 767
 ABD25044
 ID ABD25044 standard; DNA; 20 BP.
 AC ABD25044;
 XX
 XX 29-JUL-2004 (first entry)
 DT
 XX
 DE A1128305-derived oligonucleotide SEQ ID 4056.
 XX
 XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
 XX respiratory tract inflammation; adenosine sensitivity; lung; cancer;
 XX surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
 XX analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
 XX beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
 XX respiratory distress syndrome; allergic rhinitis; pulmonary hyperextension;
 XX emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
 XX pulmonary transplantation rejection; ss; primer.
 XX
 OS Homo sapiens.
 XX
 XX WO200285309-A2.
 XX
 XX 31-OCT-2002.
 XX
 XX 23-APR-2002; 2002WO-US013143.
 XX
 XX 24-APR-2001; 2001US-0286036P.
 XX
 XX (EPIG-) EPIGENESIS PHARM INC.
 XX
 XX NYCE JW, Li Y, Sandrasagra A, Katz E, Fabalan J, Aguilar D,
 XX Pi Miller S, Tang L, Shahbuddin S,
 XX
 XX WPI; 2003-093058/08.

XX
 PT pharmaceutical composition for treating asthma, has antisense
 PT oligonucleotide containing less percentage of adenosine, targeted to
 PT nucleic acids associated with lung airway or lung dysfunction, and
 PT bronchodilating agent.

XX
 PS Claim 15; SEQ ID NO 4056; 763bp; English.

XX
 XX This invention describes a novel composition (a) a first active agent,
 CC comprising oligonucleotides, effective for alleviating
 CC bronchoconstriction, respiratory tract inflammation, allergies and
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
 CC surfactant depletion or hyposecretion, when administered to a mammal. The
 CC oligonucleotides are derived from a gene encoding or regulating
 CC expression of a target polypeptide associated with lung airway or lung
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
 CC The invention also describes a kit, that comprises: (a) a delivery
 CC device, in separate containers, (b) the oligonucleotides, (c)
 CC instructions for adding a carrier and for use of the kit. The composition
 CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
 CC beta-adrenergic agonist. The composition is useful for preventing or
 CC treating a respiratory, lung or malignant disease. The administered
 CC composition comprises oligo and is administered to reduce the production
 CC or availability, or to increase the degradation of the target mRNA or to
 CC reduce the amount of target polypeptide present in the lungs. The
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung
 CC inflammation, allergies and/or surfactant hypoproduction are associated
 CC with a disease or condition such as pulmonary vasoconstriction,
 CC inflammation, allergies, asthma, impeded respiration, respiratory
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
 CC hyperextension, emphysema, chronic obstructive pulmonary disease, pulmonary
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.
 CC The reduced adenosine content of the anti-sense oligos corresponding to
 CC thymidines present in the target RNA serves to prevent the breakdown of
 CC the oligonucleotides into products that free adenosine into the system
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
 CC prevent any unwanted effects due to it

XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 4.4e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
 Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 768
 ABD25111
 ID ABD25111 standard; DNA; 20 BP.
 AC ABD25111;
 XX
 XX 29-JUL-2004 (first entry)
 DT
 XX
 XX A112528-derived oligonucleotide SEQ ID 4123.
 XX
 XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
 XX respiratory tract inflammation; adenosine sensitivity; lung; cancer;
 XX surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
 XX analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
 XX beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
 XX respiratory distress syndrome; allergic rhinitis; pulmonary hyperextension;
 XX emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
 XX pulmonary transplantation rejection; ss; primer.
 XX
 OS Homo sapiens.
 XX
 XX WO200285309-A2.

PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIC-) EPIGENESIS PHARM INC.
XX
PI Nyece JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D,
PI Miller S, Teng L, Shahbuddin S;
XX
DR WPI; 2003-093058/08.
XX
PT Pharmaceutical composition for treating asthma, has antilasease
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 4123; 763pp; English.
XX
CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, antihastmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasooconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidine present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAGTAAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 18
XX
RESULT 769
ADH08684
ID ADH08684 standard; DNA; 20 BP.
XX
AC ADH08684;
XX
DT 11-MAR-2004 (first entry)
XX
DE Nanotechnology nucleic acid detection method associated #54.
XX
KW Linking oligonucleotide; ss; nucleic acid detection;

KW nanoparticle-oligonucleotide conjugate.
XX
OS Synthetic.
XX
PN US2002137070-A1.
XX
PD 26-SEP-2002.
XX
PE 10-OCT-2001; 2001US-00973638.
XX
PR 29-JUL-1996; 96US-0011809P.
PR 21-JUL-1997; 97WO-US012783.
PR 29-JAN-1999; 99US-00240755.
PR 25-JUN-1999; 99US-00344667.
PR 26-APR-2000; 2000US-0200161P.
PR 26-JUN-2000; 2000US-00603830.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI MicKin CA, Letsinger RL, Mucic RC, Stornhoff JJ, Elghanian R;
PI Taton TA;
XX
DR WPI; 2004-059018/06.
XX
PT Detecting nucleic acid used for e.g. diagnosis of diseases, forensics and
PT DNA sequencing, comprises observing detectable change caused by
PT hybridization of nucleic acid with substrate or particle bound
PT oligonucleotides.
XX
PS Example 18; SEQ ID NO 55; 130pp; English.
XX
CC The invention relates to a method of detecting a nucleic acid with at
CC least two portions by providing a type of nanoparticle-oligonucleotide
CC conjugate, contacting the nucleic acid and nanoparticles to allow
CC hybridisation of the oligonucleotides with the two or more portions of
CC the nucleic acid and observing a detectable change brought about by
CC hybridisation. The oligonucleotides have a sequence complementary to the
CC sequence of at least two portions of the nucleic acid. Hybridisation of
CC the oligonucleotides on the nanoparticles with the nucleic acid results
CC in a detectable change. This sequence represents a linking
CC oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAGTAAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 18
XX
RESULT 770
ADH08814
ID ADH08814 standard; DNA; 20 BP.
XX
AC ADH08814;
XX
DT 11-MAR-2004 (first entry)
XX
DE Nanotechnology nucleic acid detection method associated #54.
XX
KW Linking oligonucleotide; ss; nucleic acid detection;
KW nanoparticle-oligonucleotide conjugate.
XX
OS Synthetic.
XX
PN US2002137072-A1.
XX
PD 26-SEP-2002.
XX
PF 12-OCT-2001; 2001US-00976617.


```
XX 29-JUL-1996; 96US-0031809P.
PR 21-JUL-1997; 97WO-US012783.
PR 29-JAN-1999; 99US-00240755.
PR 25-JUN-1999; 99US-00344667.
PR 26-APR-2000; 2000US-0200161P.
PR 26-JUN-2000; 2000US-00603830.
XX
XX (NANO-) NANOSPHERE INC.
PA
PI Mirkin CA, Letsinger RL, Mucic RC, Storchhoff JU, Elghanian R;
PI Taton TA;
DR WPI; 2004-059020/06.
XX
XX Detecting nucleic acid used for e.g. diagnosis of diseases, forensics and
PT DNA sequencing, comprises observing detectable change caused by
PT hybridization of nucleic acid with substrate or particle bound
PT oligonucleotides.
XX
XX Example 18; SEQ ID NO 55; 130pp; English.
XX
XX The invention relates to a method of detecting a nucleic acid with at
CC least two portions by providing a type of nanoparticle-oligonucleotide
CC conjugate, contacting the nucleic acid and nanoparticles to allow
CC hybridisation of the oligonucleotides with the two or more portions of
CC the nucleic acid and observing a detectable change brought about by
CC hybridisation. The oligonucleotides have a sequence complementary to the
CC sequence of at least two portions of the nucleic acid. Hybridisation of
CC the oligonucleotides on the nanoparticles with the nucleic acid results
CC in a detectable change. This sequence represents a linking
CC oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 86.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAGTAAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 18
RESULT 771
ADH08749
ID ADH08749 standard; DNA; 20 BP.
AC ADH08749;
XX
XX 11-MAR-2004 (first entry)
XX
XX Nanotechnology nucleic acid detection method associated #54.
DE
XX Linking oligonucleotide; ss; nucleic acid detection;
KW nanoparticle-oligonucleotide conjugate.
XX
XX Synthetic.
OS
XX US2002137071-A1.
PN
XX
XX 26-SEP-2002.
PD
XX
XX 10-OCT-2001; 2001US-00974007.
PF
XX
XX 29-JUL-1996; 96US-0031809P.
PR 21-JUL-1997; 97WO-US012783.
PR 29-JAN-1999; 99US-00240755.
PR 25-JUN-1999; 99US-00344667.
PR 26-APR-2000; 2000US-0200161P.
PR 26-JUN-2000; 2000US-00603830.
XX
XX (NANO-) NANOSPHERE INC.
PA
```

```
XX Mirkin CA, Letsinger RL, Mucic RC, Storchhoff JU, Elghanian R;
PI Taton TA;
XX
XX WPI; 2004-059019/06.
DR
XX
XX Detecting nucleic acid used for e.g. diagnosis of diseases, forensics and
PT DNA sequencing, comprises observing detectable change caused by
PT hybridization of nucleic acid with substrate or particle bound
PT oligonucleotides.
XX
XX Example 18; SEQ ID NO 55; 130pp; English.
XX
XX The invention relates to a method of detecting a nucleic acid with at
CC least two portions by providing a type of nanoparticle-oligonucleotide
CC conjugate, contacting the nucleic acid and nanoparticles to allow
CC hybridisation of the oligonucleotides with the two or more portions of
CC the nucleic acid and observing a detectable change brought about by
CC hybridisation. The oligonucleotides have a sequence complementary to the
CC sequence of at least two portions of the nucleic acid. Hybridisation of
CC the oligonucleotides on the nanoparticles with the nucleic acid results
CC in a detectable change. This sequence represents a linking
CC oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAGTAAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 18
RESULT 772
ADH65941/C
ID ADH65941 standard; DNA; 20 BP.
XX
XX ADH65941;
AC
XX
XX 25-MAR-2004 (first entry)
DT
XX
XX Human glucocorticoid receptor-specific antisense oligonucleotide #2775.
DE
XX antisense oligonucleotide; glucocorticoid receptor; infection;
KW inflammation; tumour formation; diabetes; obesity;
KW cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; ss;
KW phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.
XX
XX Homo sapiens.
OS
XX
XX WO2003099215-A2.
PN
XX
XX 04-DEC-2003.
PD
XX
XX 20-MAY-2003; 2003WO-US016084.
PF
XX
XX 20-MAY-2002; 2002US-0381857P.
PR
XX (PAAA ) PHARMACIA CORP.
PA
XX
XX Crosby SD, Nalseth AE;
PI
XX
XX WPI; 2004-035034/03.
DR
XX
XX New antisense compound targeted to a nucleic acid molecule encoding
PT mammalian glucocorticoid receptor, useful for treating diabetes, obesity,
PT cardiovascular disorder, hyperlipidemia or Cushing's syndrome.
XX
XX Claim 4; SEQ ID NO 2775; 985pp; English.
XX
XX The invention comprises an antisense oligonucleotides that are targeted
CC
```

CC to nucleic acids encoding a mammalian glucocorticoid receptor. The
CC antisense oligonucleotides of the invention are useful for preventing or
CC delaying infection, inflammation or tumour formation. The antisense
CC oligonucleotides are also useful for treating diabetes, obesity, the
CC cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The
CC present DNA sequence represents an antisense oligonucleotide that targets
CC the human glucocorticoid receptor gene. NOTE: The present sequence
CC contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
XX
SQ Sequence 20 BP; 1 A; 3 C; 1 G; 15 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1522 AAAAAAAAAAGTAAAG 1538
DB 19 AAGAGAAAAATTAAGG 2
RESULT 775
ADH67409/C
ID ADH67409 standard; DNA; 20 BP.
XX
AC ADH67409;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human glucocorticoid receptor-specific antisense oligonucleotide #4243.
XX
XX antisense oligonucleotide; glucocorticoid receptor; infection;
KM inflammation; tumour formation; diabetes; obesity;
KM cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; ss;
KM phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.
XX
XX Homo sapiens.
XX
XX OS
XX PN WO2003099215-A2.
XX
PD 04-DEC-2003.
XX
PF 20-MAY-2003; 2003WO-US016084.
XX
PR 20-MAY-2002; 2002US-0381857P.
XX
PA (PHAA) PHARMACIA CORP.
PI Crobby SD, Nalseth AE;
XX
DR WPI; 2004-035034/03.
XX
XX New antisense compound targeted to a nucleic acid molecule encoding
PT mammalian glucocorticoid receptor, useful for treating diabetes, obesity,
PT cardiovascular disorder, hyperlipidaemia or Cushing's syndrome.
XX
PS Claim 4; SEQ ID NO 4243; 985bp; English.
XX
CC The invention comprises an antisense oligonucleotide that are targeted
CC to nucleic acids encoding a mammalian glucocorticoid receptor. The
CC antisense oligonucleotides of the invention are useful for preventing or
CC delaying infection, inflammation or tumour formation. The antisense
CC oligonucleotides are also useful for treating diabetes, obesity, the
CC cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The
CC present DNA sequence represents an antisense oligonucleotide that targets
CC the human glucocorticoid receptor gene. NOTE: The present sequence
CC contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
XX
SQ Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1521 AAAAAAAAAAGTAAAG 1538
DB 20 AAAAAAAAAAAAAAAAAAG 3
RESULT 774
AD134492
ID AD134492 standard; DNA; 20 BP.
XX
AC AD134492;
XX
DT 22-APR-2004 (first entry)
XX
DE Nucleotide sequence of a dA20 oligonucleotide.
XX
XX Nucleic acid amplification; RNA transcription; RNA polymerase; ss; T7.
XX
XX Synthetic.
XX
XX OS
XX PN WO2003102243-A1.
XX
PD 11-DEC-2003.
XX
XX 30-MAY-2003; 2003WO-US017103.
XX
XX 31-MAY-2002; 2002US-0384454P.
XX
PA (JANC) JANSSEN PHARM NV.
XX
XX Kamme FC, Zhu JY;
XX
XX WPI; 2004-035466/03.
XX
PT Amplifying for RNA in a sample, useful for improving RNA polymerase based
PT RNA transcription from a polynucleotide template, comprises eliminating
PT single-stranded oligonucleotide from the transcription sample.
XX
PS Example 2; SEQ ID NO 11; 26pp; English.
XX
XX The invention relates to amplifying for RNA in a sample comprises
CC eliminating single-stranded oligonucleotide from the transcription
CC sample. The method involves synthesizing single-stranded cDNA by
CC incubating the sample RNA with reverse transcriptase and an
CC oligonucleotide primer that primes synthesis in a direction toward 5' end
CC of the RNA; converting the single-stranded cDNA into double-stranded cDNA
CC to form a transcription sample containing a cDNA template; eliminating
CC single-stranded oligonucleotide from the transcription sample; and
CC transcribing the cDNA template into RNA using an RNA polymerase. The
CC method is useful for improving RNA polymerase based RNA transcription
CC from a polynucleotide template. The method inhibits the undesired non-
CC template derived production of RNA in the transcription reaction. The
CC present sequence represents an oligonucleotide used to exemplify RNA
CC transcription in the presence of single- and double-stranded
CC oligonucleotides.
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAGTAAAG 1537
DB 1 AAAAAAAAAAAAAAAAAAAAA 18
RESULT 775
AD147212
ID AD147212 standard; DNA; 20 BP.
XX
AC AD147212;
XX
DT 22-APR-2004 (first entry)

```
XX DE Molecule analysing microchannel method related probe #2.
XX KM laminar flow; micro channel; complex; selectively promoted; fluorescence;
XX KW probe; ss.
XX OS Unidentified.
XX XX WO2004010140-A1.
XX PN 29-JAN-2004.
XX PD 18-JUL-2003; 2003WO-JP009142.
XX PF 19-JUL-2002; 2002JP-00211462.
XX PR 19-JUL-2002; 2002JP-00211462.
XX PA (NABAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
XX XX Yamashita K, Maeda H, Shimizu H, Miyazaki M, Nakamura H,
PI Yamaguchi Y;
XX WPI; 2004-180318/17.
XX PT Analysis of sample molecules such as DNA fragment, by using micro channel
PT to form laminar flow of specimen molecule-containing solution and complex
PT forming molecule containing solution.
XX PS Example 1; Page 9; 19pp; Japanese.
XX CC The invention relates to a novel method involving forming a laminar flow,
CC by passing into a micro channel, a solution containing the specimen
CC molecules, and a solution containing probe molecules capable of forming a
CC complex with the specimen molecules. The dispersion of the formed complex
CC is selectively promoted, based on their affinity, and the degree of
CC dispersion of the complex formed between the specimen molecules and the
CC probe molecules is detected and analysed. The probe molecules are capable
CC of producing fluorescence. This polynucleotide sequence represents an
CC oligo used in the exemplification of the invention.
XX SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX Query Match 1.1%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 4.4e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX QY 1520 AAAAAAAAAAGTAAAA 1537
XX DB 1 AAAAAAAAAAAAAAAAAA 18
XX RESULT 776
XX ADX51142/C
XX ID ADX51142 standard; DNA; 20 BP.
XX AC ADX51142;
XX DT 06-MAY-2004 (first entry)
XX DE Polyalkyleneamine-conjugated oligonucleotide #1.
XX SS; Antimicrobial; Antiinflammatory; Cytostatic; prodrug; infection;
XX inflammation; tumour.
XX OS Synthetic.
XX XX
XX Key Location/Qualifiers
XX modified_base 20
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "Optionally conjugated with spermine,
XX FT polyethyleneimine (PEI) 600 or PEI 1200,
XX FT tetraethylenepentamine. Also optionally 5'-protected with
XX FT DMT."
```

```
XX XX US2004019000-A1.
XX PN 23-JAN-2004.
XX PD 19-JUL-2002; 2002US-00199585.
XX PF 19-JUL-2002; 2002US-00199585.
XX PR 19-JUL-2002; 2002US-00199585.
XX XX (MANO/) MANOHARAN M.
XX PA (GUZA/) GUZAEV A P.
XX PA (MAIE/) MAIER M A.
XX XX Manoharan M, Guzaev AP, Maier MA;
XX WPI; 2004-224429/21.
XX DR
XX PT Novel polyalkyleneamine-containing oligomeric compound useful for
PT preventing or delaying infection, inflammation or tumor formation in
PT organisms.
XX PS Example 3; Page 22; 37pp; English.
XX CC The invention relates to a polyalkyleneamine-containing oligomeric
CC compound (OC). Also described is a compound (C) comprising an oligomeric
CC part, a fusogenic part, and a targeting part; and enhancing the cellular
CC uptake of OC, by conjugating OC to a fusogenic part. In (C), the
CC fusogenic part is covalently linked to the oligomeric part. The targeting
CC part is covalently linked to the oligomeric or fusogenic part, where the
CC fusogenic part is a lipophilic polyamine, polyethylenimine,
CC polyallylamine, fusogenic peptide, oligomeric imidazole, histidine,
CC pyridine, hydroxylamine, substituted hydroxylamine, hydrazine,
CC substituted hydrazine, thiourea or imine. The targeting part is a ligand
CC that binds to a cellular reporter, where the targeting part is
CC transferrin, folate, epidermal growth factor, nerve growth factor,
CC insulin, alpha-fetoprotein, galactose, galactosamine, lactose, mannose, a
CC polyclonal antibody, monoclonal antibody, vitamin B12, ibuprofen,
CC cholesterol, low-density lipoprotein, peptide comprising an arginine-
CC glycine-aspartic acid sequence. The oligomeric part is an
CC oligonucleotide, and oligonucleotide analogue, a peptide nucleic acid or
CC a peptide nucleic acid analogue. OC is useful as a prodrug, useful in
CC diagnostics, therapeutics and as research reagents and kits. OC is useful
CC for preventing or delaying infection, inflammation or tumour formation in
CC organisms. The present sequence represents an oligonucleotide used in the
CC method of the invention.
XX SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
XX Query Match 1.1%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 4.4e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX QY 1520 AAAAAAAAAAGTAAAA 1537
XX DB 20 AAAAAAAAAAAAAAAAAA 3
XX RESULT 777
XX ADX98410/C
XX ID ADX98410 standard; DNA; 20 BP.
XX AC ADX98410;
XX DT 06-MAY-2004 (first entry)
XX DE Primer of the invention #4130.
XX XX human; single nucleotide polymorphism; SNP; ss; primer.
XX OS Synthetic.
XX XX
XX JP2003259875-A.
XX PN
```

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PD 16-SEP-2003.
XX
XX 08-MAR-2002; 2002JP-00064373.
XX
XX 08-MAR-2002; 2002JP-00064373.
XX
XX (KAGA-) KAGAKU GIUTSU SHINKO JIGYODAN.
XX
XX WPI; 2004-093977/10.
XX
XX Novel polynucleotide useful for PCR amplification along with two DNA
XX fragment from another set of sequences, or for detecting single
XX polynucleotide polymorphism in human gene.
XX
XX Claim 2; SEQ ID NO 7439; 2627bp; Japanese.
XX
XX The present invention relates to a polynucleotide isolated from a human
XX gene and is useful for detecting a single nucleotide polymorphism in a
XX human gene or for diagnosing of disease. The invention enables the
XX detection of a single nucleotide polymorphism in a human gene. The
XX present sequence represents a primer of the invention.
XX
XX Sequence 20 BP; 5 A; 5 C; 8 G; 2 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 668 CTCACCTCTGAGCGCCT 685
Db 19 CTCACCTCTGAGCGCCT 2
RESULT 778
ADJ60935/C
ID ADJ60935 standard; DNA; 20 BP.
XX
XX ADJ60935;
AC
XX
XX 06-MAY-2004 (first entry)
DT
XX
XX Oligonucleotide associated to PDE4C #1.
XX
XX interleukin; IL-4 receptor; IL-5 receptor; lung disease;
XX airway inflammation; allergy; asthma; impeded respiration;
XX cystic fibrosis; acute respiratory distress syndrome;
XX pulmonary hypertension; lung inflammation; bronchitis; oligonucleotide;
XX ss.
XX
XX Homo sapiens.
XX
XX WO2004011613-A2.
XX
XX 05-FEB-2004.
PD
XX
XX 25-JUL-2003; 2003WO-US023509.
PF
XX
XX 29-JUL-2002; 2002US-0399076P.
PR
XX
XX (EPIC-) EPICGENESIS PHARM INC.
PA
XX
XX Nyce JM, Tang L, Sandraesgra A, Aguilar D, Miller S;
XX Shahabuddin S, Lu H, Cong H;
XX WPI; 2004-203534/19.
XX
XX Novel single or multiple target oligonucleotide anti-sense to e.g.,
XX initiation codons and introns of respiratory disease-relevant genes e.g.,
XX CCR1, RANTES, MCP4, useful for prophylaxis or treating respiratory
XX disease e.g., asthma.
XX
XX Claim 2; SEQ ID NO 1791; 85pp; English.
XX
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CC The present invention relates to an oligonucleotide anti-sense to e.g.,
CC initiation codon, coding region with 2-10 nucleotides of 5'-end and 3'-
CC end of nucleic acid target comprising gene(s) chosen from e.g.
CC interleukin (IL)-4 receptor, IL-5 receptor or sales of the
CC oligonucleotide and optionally surfactant operatively linked to the
CC oligonucleotide. The method is useful for preventing or treating a
CC respiratory or lung disease, which involves administering to the airways
CC of a subject an effective amount of an inhibitor. The oligonucleotide is
CC useful for production of a medicament for the prevention and/or treatment
CC of a respiratory or lung disease. The respiratory or lung disease is
CC chosen from airway inflammation, allergy(ies), asthma, impeded
CC respiration, cystic fibrosis (CF), chronic obstructive pulmonary diseases
CC (COPD), allergic rhinitis (AR), acute respiratory distress syndrome
CC (ARDS), pulmonary hypertension, lung inflammation, bronchitis, airway
CC obstruction. The present sequence represents an oligonucleotide of the
CC invention.
XX
XX Sequence 20 BP; 0 A; 1 C; 0 G; 19 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAAAGTAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2
RESULT 779
ADJ32920
ID ADJ32920 standard; DNA; 20 BP.
XX
XX ADJ32920;
AC
XX
XX 06-MAY-2004 (first entry)
DT
XX
XX Oligo related to thiol oligo-gold colloid conjugate probe SEQ 70.
XX
XX nanoparticle; gold; disease; forensic; paternity testing;
XX cell line authentication; gene therapy; ss; gold colloid conjugate.
XX
XX Synthetic.
XX
XX US2003207296-A1.
XX
XX 06-NOV-2003.
PD
XX
XX 08-OCT-2002; 2002US-00266983.
PF
XX
XX 29-JUL-1996; 96US-0031809P.
PR
XX
XX 21-JUL-1997; 97WO-US012783.
PR
XX
XX 29-JAN-1999; 99US-00240755.
PR
XX
XX 25-JUN-1999; 99US-00344667.
PR
XX
XX 13-JAN-2000; 2000US-0176409P.
PR
XX
XX 28-MAR-2000; 2000US-0192699P.
PR
XX
XX 26-APR-2000; 2000US-0200161P.
PR
XX
XX 26-JUN-2000; 2000US-00603830.
PR
XX
XX 26-JUN-2000; 2000US-0213906P.
PR
XX
XX 11-AUG-2000; 2000US-0224631P.
PR
XX
XX 08-DEC-2000; 2000US-0254392P.
PR
XX
XX 08-DEC-2000; 2000US-0254418P.
PR
XX
XX 11-DEC-2000; 2000US-0255235P.
PR
XX
XX 11-DEC-2000; 2000US-0255236P.
PR
XX
XX 12-JAN-2001; 2001US-00760500.
PR
XX
XX 28-MAR-2001; 2001US-00820279.
PR
XX
XX 09-APR-2001; 2001US-0282640P.
PR
XX
XX 10-AUG-2001; 2001US-00927777.
PR
XX
XX 09-OCT-2001; 2001US-0327864P.
PR
XX
XX 07-DEC-2001; 2001US-00008978.
XX
XX (PARK/) PARK S.
XX (TATO/) TATON T A.
XX (MIRK/) MIRKIN C A.
XX
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XX Park S, Taton TA, Mirkin CA;
XX WPI; 2004-059754/06.
XX
PT Detection of nucleic acid, e.g. viral RNA or DNA, comprises contacting
PT nucleic acid with different types of nanoparticles having attached
PT oligonucleotides and observing detectable change brought about by
PT hybridization.
XX
PS Example 24; SEQ ID NO 70; 206pp; English.
XX
CC The invention relates to a novel method for detecting a nucleic acid
CC having at least two portions comprising contacting the nucleic acid with
CC at least two types of nanoparticles, such as gold, having attached
CC oligonucleotides and observing a detectable change brought about by
CC hybridisation of the oligonucleotides on the nanoparticles with the
CC nucleic acid. The method of the invention may be useful for detecting a
CC nucleic acid, preferably viral RNA or DNA, bacterial DNA, a gene
CC associated with a disease, a fungal DNA, synthetic DNA or RNA,
CC structurally modified natural or synthetic DNA or RNA or a product of a
CC polymerase chain reaction amplification. The detected nucleic acid may be
CC utilised for diagnosis of disease, sequencing of nucleic acids,
CC forensics, paternity testing, cell line authentication and monitoring
CC gene therapy. The method for detecting the nucleic acids is based on
CC observing a colour change with the naked eye and is cheap, fast, simple,
CC and robust, requiring no specialised or expensive equipment. The current
CC sequence is that of the oligonucleotide which is related to a thiol-
CC modified oligonucleotide-gold colloid conjugate probe of the invention.
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAGTAAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 18
XX
RESULT 780
AD132905
ID AD132905 standard; DNA; 20 BP.
XX
AC AD132905;
XX
XX 06-MAY-2004 (first entry)
XX
DE Synthetic thiol-modified oligo-gold colloid conjugate probe - SEQ 55.
XX
KW nanoparticle; gold; disease; forensic; paternity testing;
KW cell line authentication; gene therapy; ss; gold colloid conjugate;
KW probe.
XX
OS Synthetic.
XX
XX US2003207296-A1.
XX
PN 06-NOV-2003.
XX
PD 06-NOV-2003.
XX
PF 08-OCT-2002; 2002US-00266983.
XX
XX
PR 29-JUL-1996; 96US-0031809P.
PR 21-JUL-1997; 97WO-US0122783.
PR 29-JAN-1999; 99US-00240755.
PR 25-JUN-1999; 99US-00344667.
PR 13-JAN-2000; 2000US-0176409P.
PR 28-MAR-2000; 2000US-0192699P.
PR 26-APR-2000; 2000US-0200161P.
PR 26-JUN-2000; 2000US-00603830.
PR 26-JUN-2000; 2000US-0213906P.
PR 11-AUG-2000; 2000US-0224631P.
PR
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PR 08-DEC-2000; 2000US-0254392P.
PR 08-DEC-2000; 2000US-0254418P.
PR 11-DEC-2000; 2000US-0255235P.
PR 11-DEC-2000; 2000US-0255236P.
PR 12-JAN-2001; 2001US-00760500.
PR 28-MAR-2001; 2001US-00820279.
PR 09-APR-2001; 2001US-0282640P.
PR 10-AUG-2001; 2001US-00927777.
PR 09-OCT-2001; 2001US-0327864P.
PR 07-DEC-2001; 2001US-00008978.
XX
XX (PARK/) PARK S.
XX (TATON/) TATON T A.
XX (MIRK/) MIRKIN C A.
XX
PI Park S, Taton TA, Mirkin CA;
XX WPI; 2004-059754/06.
XX
DR WPI; 2004-059754/06.
XX
XX
XX Detection of nucleic acid, e.g. viral RNA or DNA, comprises contacting
XX nucleic acid with different types of nanoparticles having attached
XX oligonucleotides and observing detectable change brought about by
XX hybridization.
XX
PS Example 18; SEQ ID NO 55; 206pp; English.
XX
XX
XX The invention relates to a novel method for detecting a nucleic acid
XX having at least two portions comprising contacting the nucleic acid with
XX at least two types of nanoparticles, such as gold, having attached
XX oligonucleotides and observing a detectable change brought about by
XX hybridisation of the oligonucleotides on the nanoparticles with the
XX nucleic acid. The method of the invention may be useful for detecting a
XX nucleic acid, preferably viral RNA or DNA, bacterial DNA, a gene
XX associated with a disease, a fungal DNA, synthetic DNA or RNA,
XX structurally modified natural or synthetic DNA or RNA or a product of a
XX polymerase chain reaction amplification. The detected nucleic acid may be
XX utilised for diagnosis of disease, sequencing of nucleic acids,
XX forensics, paternity testing, cell line authentication and monitoring
XX gene therapy. The method for detecting the nucleic acids is based on
XX observing a colour change with the naked eye and is cheap, fast, simple,
XX and robust, requiring no specialised or expensive equipment. The current
XX sequence is that of the synthetic thiol-modified oligonucleotide-gold
XX colloid conjugate probe of the invention which is linked via a thiol
XX group to a gold nanoparticle.
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAGTAAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 18
XX
RESULT 781
ADK70840
ID ADK70840 standard; DNA; 20 BP.
XX
AC ADK70840;
XX
XX 06-MAY-2004 (first entry)
XX
DE 5' mRNA DNA preparation method related tag DNA sequence #8.
XX
KW DNA preparation; 5' mRNA; linker synthesis; primer synthesis;
KW gene regulation; gene expression; ss; tag.
XX
OS Unidentified.
XX
XX W02003106672-A2.
XX
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PD 24-DEC-2003.
XX
XX 12-JUN-2003; 2003WO-JP007514.
XX
XX 12-JUN-2002; 2002JP-00171851.
PR 12-AUG-2002; 2002JP-00235294.
XX
XX (RIKE) RIKEN KK.
PA (DNAF-) DNAFORM KK.
XX
XX Hayashizaki Y, Carninci P, Harbers MT;
PI MPI; 2004-082194/08.
XX
XX Preparing DNA fragment corresponding to nucleotide sequence of 5' end
XX region of mRNA, by preparing nucleic acid corresponding to nucleotide
PT sequence of 5' end of mRNA, cleaving nucleic acid with restriction
PT enzyme.
XX
XX Example 5; SEQ ID NO 40; 121pp; English.
PS
XX The invention comprises a method for preparing a DNA fragment
XX corresponding to a nucleotide sequence of a 5' end of an mRNA. The method
XX is useful for synthesizing a nucleotide sequence to be used as a linker
XX or primer and selectively collecting multiple nucleic acid fragments
XX containing information on the nucleotide sequences at the 5' end of
XX multiple mRNA in a sample. The method is also useful for identifying
XX regions in the genome, which are required for gene regulation and gene
XX expression. The present DNA sequence was used in an example of the
XX invention.
XX
XX Sequence 20 BP; 0 A; 1 C; 10 G; 9 T; 0 U; 0 Other;

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Query Match          1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred.No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps
OY      545  TGTGTCGCTGTGTCGTG 562
          ||||| |||||
Db      2    TGTGTGTGTGTGTCGTG 19

RESULT 782
ADK69880/c
ADK69880 standard; DNA; 20 BP.
XX
AC      ADK69880;
XX
DT      06-MAY-2004 (first entry)
XX
DE      Sulphurised oligonucleotide #10.
XX
KM      Phosphorothioate backbone; sulphurised oligonucleotide; ss.
XX
OS      Unidentified.
XX
XX      Key      Location/Qualifiers
FH      modified_base 1..20
FT      /*tag= a
FT      /mod_base= OTHER
FT      /note= "Phosphorothioate backbone; 2'-O-methoxyethyl
FT      residues"
XX
XX      US2003212267-A1.
XX
XX      13-NOV-2003.
XX
XX      12-DEC-2002; 2002US-00181200.
XX
XX      11-JAN-2000; 2000US-00481486.
XX      10-JAN-2001; 2001WO-US000715.
XX
XX      (COLE/) COLE D L.

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PA      (RAVI//) RAVIKUMAR V T.
EA      (CHER//) CHERUVALLATH Z S.
XX
XX
PI      Cole DL, Ravikumar VT, Cheruvallath ZS;
DR      WPI; 2004-069376/07.
XX
XX
PT      Preparation of phosphorothioate oligonucleotides involves oxidizing
FT      phosphate intermediate with acetyl disulfide in acetonitrile for time to
PT      effect conversion of phosphate intermediate to phosphorothioate.
XX
PS      Example 12; SEQ ID NO 10; 8pp; English.
XX
CC      The invention relates to phosphorothioate oligonucleotides having
CC      nucleoside with 240 modification are prepared by phosphorylating 5'-
CC      hydroxyl of a nucleic acid moiety having a nucleoside with 2'
CC      modification in an acetonitrile containing solvent mixture to form a
CC      phosphate intermediate; and oxidising the phosphate intermediate with an
CC      acetyl disulfide in an acetonitrile for a time to effect conversion of
CC      the phosphate intermediate to phosphorothioate. The invented method
CC      achieves high yields and greater efficiency. The present sequence is
CC      sulphurised oligonucleotide used in the exemplification of the invention.
SQ      Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match          1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative % 0; Mismatches 2; Indels 0; Gaps 0;

QY      1520 AAAAAAAAAAGTAAAA 1537
        |||||||||         |||
DB      20 AAAAAAAAAAAAAAAAAA 3

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RESULT	783
ADK6985/c	
ID	ADK6985 standard; DNA; 20 BP.
AC	
XX	ADK6985;
DT	06-MAY-2004 (first entry)
XX	
DE	Sulphurised oligonucleotide #15.
XX	
KM	Phosphorothioate backbone; sulphurised oligonucleotide; ss.
XX	
OS	Unidentified.
XX	
FH	Key/Location/Qualifiers
FT	modified_base 1..20
FT	/tag= a
FT	/mod_base= OTHER
FT	/note= "Phosphorothioate backbone; 2'-O-methoxyethyl residues"
PN	US2003212267-A1.
PD	
XX	13-NOV-2003.
PP	
XX	12-DEC-2002; 2002US-00181200.
PR	
XX	11-JAN-2000; 2000US-00481486.
PA	10-JAN-2001; 2001WO-US000715.
PA	(COLE/) COLE D L.
PA	(RAVI/) RAVIKUMAR V T.
PA	(CHER/) CHERUVALLATH Z S.
PI	
XX	Cole DL, Ravikumar VT, Cheruvallath ZS;
DR	
XX	WPI; 2004-069376/07.
XX	
PT	Preparation of phosphorothioate oligonucleotides involves oxidizing

PT phosphite intermediate with acetyl disulfide in acetonitrile for time to
PT effect conversion of phosphite intermediate to phosphorothioate.
XX
PS Example 22; SEQ ID NO 15; 8bp; English.
XX
CC The invention relates to phosphorothioate oligonucleotides having
CC nucleoside with 240 modification are prepared by phosphorylating 5'-
CC hydroxyl of a nucleic acid moiety having a nucleoside with 2'
CC modification in an acetonitrile containing solvent mixture to form a
CC phosphite intermediate, and oxidizing the phosphite intermediate with an
CC acetyl disulfide in an acetonitrile for a time to effect conversion of
CC the phosphite intermediate to phosphorothioate. The invented method
CC achieves high yields and greater efficiency. The present sequence is
CC sulphurised oligonucleotide used in the exemplification of the invention.
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAGTAAA 1537
DB 20 AAAAAAAAAAAAAAAAAA 3

RESULT 784
ADK74647/c
ID ADK74647 standard; DNA; 20 BP.
XX
AC ADK74647;
XX
DT 20-MAY-2004 (first entry)
XX
DE Chimeric phosphorothioate oligonucleotide to target Nav1.3 #1981.
XX
KM Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
KM diabetic neuropathy; arthritic pain; migraine headache;
KM infantile epilepsy; ataxia; ss.
XX
OS Synthetic.
XX
PN WO2004016754-A2.
XX
PD 26-FEB-2004.
XX
PF 14-AUG-2003; 2003WO-US025465.
XX
PR 14-AUG-2002; 2002US-0403416P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Roberts SL;
XX
DR WPI; 2004-203785/19.
XX
PT New antisense compound targeted to a nucleic acid molecule encoding
PT Nav1.3, useful for treating a disease or condition associated
PT with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
PT disorder, or ataxia.
XX
PS Claim 4; SEQ ID NO 1981; 417bp; English.
XX
CC The present invention relates to an antisense compound targeted to a
CC nucleic acid molecule encoding Nav1.3, where the antisense compound
CC specifically hybridizes with and inhibits the expression of Nav1.3. The
CC compound and composition are useful for treating a disease or condition
CC associated with Nav1.3, e.g. pain including but not limited to
CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
CC pain from burns, migraine headache, cluster headache, mild-to-moderate
CC headache; seizure disorder such as childhood seizure disorder, including
CC but not limited to neonatal or infantile epilepsy; or ataxia. The present

CC sequence represents a chimeric phosphorothioate oligonucleotide with
CC 2' MOE wings and a deoxy gap. Used during the antisense inhibition of
CC human Nav1.3 expression, the oligonucleotides are designed to target
CC different regions of the human Nav1.3 RNA.
XX
SQ Sequence 20 BP; 0 A; 0 C; 1 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAGTAAA 1537
DB 19 AAAAAAAAAAAAAAAAAA 2

RESULT 785
ADK74188/c
ID ADK74188 standard; DNA; 20 BP.
XX
AC ADK74188;
XX
DT 20-MAY-2004 (first entry)
XX
DE Chimeric phosphorothioate oligonucleotide to target Nav1.3 #1522.
XX
KM Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
KM diabetic neuropathy; arthritic pain; migraine headache;
KM infantile epilepsy; ataxia; ss.
XX
OS Synthetic.
XX
PN WO2004016754-A2.
XX
PD 26-FEB-2004.
XX
PF 14-AUG-2003; 2003WO-US025465.
XX
PR 14-AUG-2002; 2002US-0403416P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Roberts SL;
XX
DR WPI; 2004-203785/19.
XX
PT New antisense compound targeted to a nucleic acid molecule encoding
PT Nav1.3, useful for treating a disease or condition associated
PT with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
PT disorder, or ataxia.
XX
PS Claim 4; SEQ ID NO 1522; 417bp; English.
XX
CC The present invention relates to an antisense compound targeted to a
CC nucleic acid molecule encoding Nav1.3, where the antisense compound
CC specifically hybridizes with and inhibits the expression of Nav1.3. The
CC compound and composition are useful for treating a disease or condition
CC associated with Nav1.3, e.g. pain including but not limited to
CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
CC pain from burns, migraine headache, cluster headache, mild-to-moderate
CC headache; seizure disorder such as childhood seizure disorder, including
CC but not limited to neonatal or infantile epilepsy; or ataxia. The present
CC sequence represents a chimeric phosphorothioate oligonucleotide with
CC 2' MOE wings and a deoxy gap. Used during the antisense inhibition of
CC human Nav1.3 expression, the oligonucleotides are designed to target
CC different regions of the human Nav1.3 RNA.
XX
SQ Sequence 20 BP; 0 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;


```
OY      1520 AAAAAAAAAAGTAAA 1537
      |||||
DB      19 AAAAAAAAAAAAAAA 2
      |||||

RESULT 786
ID      ADK74969/C
      ADK74969 standard; DNA; 20 BP.
XX
AC      ADK74969;
XX
DT      20-MAY-2004 (first entry)
XX
DE      Chimeric phosphorothioate oligonucleotide to target Nav1.3 #2303.
XX
KW      Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
      diabetic neuropathy; arthritic pain; migraine headache;
      infantile epilepsy; ataxia; ss.
XX
OS      Synthetic.
XX
PN      WO2004016754-A2.
XX
PD      26-FEB-2004.
XX
PP      14-AUG-2003; 2003WO-US025465.
XX
PR      14-AUG-2002; 2002US-0403416P.
XX
PA      (PHAA ) PHARMACIA CORP.
XX
PI      Roberds SL;
XX
DR      WPI; 2004-203785/19.
XX
PT      New antisense compound targeted to a nucleic acid molecule encoding
      Nav1.3, useful for treating a disease or condition associated
      with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
      disorder, or ataxia.
XX
PS      Claim 4; SEQ ID NO 2303; 417pp; English.
XX
CC      The present invention relates to an antisense compound targeted to a
      nucleic acid molecule encoding Nav1.3, where the antisense compound
      specifically hybridizes with and inhibits the expression of Nav1.3. The
      compound and composition are useful for treating a disease or condition
      associated with Nav1.3, e.g. pain including but not limited to
      neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
      diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
      pain from burns, migraine headache, cluster headache, mild-to-moderate
      headache; seizure disorder such as childhood seizure disorder, including
      but not limited to neonatal or infantile epilepsy; or ataxia. The present
      sequence represents a chimeric phosphorothioate oligonucleotide with
      2'OH wings and a deoxy gap. Used during the antisense inhibition of
      human Nav1.3 expression, the oligonucleotides are designed to target
      different regions of the human Nav1.3 RNA.
XX
SQ      Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match      1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      1520 AAAAAAAAAAGTAAA 1537
      |||||
DB      20 AAAAAAAAAAAAAAA 3
      |||||

RESULT 787
ID      ADK75847
      ADK75847 standard; DNA; 20 BP.
XX
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AC      ADK75847;
XX
DT      20-MAY-2004 (first entry)
XX
DE      Chimeric phosphorothioate oligonucleotide to target Nav1.3 #3181.
XX
KW      Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
      diabetic neuropathy; arthritic pain; migraine headache;
      infantile epilepsy; ataxia; ss.
XX
OS      Synthetic.
XX
PN      WO2004016754-A2.
XX
PD      26-FEB-2004.
XX
PP      14-AUG-2003; 2003WO-US025465.
XX
PR      14-AUG-2002; 2002US-0403416P.
XX
PA      (PHAA ) PHARMACIA CORP.
XX
PI      Roberds SL;
XX
DR      WPI; 2004-203785/19.
XX
PT      New antisense compound targeted to a nucleic acid molecule encoding
      Nav1.3, useful for treating a disease or condition associated
      with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
      disorder, or ataxia.
XX
PS      Claim 4; SEQ ID NO 3181; 417pp; English.
XX
CC      The present invention relates to an antisense compound targeted to a
      nucleic acid molecule encoding Nav1.3, where the antisense compound
      specifically hybridizes with and inhibits the expression of Nav1.3. The
      compound and composition are useful for treating a disease or condition
      associated with Nav1.3, e.g. pain including but not limited to
      neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
      diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
      pain from burns, migraine headache, cluster headache, mild-to-moderate
      headache; seizure disorder such as childhood seizure disorder, including
      but not limited to neonatal or infantile epilepsy; or ataxia. The present
      sequence represents a chimeric phosphorothioate oligonucleotide with
      2'OH wings and a deoxy gap. Used during the antisense inhibition of
      human Nav1.3 expression, the oligonucleotides are designed to target
      different regions of the human Nav1.3 RNA.
XX
SQ      Sequence 20 BP; 7 A; 1 C; 4 G; 8 T; 0 U; 0 Other;

Query Match      1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      1165 AGTATTGTTGAATAGT 1182
      |||||
DB      3 AGTATTGTTAAACAGT 20
      |||||

RESULT 788
ID      ADK79524/C
      ADK79524 standard; DNA; 20 BP.
XX
AC      ADK79524;
XX
DT      20-MAY-2004 (first entry)
XX
DE      Chimeric phosphorothioate oligonucleotide to target Nav1.3 #6858.
XX
KW      Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
      diabetic neuropathy; arthritic pain; migraine headache;
      infantile epilepsy; ataxia; ss.
XX
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```
OS Synthetic.
XX
XX WO2004016754-A2.
XX
XX 26-FEB-2004.
XX
XX 14-AUG-2003; 2003WO-US025465.
XX
XX 14-AUG-2002; 2002US-0403416P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Roberda SL;
XX
XX WPI; 2004-203785/19.
XX
XX
XX New antisense compound targeted to a nucleic acid molecule encoding
XX Nav1.3, useful for useful for treating a disease or condition associated
XX with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
XX disorder, or ataxia.
XX
XX Claim 4; SEQ ID NO 6858; 417bp; English.
XX
XX The present invention relates to an antisense compound targeted to a
XX nucleic acid molecule encoding Nav1.3, where the antisense compound
XX specifically hybridizes with and inhibits the expression of Nav1.3. The
XX compound and composition are useful for treating a disease or condition
XX associated with Nav1.3, e.g. pain including but not limited to
XX neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
XX diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
XX pain from burns, migraine headache, cluster headache, mild-to-moderate
XX headache; seizure disorder such as childhood seizure disorder, including
XX but not limited to neonatal or infantile epilepsy; or ataxia. The present
XX sequence represents a chimeric phosphorothioate oligonucleotide with
XX 2'MOE wings and a deoxy gap. Used during the antisense inhibition of
XX human Nav1.3 expression, the oligonucleotides are designed to target
XX different regions of the human Nav1.3 RNA.
XX
XX Sequence 20 BP; 11 A; 1 C; 2 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 4.4e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1252 TTTTGTTTTTAAATCAGA 1269
XX ||||| ||||| |||||
XX Db TTTTGATTTTAAATCACA 3
XX
XX RESULT 789
XX ADK74688/C
XX ID ADK74688 standard; DNA; 20 BP.
XX
XX AC ADK74688;
XX
XX 20-MAY-2004 (first entry)
XX
XX Chimeric phosphorothioate oligonucleotide to target Nav1.3 #2022.
XX
XX Nav1.3; Analgesic; Nociceptive; Neuroprotective; post-herpetic neuralgia;
XX diabetic neuropathy; arthritic pain; migraine headache;
XX infantile epilepsy; ataxia; ss.
XX
XX Synthetic.
XX
XX WO2004016754-A2.
XX
XX 26-FEB-2004.
XX
XX 14-AUG-2003; 2003WO-US025465.
XX
XX 14-AUG-2002; 2002US-0403416P.
XX
XX
```

```
PA (PHAA ) PHARMACIA CORP.
XX
XX Roberda SL;
XX
XX WPI; 2004-203785/19.
XX
XX
XX New antisense compound targeted to a nucleic acid molecule encoding
XX Nav1.3, useful for useful for treating a disease or condition associated
XX with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
XX disorder, or ataxia.
XX
XX Claim 4; SEQ ID NO 2022; 417bp; English.
XX
XX The present invention relates to an antisense compound targeted to a
XX nucleic acid molecule encoding Nav1.3, where the antisense compound
XX specifically hybridizes with and inhibits the expression of Nav1.3. The
XX compound and composition are useful for treating a disease or condition
XX associated with Nav1.3, e.g. pain including but not limited to
XX neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
XX diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
XX pain from burns, migraine headache, cluster headache, mild-to-moderate
XX headache; seizure disorder such as childhood seizure disorder, including
XX but not limited to neonatal or infantile epilepsy; or ataxia. The present
XX sequence represents a chimeric phosphorothioate oligonucleotide with
XX 2'MOE wings and a deoxy gap. Used during the antisense inhibition of
XX human Nav1.3 expression, the oligonucleotides are designed to target
XX different regions of the human Nav1.3 RNA.
XX
XX Sequence 20 BP; 0 A; 2 C; 0 G; 18 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 4.4e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1520 AAAAAAAAAAAGTAAAA 1537
XX ||||| ||||| |||||
XX Db AAAAAAAAAAAGTAAAA 1
XX
XX RESULT 790
XX ADK74889/C
XX ID ADK74889 standard; DNA; 20 BP.
XX
XX AC ADK74889;
XX
XX 20-MAY-2004 (first entry)
XX
XX Chimeric phosphorothioate oligonucleotide to target Nav1.3 #2223.
XX
XX Nav1.3; Analgesic; Nociceptive; Neuroprotective; post-herpetic neuralgia;
XX diabetic neuropathy; arthritic pain; migraine headache;
XX infantile epilepsy; ataxia; ss.
XX
XX Synthetic.
XX
XX WO2004016754-A2.
XX
XX 26-FEB-2004.
XX
XX 14-AUG-2003; 2003WO-US025465.
XX
XX 14-AUG-2002; 2002US-0403416P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Roberda SL;
XX
XX WPI; 2004-203785/19.
XX
XX New antisense compound targeted to a nucleic acid molecule encoding
XX Nav1.3, useful for useful for treating a disease or condition associated
XX with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
XX disorder, or ataxia.
XX
```

XX Claim 4, SEQ ID NO 2223; 417bp; English.
PS
XX The present invention relates to an antisense compound targeted to a
CC nucleic acid molecule encoding Nav1.3, where the antisense compound
CC specifically hybridizes with and inhibits the expression of Nav1.3. The
CC compound and composition are useful for treating a disease or condition
CC associated with Nav1.3, e.g. pain including but not limited to
CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
CC pain from burns, migraine headache, cluster headache, mild-to-moderate
CC headache; seizure disorder such as childhood seizure disorder, including
CC but not limited to neonatal or infantile epilepsy; or ataxia. The present
CC sequence represents a chimeric phosphorothioate oligonucleotide with
CC 2'MOE wings and a deoxy gap. Used during the antisense inhibition of
CC human Nav1.3 expression, the oligonucleotides are designed to target
CC different regions of the human Nav1.3 RNA.
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAATAAAA 1537
|||
20 AAAAAAAAAAAAAAAAAA 3
Db
RESULT 791
ID ADK80788/C
ID ADK80788 standard; DNA; 20 BP.
AC ADK80788;
XX 20-MAY-2004 (first entry)
DT
XX Chimeric phosphorothioate oligonucleotide to target Nav1.3 #8122.
DE
XX Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
XX diabetic neuropathy; arthritic pain; migraine headache;
XX infantile epilepsy; ataxia; ss.
XX
OS Synthetic.
XX
XX WO2004016754-A2.
XX
XX 26-FEB-2004.
XX
XX 14-AUG-2003; 2003WO-US025465.
XX
XX 14-AUG-2002; 2002US-0403416P.
XX
XX (PHAA) PHARMACIA CORP.
XX
XX Roberds SL;
XX
XX WPI; 2004-203785/19.
XX
XX New antisense compound targeted to a nucleic acid molecule encoding
XX Nav1.3, useful for treating a disease or condition associated
XX with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
XX disorder, or ataxia.
XX
XX Claim 4; SEQ ID NO 8122; 417bp; English.
XX
XX The present invention relates to an antisense compound targeted to a
XX nucleic acid molecule encoding Nav1.3, where the antisense compound
XX specifically hybridizes with and inhibits the expression of Nav1.3. The
XX compound and composition are useful for treating a disease or condition
XX associated with Nav1.3, e.g. pain including but not limited to
XX neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
XX diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
XX pain from burns, migraine headache, cluster headache, mild-to-moderate
XX headache; seizure disorder such as childhood seizure disorder, including
XX but not limited to neonatal or infantile epilepsy; or ataxia. The present
XX sequence represents a chimeric phosphorothioate oligonucleotide with
XX 2'MOE wings and a deoxy gap. Used during the antisense inhibition of
XX human Nav1.3 expression, the oligonucleotides are designed to target
XX different regions of the human Nav1.3 RNA.
SQ Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

CC pain from burns, migraine headache, cluster headache, mild-to-moderate
CC headache; seizure disorder such as childhood seizure disorder, including
CC but not limited to neonatal or infantile epilepsy; or ataxia. The present
CC sequence represents a chimeric phosphorothioate oligonucleotide with
CC 2'MOE wings and a deoxy gap. Used during the antisense inhibition of
CC human Nav1.3 expression, the oligonucleotides are designed to target
CC different regions of the human Nav1.3 RNA.
SQ Sequence 20 BP; 10 A; 2 C; 3 G; 5 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1252 TTTTGTATTAATCACA 1269
|||
18 TTTGATTTTAATCACA 1
Db
RESULT 792
ID ADK74838/C
ID ADK74838 standard; DNA; 20 BP.
AC ADK74838;
XX 20-MAY-2004 (first entry)
DT
XX Chimeric phosphorothioate oligonucleotide to target Nav1.3 #2172.
DE
XX Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
XX diabetic neuropathy; arthritic pain; migraine headache;
XX infantile epilepsy; ataxia; ss.
XX
OS Synthetic.
XX
XX WO2004016754-A2.
XX
XX 26-FEB-2004.
XX
XX 14-AUG-2003; 2003WO-US025465.
XX
XX 14-AUG-2002; 2002US-0403416P.
XX
XX (PHAA) PHARMACIA CORP.
XX
XX Roberds SL;
XX
XX WPI; 2004-203785/19.
XX
XX New antisense compound targeted to a nucleic acid molecule encoding
XX Nav1.3, useful for treating a disease or condition associated
XX with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
XX disorder, or ataxia.
XX
XX Claim 4; SEQ ID NO 2172; 417bp; English.
XX
XX The present invention relates to an antisense compound targeted to a
XX nucleic acid molecule encoding Nav1.3, where the antisense compound
XX specifically hybridizes with and inhibits the expression of Nav1.3. The
XX compound and composition are useful for treating a disease or condition
XX associated with Nav1.3, e.g. pain including but not limited to
XX neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
XX diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
XX pain from burns, migraine headache, cluster headache, mild-to-moderate
XX headache; seizure disorder such as childhood seizure disorder, including
XX but not limited to neonatal or infantile epilepsy; or ataxia. The present
XX sequence represents a chimeric phosphorothioate oligonucleotide with
XX 2'MOE wings and a deoxy gap. Used during the antisense inhibition of
XX human Nav1.3 expression, the oligonucleotides are designed to target
XX different regions of the human Nav1.3 RNA.
SQ Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1521 AAAAAAAAAAGTAAAG 1538
Db 20 AAAAAAAAAAAAAAAAAAG 3

RESULT 793

ADK77218
ID ADK77218 standard; DNA; 20 BP.

XX ADK77218;

XX 20-MAY-2004 (first entry)

XX Chimeric phosphorothioate oligonucleotide to target Nav1.3 #4552.

XX Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;

KM diabetic neuropathy; arthritic pain; migraine headache;

KW infantile epilepsy; ataxia; ss.

XX Synthetic.

XX MO2004016754-A2.

XX 26-FEB-2004.

XX 14-AUG-2003; 2003MO-US025465.

XX 14-AUG-2002; 2002US-0403416P.

XX (PHAA) PHARMACIA CORP.

XX Roberds SL;

XX WPI; 2004-203785/19.

XX New antisense compound targeted to a nucleic acid molecule encoding

PT Nav1.3, useful for treating a disease or condition associated

PT with Nav1.3, e.g. pain, seizure disorder such as childhood seizure

PT disorder, or ataxia.

XX Claim 4; SEQ ID NO 4552; 417p; English.

XX The present invention relates to an antisense compound targeted to a

CC nucleic acid molecule encoding Nav1.3, where the antisense compound

CC specifically hybridizes with and inhibits the expression of Nav1.3. The

CC compound and composition are useful for treating a disease or condition

CC associated with Nav1.3, e.g. pain including but not limited to

CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,

CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,

CC pain from burns, migraine headache, cluster headache, mild-to-moderate

CC headache; seizure disorder such as childhood seizure disorder, including

CC but not limited to neonatal or infantile epilepsy; or ataxia. The present

CC sequence represents a chimeric phosphorothioate oligonucleotide with

CC 2'MOE wings and a deoxy gap. Used during the antisense inhibition of

CC human Nav1.3 expression, the oligonucleotides are designed to target

CC different regions of the human Nav1.3 RNA.

XX Sequence 20 BP; 7 A; 2 C; 4 G; 7 T; 0 U; 0 Other;

XX Query Match 1.1%; Score 14.8; DB 1; Length 20;

XX Best Local Similarity 88.9%; Pred. No. 4.4e+02;

XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1165 AGTATTTGTTGAAATAGT 1182

Db 2 AGTATTTGTTAAACAGT 19

RESULT 794

ADK80450/C
ID ADK80450 standard; DNA; 20 BP.

XX ADK80450;

XX 20-MAY-2004 (first entry)

XX Chimeric phosphorothioate oligonucleotide to target Nav1.3 #7784.

XX Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;

KM diabetic neuropathy; arthritic pain; migraine headache;

KW infantile epilepsy; ataxia; ss.

XX Synthetic.

XX MO2004016754-A2.

XX 26-FEB-2004.

XX 14-AUG-2003; 2003MO-US025465.

XX 14-AUG-2002; 2002US-0403416P.

XX (PHAA) PHARMACIA CORP.

XX Roberds SL;

XX WPI; 2004-203785/19.

XX New antisense compound targeted to a nucleic acid molecule encoding

PT Nav1.3, useful for treating a disease or condition associated

PT with Nav1.3, e.g. pain, seizure disorder such as childhood seizure

PT disorder, or ataxia.

XX Claim 4; SEQ ID NO 7784; 417p; English.

XX The present invention relates to an antisense compound targeted to a

CC nucleic acid molecule encoding Nav1.3, where the antisense compound

CC specifically hybridizes with and inhibits the expression of Nav1.3. The

CC compound and composition are useful for treating a disease or condition

CC associated with Nav1.3, e.g. pain including but not limited to

CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,

CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,

CC pain from burns, migraine headache, cluster headache, mild-to-moderate

CC headache; seizure disorder such as childhood seizure disorder, including

CC but not limited to neonatal or infantile epilepsy; or ataxia. The present

CC sequence represents a chimeric phosphorothioate oligonucleotide with

CC 2'MOE wings and a deoxy gap. Used during the antisense inhibition of

CC human Nav1.3 expression, the oligonucleotides are designed to target

CC different regions of the human Nav1.3 RNA.

XX Sequence 20 BP; 10 A; 1 C; 3 G; 6 T; 0 U; 0 Other;

XX Query Match 1.1%; Score 14.8; DB 1; Length 20;

XX Best Local Similarity 88.9%; Pred. No. 4.4e+02;

XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1252 TTTTGTGTTTAAATCAGA 1269

Db 19 TTTTGTGTTTAAATCACA 2

RESULT 795

ADK69507

ID ADK69507 standard; DNA; 20 BP.

XX ADK69507;

XX 03-JUN-2004 (first entry)

XX Plant gene polymorphism marker related primer, SEQ ID 386.

XX Primer; variation mapping; mutation mapping; plant;

KW gene polymorphism marker; ss.
XX Synthetic.
XX JP2003289885-A.
XX 14-OCT-2003.
XX 31-JAN-2003; 2003JP-00024620.
XX 01-FEB-2002; 2002JP-00025338.
XX (RIKA) RIKAGAKU KENKYUSHO.
XX (SAIM-) SAI MEDIA KK.
XX (MATSU) MATSUI M.
XX (NAKA/) NAKAZAWA M.
XX WPI; 2004-126231/13.
XX A primer set and method useful for mapping at least the
PT variation/mutation part of a plant gene using a gene polymorphism marker.
PS Claim 7; SEQ ID NO 386; 120bp; Japanese.
XX The present invention relates to a primer set and method for mapping at
CC least the variation/mutation part of the plant gene using a gene
CC polymorphism marker. A mutation site of the plant gene is mapped by
CC utilizing a genetic polymorphism marker as follows: (a) genomic DNA is
CC prepared from a plant homozygously having a mutation to be an object of
CC the mapping; (b) A forward primer 1 containing a base corresponding to
CC the gene polymorphic maker of one ecotype plant, a forward primer 2
CC containing a base corresponding to the genetic polymorphism of the other
CC ecotype plant and a reverse primer 3 based on the base sequence common
CC with both the ecotype plants are prepared; (c) two kinds of
CC oligonucleotides emitting fluorescence of different colors when the
CC genetic polymorphism marker is detected are prepared; (d) an
CC amplification reaction of the genomic DNA is carried out in the presence
CC of the primers 1, 2 and 3 and the two kinds of the oligonucleotides; (e)
CC the fluorescence intensity emitted from the resultant reactional product
CC is detected and (f) the position on the genome of the mutation site is
CC determined from the results of detection. The present sequence is a
CC primer, used to illustrate the invention.
XX Sequence 20 BP; 6 A; 3 C; 7 G; 4 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1462 AGAAGTGACAAATTCA 1479
DB 1 AGAAGTGACACTTCA 18
RESULT 796
ADM69506 standard; DNA; 20 BP.
XX ADM69506;
XX 03-JUN-2004 (first entry)
XX Plant gene polymorphism marker related primer, SEQ ID 385.
XX primer; variation mapping; mutation mapping; plant;
KW gene polymorphism marker; ss.
XX Synthetic.
XX JP2003289885-A.
XX 14-OCT-2003.
XX

PF 31-JAN-2003; 2003JP-00024620.
XX 01-FEB-2002; 2002JP-00025338.
XX (RIKA) RIKAGAKU KENKYUSHO.
XX (SAIM-) SAI MEDIA KK.
XX (MATSU) MATSUI M.
XX (NAKA/) NAKAZAWA M.
XX WPI; 2004-126231/13.
XX A primer set and method useful for mapping at least the
PT variation/mutation part of a plant gene using a gene polymorphism marker.
PS Claim 7; SEQ ID NO 385; 120bp; Japanese.
XX The present invention relates to a primer set and method for mapping at
CC least the variation/mutation part of a plant gene using a gene
CC polymorphism marker. A mutation site of the plant gene is mapped by
CC utilizing a genetic polymorphism marker as follows: (a) genomic DNA is
CC prepared from a plant homozygously having a mutation to be an object of
CC the mapping; (b) A forward primer 1 containing a base corresponding to
CC the gene polymorphic maker of one ecotype plant, a forward primer 2
CC containing a base corresponding to the genetic polymorphism of the other
CC ecotype plant and a reverse primer 3 based on the base sequence common
CC with both the ecotype plants are prepared; (c) two kinds of
CC oligonucleotides emitting fluorescence of different colors when the
CC genetic polymorphism marker is detected are prepared; (d) an
CC amplification reaction of the genomic DNA is carried out in the presence
CC of the primers 1, 2 and 3 and the two kinds of the oligonucleotides; (e)
CC the fluorescence intensity emitted from the resultant reactional product
CC is detected and (f) the position on the genome of the mutation site is
CC determined from the results of detection. The present sequence is a
CC primer, used to illustrate the invention.
XX Sequence 20 BP; 7 A; 3 C; 6 G; 4 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1462 AGAAGTGACAAATTCA 1479
DB 1 AGAAGTGACACTTCA 18
RESULT 797
ADL33726/C
ID ADL33726 standard; DNA; 20 BP.
XX ADL33726;
XX 03-JUN-2004 (first entry)
XX LNA oligomer #5.
XX Detection; isolation; locked nucleic acid; LNA; ss.
XX Synthetic.
XX Key location/Qualifiers
XX modified_base 1..20
XX /*tag= b
FT /mod_base= OTHER
FT /note= "Optionally LNA nucleotides"
FT modified_base 1
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Optionally biotinylated or 5' A02-HRG3, where A0
FT is anthraquinone and HEG is hexa-ethylene glycol"
XX W02004020575-A2.
XX

PD	11-MAR-2004.
XX	20-JUN-2003; 2003WO-IB006354.
PF	24-JUN-2002; 2002US-0390928P.
PR	(EXIQ-) EXIQON AS.
XX	Kaupinen S, Jacobsen N;
XX	WPI; 2004-315512/29.
DR	Detecting and/or isolating nucleic acid molecule having homopolymeric
PT	sequence or repetitive element or conserved nucleotide sequence involves
PT	treating sample containing nucleic acid compounds with locked nucleic
PT	acid oligonucleotide.
XX	
PS	Claim 22; Page 51; 104pp; English.
XX	
CC	The present invention relates to a method (M1) for detecting and/or
CC	isolating a nucleic acid having a homopolymetric sequence or repetitive
CC	element or conserved nucleotide sequence. (M1) comprises treating a
CC	sample containing nucleic acid compounds with an locked nucleic acid
CC	(LNA) oligonucleotide (LO) to thereby detect and/or isolate a nucleic
CC	acid having the homopolymetric sequence or repetitive element or conserved
CC	nucleotide sequence. (M1) is useful for detecting and isolating nucleic
CC	acids released from a lysed complex biological mixture comprising nucleic
CC	acids. The present sequence is a LNA oligomer, used to illustrate the
invention.	
XX	
SQ	Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
Query Match	1.1%; Score 14.8; DB 1; Length 20;
Beat Local Similarity	88.9%; Pred.No.4.4e+02;
Matches 16; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
Oy	1520 AAAAAAAAAAAGTAAA 1537
Db	20 AAAAAAAAAAAAAAAAAAAAA 3
RESULT 798	
ID	ADLS9686
ID	ADLS9686 standard; DNA; 20 BP.
XX	
AC	ADLS9686;
XX	
DT	03-JUN-2004 (first entry)
XX	
DE	Human ESM-1 antisense oligonucleotide seqid 1935.
XX	
KW	cytotoxic; antidiabetic; immunomodulator; cardiatic; neuroprotective;
KW	gene therapy; endothelial specific molecule-1; ESM-1;
KW	ESM-1 related disorder; diabetes; cancer; ischemia; reperfusion injury;
KW	angiogenic disorder; immunological disorder; cardiovascular disorder;
KW	neurological disorder; antisense technology; ss.
XX	
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	modified_base 1..20
FT	/tag= b
FT	/mod_base= OTHER
FT	/note= "OTHER= phosphorothioate backbone. All cytidine
FT	residues are 5-methylcytidines"
FT	1..5
FT	modified_base /tag= a
FT	/mod_base= OTHER
FT	/note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"
FT	16..20
FT	/tag= c
FT	/mod_base= OTHER
FT	/note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"
FT	

XX	WO2004021978-A2.
PN	
PD	18-MAR-2004.
XX	
PF	19-AUG-2003; 2003WO-US025833.
XX	
PR	19-AUG-2002; 2002US-0404495P.
XX	
PA	(PHAA) PHARMACIA CORP.
PI	Weinstein EJ, Griggs DW;
DR	WPI: 2004-248358/23.
XX	
PT	New antisense compound, having a sequence targeted to a nucleic acid encoding endothelial specific molecule-1 (ESM-1), useful for preparing a composition for treating e.g., diabetes, cancer or cardiovascular disorder.
XX	
PS	Claim 3; SEQ ID NO 1935; 555pp; English.
XX	
CC	The invention describes a new antisense compound, having a sequence comprising 8-30 bp targeted to a nucleic acid encoding endothelial specific molecule-1 (ESM-1), that specifically hybridises with the nucleic acid ESM-1 and inhibits its expression. Also described are: a composition; inhibiting the expression of ESM-1 in cells or tissues; and treating an animal having a disease or condition associated with ESM-1.
CC	The compound is useful for preparing a composition for treating diabetes, cancer, ischemia or reperfusion injury, or angiodenic, immunological, cardiovascular or neurological disorder. This sequence represents an antisense oligonucleotide that can be used to modulate expression of endothelial specific molecule-1 (ESM-1).
SQ	Sequence 20 BP; 15 A; 2 C; 1 G; 2 T; 0 U; 0 Other;
Oy	Query March 1.1%; Score 14.8; DB 1; Length 20; Best Local Similarity 88.9%; Pred.No. 4.4e+02; Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Dn	1520 AAAAAAAAAAGTAAAA 1537 1 AAAAAAAAAAAGCACA 18
RESULT 799	
ID	ADL59703
XX	ADL59703 standard; DNA; 20 BP.
XX	
AC	ADL59703;
DT	03-JUN-2004 (first entry)
XX	
DE	Human ESM-1 antisense oligonucleotide seqid 1952.
KX	cytostatic; antidiabetic; immunomodulator; cardiac; neuroprotective;
KW	gene therapy; endothelial specific molecule-1; ESM-1;
KV	ESM-1 related disorder; diabetes; cancer; ischaemia; reperfusion injury;
KW	angiogenic disorder; immunological disorder; cardiovascular disorder;
KM	neurological disorder; antisense technology; ss.
XX	
OS	Homo sapiens.
XX	
PH	Key Location/Qualifiers
FT	modified_base 1..20
FT	/+tag= b
FT	/mod_base= OTHER
FT	/note= "OTHER= phosphorothioate backbone. All cytidine residues are 5-methylcytidines"
FT	modified_base 1..5
FT	/+tag= a
FT	/mod_base= OTHER
FT	/note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"

```
FT modified_base 16.20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"
XX
XX WO2004021978-A2.
XX
XX 18-MAR-2004.
XX
XX 19-AUG-2003; 2003WO-US025833.
XX
XX 19-AUG-2002; 2002US-040495P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Weinstein EJ, Griggs DW;
XX WPI; 2004-248358/23.
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding endothelial specific molecule-1 (ESM-1), useful for preparing a
XX composition for treating e.g., diabetes, cancer or cardiovascular
XX disorder.
XX
XX Claim 3; SEQ ID NO 1952; 555bp; English.
XX
XX The invention describes a new antisense compound, having a sequence
XX comprising 8-30 bp targeted to a nucleic acid encoding endothelial
XX specific molecule-1 (ESM-1), that specifically hybridises with the
XX nucleic acid ESM-1 and inhibits its expression. Also described are: a
XX composition; inhibiting the expression of ESM-1 in cells or tissues; and
XX treating an animal having a disease or condition associated with ESM-1.
XX The compound is useful for preparing a composition for treating diabetes,
XX cancer, ischaemia or reperfusion injury, or angiogenic, immunological,
XX cardiovascular or neurological disorder. This sequence represents an
XX antisense oligonucleotide that can be used to modulate expression of
XX endothelial specific molecule-1 (ESM-1).
XX
XX Sequence 20 BP; 16 A; 2 C; 1 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 4.4e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX Oy 1520 AAAAAAAAAAGTAAA 1537
XX |||||
XX 2 AAAAAAAAAAGCACAA 19
XX
XX RESULT 800
XX ADL59724
XX ID ADL59724 standard; DNA; 20 BP.
XX
XX AC ADL59724;
XX
XX DT 03-JUN-2004 (first entry)
XX
XX Human ESM-1 antisense oligonucleotide seqid 1973.
XX
XX DE Human ESM-1 antisense oligonucleotide; cardiant; neuroprotective;
XX cytosolic; antidiabetic; immunomodulator; cardiant; neuroprotective;
XX gene therapy; endothelial specific molecule-1; ESM-1;
XX ESM-1 related disorder; diabetes; cancer; ischaemia; reperfusion injury;
XX angiogenic disorder; immunological disorder; cardiovascular disorder;
XX neurological disorder; antisense technology; ss.
XX
XX OS Homo sapiens.
XX
XX PH Key Location/Qualifiers
XX FT modified_base 1.20
XX FT /*tag= b
XX FT /mod_base= OTHER
XX FT /note= "OTHER= phosphorothioate backbone. All cytidine
XX residues are 5-methylcytidines"
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FT modified_base 1.5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"
XX
XX modified_base 16.20
XX /*tag= c
XX /mod_base= OTHER
XX /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"
XX
XX WO2004021978-A2.
XX
XX 18-MAR-2004.
XX
XX 19-AUG-2003; 2003WO-US025833.
XX
XX 19-AUG-2002; 2002US-040495P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Weinstein EJ, Griggs DW;
XX WPI; 2004-248358/23.
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding endothelial specific molecule-1 (ESM-1), useful for preparing a
XX composition for treating e.g., diabetes, cancer or cardiovascular
XX disorder.
XX
XX Claim 3; SEQ ID NO 1973; 555bp; English.
XX
XX The invention describes a new antisense compound, having a sequence
XX comprising 8-30 bp targeted to a nucleic acid encoding endothelial
XX specific molecule-1 (ESM-1), that specifically hybridises with the
XX nucleic acid ESM-1 and inhibits its expression. Also described are: a
XX composition; inhibiting the expression of ESM-1 in cells or tissues; and
XX treating an animal having a disease or condition associated with ESM-1.
XX The compound is useful for preparing a composition for treating diabetes,
XX cancer, ischaemia or reperfusion injury, or angiogenic, immunological,
XX cardiovascular or neurological disorder. This sequence represents an
XX antisense oligonucleotide that can be used to modulate expression of
XX endothelial specific molecule-1 (ESM-1).
XX
XX Sequence 20 BP; 17 A; 2 C; 1 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 4.4e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX Oy 1520 AAAAAAAAAAGTAAA 1537
XX |||||
XX 3 AAAAAAAAAAGCACAA 20
XX
XX RESULT 801
XX ADM93653/C
XX ID ADM93653 standard; DNA; 20 BP.
XX
XX AC ADM93653;
XX
XX DT 01-JUL-2004 (first entry)
XX
XX Human NOVX PCR primer #2.
XX
XX DE Human NOVX PCR primer #2.
XX
XX XX Human; NOVX; PCR; ss; congenital heart defect; cardiomyopathy;
XX atherosclerosis; hypertension; pulmonary stenosis; scleroderma;
XX adenocarcinoma; haemophilia; graft-versus-host disease; cancer;
XX neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
XX multiple sclerosis; diabetes; obesity; bronchial asthma;
XX acquired immunodeficiency syndrome; AIDS; Crohn's disease;
XX infectious disease; anorexia; immune disorder; primer.
XX
XX OS Homo sapiens.
```


PN	US2004067892-A1.	
XD		
XX	08-APR-2004.	
PF	05-NOV-2002; 2002US-00287971.	
XX		
PR	22-OCT-2001; 2001US-00035568	
PR	05-NOV-2001; 2001US-0338626P	
PR	09-NOV-2001; 2001US-033072P	
PR	06-NOV-2001; 2001US-0345398P	
PR	09-NOV-2001; 2001US-0348283P	
PR	15-NOV-2001; 2001US-035610P	
PR	21-NOV-2001; 2001US-0332152P	
PR	28-NOV-2001; 2001US-0333912P	
PR	29-NOV-2001; 2001US-00997425	
PR	04-DEC-2001; 2001US-034300P	
PR	04-DEC-2001; 2001US-0336576P	
PR	05-FEB-2002; 2002US-0354807P	
PR	15-MAY-2002; 2002US-0380968P	
PR	16-MAY-2002; 2002US-0381043P	
PR	02-JUL-2002; 2002US-0393148P	
PR	02-JUL-2002; 2002US-0393262P	
PR	06-AUG-2002; 2002US-0401476P	
PR	06-AUG-2002; 2002US-0401626P	
PR	07-AUG-2002; 2002US-0401593P	
PR	07-AUG-2002; 2002US-0401695P	
PR	26-AUG-2002; 2002US-0406181P	
XX		
PA	(ALSO/) ALSOBROOK J P.	
PA	(ALVA) ALVAREZ E.	
PA	(ANDE) ANDERSON D W.	
PA	(BARO) BARON W.	
PA	(BOLD) BOLDG F L.	
PA	(BURG) BURGESS C E.	
PA	(CASW) CASMAN S J.	
PA	(CHAP) CASPAVAL A.	
PA	(DHAN) DHANABAI M.	
PA	(EDIN) EDINGER S R.	
PA	(EISE) EISEN A.	
PA	(ELLE) ELLERMAN K.	
PA	(ETTE) ETTENBERG S.	
PA	(GANG) GANGOLI E A.	
PA	(GERL) GERLACH V.	
PA	(GORM) GORMAN L.	
PA	(GROS) GROSSE W M.	
PA	(GUOX) GUO X.	
PA	(HACK) HACKETT C.	
PA	(JIRM) JI W.	
PA	(KERU) KERUDA R.	
PA	(KHTA) KHRATSOV N V.	
PA	(LEPL) LEPLEY D M.	
PA	(LIIL) LI L.	
PA	(MACD) MACDOUGALL J R.	
PA	(MALY) MALYANKAR U W.	
PA	(MAZU) MAZOR A.	
PA	(MCOU) MCCOUBENY K.	
PA	(MEZE) MEZES P S.	
PA	(MILL) MILLER C E.	
PA	(MILL) MILLET I.	
PA	(MISH) MISHRA V.	
PA	(PADI) PADIGAR V M.	
PA	(PENT) PATTURAJAN M.	
PA	(PENR) PENA C E A.	
PA	(PEYM) PEYMAN J A.	
PA	(RAST) RASTELLI L.	
PA	(RIEG) RIEGER D K.	
PA	(ROTH) ROTHENBERG M E.	
PA	(SHEN) SHENOY S G.	
PA	(SHIM) SHIMKETS R A.	
PA	(SMIT) SMITHSON G.	
PA	(SPAD) SPADERNA S K.	
PA	(STAR) STARKING G.	
PA	(STAR) STAYER K A.	

(STON/) STONE D J.
PA (TCHE/) TCHERNEV V T.
PA (TWOH/) TWOHLOW N.
PA (VERN/) VERNET C A M.
PA (ZERN/) ZERHUSEN B D.
PA (VOSS/) VOSS E Z.
PA (ZHON/) ZHONG M.

XX
PI Alsobrook JP, Alvarez E, Anderson DM, Baron M, Boldog FL,
PI Burgess CE, Caeman SJ, Chapoval A, Dhanabal M, Edinger SR, Eisen A;
PI Ellerman K, Gonenberg S, Gangoli EA, Gerlach V, Gorman L;
PI Grose WM, Guo X, Hackett C, Ji W, Kekula R, Khramsov NV;
PI Lepley LM, Li L, Macdonald JR, Malvanar UM, Mazur A, McQueney K;
PI Meares PS, Miller CE, Millet I, Mishra V, Padigaru M, Paturajan M;
PI Pena CE, Peyman JA, Raetelli L, Rieger DK, Rothenberg MB;
PI Shenoy SG, Shinkels RA, Smithson G, Spaderna SK, Starling G;
PI Speyer KA, Stone DJ, Tchernenk VT, Twohlow N, Vernet CAM,
PI Zerhusen BD, Voss Ez, Zhong M;

DR WPI; 2004-355303/33.

XX
PT Novel isolated NOVX polypeptide useful treating or preventing disorders
PT or syndromes such as Alzheimer's disease, Parkinson's disease, multiple
PT sclerosis, diabetes, obesity, cancer, bronchial asthma, Crohn's disease.

XX
PS Example C; SEQ ID NO 285; 330bp; English.

XX
CC The invention relates to human NOVX polypeptides and the polynucleotides
CC encoding them. The NOVX polypeptides and polynucleotides are useful for
CC determining the presence of or predisposition to a disease associated
CC with altered levels of the sequences in a mammalian subject, and for
CC treating or preventing a pathology associated with NOVX. The
CC polypeptides, polynucleotides and antibodies that bind immunospecifically
CC to the polypeptides are useful for treating or preventing disorders or
CC syndromes such as congenital heart defects, cardiomyopathy,
CC atherosclerosis, hypertension, pulmonary stenosis, scleroderma,
CC adenocarcinoma, haemophilia, graft-versus-host disease, cancer,
CC neurodegenerative disorders, Alzheimer's disease, Parkinson's disease,
CC multiple sclerosis, diabetes, obesity, bronchial asthma, acquired
CC immunodeficiency syndrome (AIDS), Crohn's disease, infectious disease,
CC anorexia and immune disorders. This sequence represents a PCR primer used
CC to amplify a human NOVX polynucleotide of the invention. Note: The
CC sequence data for this patent is also available from USPTO at
CC SeqData.uspto.gov/sequence.html.

XX
SQ Sequence 20 BP; 5 A; 7 C; 5 G; 3 T; 0 U; 0 Other;

KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
OS Homo sapiens.
OS Synthetic.
FH Key
FT modified_base
FT 1..20
FT /tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT 1..5
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT 16..20
FT /tag= C
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX WO2004028458-A2.
XX 08-APR-2004.
XX 25-SEP-2003; 2003WO-US030374.
XX 25-SEP-2002; 2002US-043549P.
XX (PHAA) PHARMACIA CORP.
XX Glerse JK;
XX WPI; 2004-305094/28.
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischemia.
XX
XX Claim 4; SEQ ID NO 179; 132pp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX human mPGES-1 gene is located on chromosome 9, more specifically to
XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
XX inhibits its expression; (2) a method of inhibiting the expression of
XX mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX antisense oligonucleotides and antisense compounds have cytostatic,
XX antidiabetic, immunomodulatory, cardiant, neuroprotective,
XX antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
XX ophthalmological, immunomodulatory and cardiovascular activities, and can
XX be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
XX can be used for preparing a composition for treating a disease or
XX condition associated with mPGES-1 e.g., inflammation, Alzheimer's
XX disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
XX ophthalmic, immunological, cardiovascular or neurological disorder.
XX
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 4.4e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1520 AAAAAAAAAAGTAAA 1537
XX |||||||||||||
XX 20 AAAAAAAAAAAAAAAAAA 3

ADM13994/C
ID ADM13994 standard; DNA; 20 BP.
XX
XX AC ADM13994;
XX
XX 01-JUL-2004 (first entry)
DE
XX Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:181.
XX
XX chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW microsomal prostaglandin E2 synthase inhibitor; cytostatic; antidiabetic;
KW immunomodulatory; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
OS Homo sapiens.
OS Synthetic.
FH Key
FT modified_base
FT 1..20
FT /tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT 1..5
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT 16..20
FT /tag= C
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX WO2004028458-A2.
XX 08-APR-2004.
XX 25-SEP-2003; 2003WO-US030374.
XX 25-SEP-2002; 2002US-043549P.
XX (PHAA) PHARMACIA CORP.
XX Glerse JK;
XX WPI; 2004-305094/28.
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischemia.
XX
XX Claim 4; SEQ ID NO 181; 132pp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX human mPGES-1 gene is located on chromosome 9, more specifically to
XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
XX inhibits its expression; (2) a method of inhibiting the expression of
XX mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX antisense oligonucleotides and antisense compounds have cytostatic,
XX antidiabetic, immunomodulatory, cardiant, neuroprotective,
XX antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
XX ophthalmological, immunomodulatory and cardiovascular activities, and can
XX be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
XX can be used for preparing a composition for treating a disease or

CC condition associated with mpGS-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX

SO Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other:
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
DB 20 AAAAAAAAAAAAAAAAAA 3

RESULT 804
ADM13999/C
ID ADM13999 standard; DNA, 20 BP.

AC ADM13999;
XX
DT 01-JUL-2004 (first entry)

DE Human mpGS-1 chimeric antisense oligonucleotide SEQ ID NO:186.

XX chimeric; antisense oligonucleotide; phosphorothioate; human;
KM microsome1 prostaglandin E2 synthase; mpGS-1; mpGS-1 inhibitor;
KM microsome1 prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
KM immunomodulator; cardiant; neuroprotective; antiinflammatory;
KM neuroprotective; neurotropic; antiarthritis; vasotropic; ophthalmological;
KM immunomodulatory; cardiovascular; gene therapy; inflammation;
KM Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KM reperfusion injury; ophthalmic disorder; immunological disorder;
KM cardiovascular disorder; neurological disorder; ss.

XX Homo sapiens.
OS Synthetic.

XX Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"

PN WO2004028458-A2.

PD 08-APR-2004.

PF 25-SEP-2003; 2003WO-US030374.

PR 25-SEP-2002; 2002US-0413549P.

PA (PHAA) PHARMACIA CORP.

PI Gliese JK;

DR WPI; 2004-305094/28.

XX New antisense compound, having a sequence targeted to a nucleic acid
PT encoding mpGS-1, useful for preparing a composition for treating e.g.,
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT ischaemia.
XX
PS Claim 4; SEQ ID NO 186; 132pp; English.

XX The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microsome1 prostaglandin E2 synthase (mpGS-1). The
CC human mpGS-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds,
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mpGS-1, which specifically hybridise with the nucleic acid mpGS-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mpGS-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mpGS-1. mpGS-1 chimeric
CC antisense oligonucleotides and antisense compounds have cytosolic,
CC antidiabetic, immunomodulator, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, neurotropic, antiarthritis, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mpGS-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mpGS-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX

SO Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other:
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
DB 20 AAAAAAAAAAAAAAAAAA 3

RESULT 805
ADM14008/C
ID ADM14008 standard; DNA, 20 BP.

AC ADM14008;

XX
DT 01-JUL-2004 (first entry)

DE Human mpGS-1 chimeric antisense oligonucleotide SEQ ID NO:195.

XX chimeric; antisense oligonucleotide; phosphorothioate; human;
KM microsome1 prostaglandin E2 synthase; mpGS-1; mpGS-1 inhibitor;
KM microsome1 prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
KM immunomodulator; cardiant; neuroprotective; antiinflammatory;
KM neuroprotective; neurotropic; antiarthritis; vasotropic; ophthalmological;
KM immunomodulatory; cardiovascular; gene therapy; inflammation;
KM Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KM reperfusion injury; ophthalmic disorder; immunological disorder;
KM cardiovascular disorder; neurological disorder; ss.

XX Homo sapiens.
OS Synthetic.

XX Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"

PN WO2004028458-A2.

PD 08-APR-2004.

XX

PF 25-SEP-2003; 2003WO-US030374.
 XX 25-SEP-2002; 2002US-0413549P.
 PR (PHAA) PHARMACIA CORP.
 PA
 XX
 PI Gliese JK;
 XX WPI; 2004-305094/28.
 DR
 XX
 PT New antisense compound, having a sequence targeted to a nucleic acid
 PT encoding mpGS-1, useful for preparing a composition for treating e.g.,
 PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
 PT ischemia.
 PS
 XX Claim 4; SEQ ID NO 195; 132pp; English.
 XX
 CC The present sequence represents a chimeric antisense oligonucleotide
 CC targeted to human microsomal prostaglandin E2 synthase (mpGS-1). The
 CC human mpGS-1 gene is located on chromosome 9, more specifically to
 CC 9q34.3. The present invention also describes: (1) antisense compounds,
 CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
 CC mpGS-1, which specifically hybridize with the nucleic acid mpGS-1 and
 CC inhibits its expression; (2) a method of inhibiting the expression of
 CC mpGS-1 in cells or tissues; and (3) a method of treating an animal
 CC having a disease or condition associated with mpGS-1. mpGS-1 chimeric
 CC antisense oligonucleotides and antisense compounds have cytostatic,
 CC antidiabetic, immunomodulatory, cardiant, neuroprotective,
 CC antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
 CC ophthalmological, immunomodulatory and cardiovascular activities, and can
 CC be used as mpGS-1 inhibitors and in gene therapy. The antisense compound
 CC can be used for preparing a composition for treating a disease or
 CC condition associated with mpGS-1 e.g., inflammation, Alzheimer's
 CC disease, arthritis, diabetes, cancer, ischemia or reperfusion injury, or
 CC ophthalmic, immunological, cardiovascular or neurological disorder.
 XX
 SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
 Query Match 1.1%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 89.9%; Pred. No. 4.4e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 1520 AAAAAAAAAAGTAA 1537
 Db 20 AAAAAAAAAAAAAAAAAA 3
 RESULT 806
 ADM14002/C
 ID ADM14002 standard; DNA; 20 BP.
 XX
 AC ADM14002;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Human mpGS-1 chimeric antisense oligonucleotide SEQ ID NO:189.
 XX
 KW chimeric; antisense oligonucleotide; phosphorothioate; human;
 KW microsomal prostaglandin E2 synthase; mpGS-1; mpGS-1 inhibitor;
 KW microsomal prostaglandin E2 synthase inhibitor; cytosstatic; antidiabetic;
 KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
 KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
 KW immunomodulatory; cardiovascular; gene therapy; inflammation;
 KW Alzheimer's disease; arthritis; diabetes; cancer; ischemia;
 KW reperfusion injury; ophthalmic disorder; immunological disorder;
 KW cardiovascular disorder; neurological disorder; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= b

FT /mod_base= OTHER
 FT /note= "phosphorothioate linkages and all cytidine
 FT residues are 5-methylcytidines"
 FT modified_base 1..5
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "2'-O-methoxyethyls"
 FT modified_base 16..20
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "2'-O-methoxyethyls"
 FT
 FT W02004028458-A2.
 XX
 XX 08-APR-2004.
 XX
 XX 25-SEP-2003; 2003WO-US030374.
 XX
 XX 25-SEP-2002; 2002US-0413549P.
 PR
 XX (PHAA) PHARMACIA CORP.
 PA
 XX
 PI Gliese JK;
 XX WPI; 2004-305094/28.
 DR
 XX
 PT New antisense compound, having a sequence targeted to a nucleic acid
 PT encoding mpGS-1, useful for preparing a composition for treating e.g.,
 PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
 PT ischemia.
 PS
 XX Claim 4; SEQ ID NO 189; 132pp; English.
 XX
 CC The present sequence represents a chimeric antisense oligonucleotide
 CC targeted to human microsomal prostaglandin E2 synthase (mpGS-1). The
 CC human mpGS-1 gene is located on chromosome 9, more specifically to
 CC 9q34.3. The present invention also describes: (1) antisense compounds,
 CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
 CC mpGS-1, which specifically hybridize with the nucleic acid mpGS-1 and
 CC inhibits its expression; (2) a method of inhibiting the expression of
 CC mpGS-1 in cells or tissues; and (3) a method of treating an animal
 CC having a disease or condition associated with mpGS-1. mpGS-1 chimeric
 CC antisense oligonucleotides and antisense compounds have cytostatic,
 CC antidiabetic, immunomodulatory, cardiant, neuroprotective,
 CC antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
 CC ophthalmological, immunomodulatory and cardiovascular activities, and can
 CC be used as mpGS-1 inhibitors and in gene therapy. The antisense compound
 CC can be used for preparing a composition for treating a disease or
 CC condition associated with mpGS-1 e.g., inflammation, Alzheimer's
 CC disease, arthritis, diabetes, cancer, ischemia or reperfusion injury, or
 CC ophthalmic, immunological, cardiovascular or neurological disorder.
 XX
 SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
 Query Match 1.1%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 89.9%; Pred. No. 4.4e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 1520 AAAAAAAAAAGTAA 1537
 Db 20 AAAAAAAAAAAAAAAAAA 3
 RESULT 807
 ADM14090/C
 ID ADM14090 standard; DNA; 20 BP.
 XX
 AC ADM14090;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Human mpGS-1 chimeric antisense oligonucleotide SEQ ID NO:277.
 XX

KM chimeric; antisense oligonucleotide; phosphorothioate; human;
KM microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KM microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
KM immunomodulator; cardiant; neuroprotective; antiinflammatory;
KM neuroprotective; neurotropic; antiarthritic; vasotropic; ophthalmological;
KM immunomodulatory; cardiovascular; gene therapy; inflammation;
KM Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KM reperfusion injury; ophthalmic disorder; immunological disorder;
KM cardiovascular disorder; neurological disorder; ss.
XX Homo sapiens.
OS Synthetic.
XX
FH Key
FT modified_base
FT 1. .20
FT /tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT 1. .5
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT 16. .20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX WO2004028458-A2.
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX
XX (PHAA) PHARMACIA CORP.
XX
XX Gierse JK;
XX
XX WPI; 2004-305094/28.
XX
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischemia.
XX
XX
XX Claim 4; SEQ ID NO 277; 132pp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX human mPGES-1 gene is located on chromosome 9, more specifically to
XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
XX inhibits its expression; (2) a method of inhibiting the expression of
XX mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX antisense oligonucleotides and antisense compounds have cytostatic,
XX antidiabetic, immunomodulator, cardiant, neuroprotective,
XX antiinflammatory, neuroprotective, neurotropic, antiarthritic, vasotropic,
XX ophthalmological, immunomodulatory and cardiovascular activities, and can
XX be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
XX can be used for preparing a composition for treating a disease or
XX condition associated with mPGES-1 e.g., inflammation, Alzheimer's
XX disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
XX ophthalmic, immunological, cardiovascular or neurological disorder.
XX
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
XX
XX Query March 1.1%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 4.4e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CY 1520 AAAAAAAAAAGTAAA 1537
DB 20 AAAAAAAAAAAAAAAAAA 3
RESULT 808
ADM14151/c
ID ADM14151 standard; DNA; 20 BP.
XX
XX ADM14151;
XX
XX 01-JUL-2004 (first entry)
XX
XX Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:338.
XX
XX chimeric; antisense oligonucleotide; phosphorothioate; human;
KM microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KM microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
KM immunomodulator; cardiant; neuroprotective; antiinflammatory;
KM neuroprotective; neurotropic; antiarthritic; vasotropic; ophthalmological;
KM immunomodulatory; cardiovascular; gene therapy; inflammation;
KM Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KM reperfusion injury; ophthalmic disorder; immunological disorder;
KM cardiovascular disorder; neurological disorder; ss.
XX Homo sapiens.
OS Synthetic.
OS
XX
XX Key
FT modified_base
FT 1. .20
FT /tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT 1. .5
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT 16. .20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX WO2004028458-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX
XX (PHAA) PHARMACIA CORP.
XX
XX Gierse JK;
XX
XX WPI; 2004-305094/28.
XX
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischemia.
XX
XX
XX Claim 4; SEQ ID NO 338; 132pp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX human mPGES-1 gene is located on chromosome 9, more specifically to
XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
XX inhibits its expression; (2) a method of inhibiting the expression of
XX mPGES-1 in cells or tissues; and (3) a method of treating an animal

Qy	1520	AAAAAAAAAGTAAA	1537			
Db	20	AAAAAAAAAAAAAAAAAAAA	3			
RESULT 809						
ADML3997/C	ID	ADML3997	standard; DNA; 20 BP.			
XX	ADML3997;					
XX	01-JUL-2004	(first entry)				
DE	Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:184.					
XX	human mPGES-1 chimeric antisense oligonucleotide; phosphorothioate; human;					
KM	microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;					
KM	microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;					
KM	immunomodulator; cardiant; neuroprotective; antiinflammatory;					
KM	neuroprotective; nocotropic; antiarthritic; vasotropic; ophthalmological;					
KM	immunomodulatory; cardiovascular; gene therapy; inflammation;					
KM	Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;					
KM	reperfusion injury; ophthalmic disorder; immunological disorder;					
KM	cardiovascular disorder; neurological disorder; se.					
XX						
OS	Homo sapiens.					
OS	Synthetic.					
XX						
FH	Key	Location/Qualifiers				
FT	modified_base	1..20				
FT		/*tag= b				
FT		/mod_base= OTHER				
FT		/note= "phosphorothioate linkages and all cytidine				
FT		residues are 5-methylcytidines"				
FT	modified_base	1..15				
FT		/*tag= a				
FT		/mod_base= OTHER				
FT		/note= "2'-O-methoxyethyls"				
FT	modified_base	16..20				
FT		/*tag= c				
FT		/mod_base= OTHER				
FT		/note= "2'-O-methoxyethyls"				
XX						
XX	WC02004028458-A2.					
XX						
XX	08-APR-2004.					
XX						
XX	25-SEP-2003; 2003WO-US030374.					
XX						
XX	25-SEP-2002; 2002US-0413549P.					
XX						
XX	(PHAA) PHARMACIA CORP.					
XX						
XX	Glerse JK.					
XX						
XX	WPI; 2004-305094/28.					

XX	New anticense compound, having a sequence targeted to a nucleic acid
PT	encoding mpGS-1, useful for preparing a composition for treating e.g.,
PT	inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT	ischemia.
XX	
PS	Claim 4; SEQ ID NO 184; 132pp; English.
XX	
CC	The present sequence represents a chimeric antisense oligonucleotide
CC	targeted to human microsomal prostaglandin E2 synthase (mpGS-1). The
CC	human mpGS-1 gene is located on chromosome 9, more specifically to
CC	9q34.3. The present invention also describes: (1) antisense compounds,
CC	having a sequence comprising 8-10 bp targeted to a nucleic acid encoding
CC	mpGS-1, which specifically hybridize with the nucleic acid mpGS-1 and
CC	inhibits its expression; (2) a method of inhibiting the expression of
CC	mpGS-1 in cells or tissues; and (3) a method of treating an animal
CC	having a disease or condition associated with mpGS-1. mpGS-1 chimeric
CC	antisense oligonucleotides and antisense compounds have cytostatic,
CC	antidiabetic, immunomodulator, cardiac, neuroprotective,
CC	antiinflammatory, neuroprotective, nociceptive, antiarthritic, vasotropic,
CC	ophthalmological, immunomodulatory and cardiovascular activities, and can
CC	be used as mpGS-1 inhibitors and in gene therapy. The antisense compound
CC	can be used for preparing a composition for treating a disease or
CC	condition associated with mpGS-1 e.g., inflammation, Alzheimer's
CC	disease, arthritis, diabetes, cancer, ischemia or reperfusion injury, or
CC	ophthalmic, immunological, cardiovascular or neurological disorder.
CC	
XX	
SQ	Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
Query Match	1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity	88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
Oy	1520 AAAAAAAAAAAGTAAA 1537 20 AAAAAAAAAAAAAAAAAA 3
Db	
RESULT 810	
ADM14017/C	
ID	ADM14017 standard; DNA; 20 BP.
XX	
AC	ADM14017;
XX	
DT	01-JUL-2004 (first entry)
XX	
DE	Human mpGS-1 chimeric antisense oligonucleotide SEQ ID NO:204.
XX	
KW	chimeric; antisense oligonucleotide; phosphorothioate; human;
KW	microsomal prostaglandin E2 synthase; mpGS-1; mpGS-1 inhibitor;
KW	microsomal prostaglandin E2 synthase inhibitor; cyclostatic; antidiabetic;
KW	immunomodulator; cardiac; neuroprotective; antiinflammatory;
KW	neuroprotective; nociceptive; antiarthritic; vasotropic; ophthalmological;
KW	immunomodulatory; cardiovascular; gene therapy; inflammation;
KW	Alzheimer's disease; arthritis; diabetes; cancer; ischemia;
KW	reperfusion injury; ophthalmic disorder; immunological disorder;
KW	cardiovascular disorder; neurological disorder; ss.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
Key	Location/Qualifiers
FT	modified_base 1..20
FT	/*tag= b
FT	/mod_base= OTHER
FT	/note="phosphorothioate linkages and all cytidine
FT	residues are 5-methylcytidines"
FT	modified_base 1..5
FT	/*tag= a
FT	/mod_base= OTHER
FT	/note="2'-O-methoxyethyls"
FT	modified_base 16..20
FT	/*tag= c

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FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX WO2004028458-A2.
XX
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Gliese JK;
XX
XX WPI; 2004-305094/28.
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mpGS-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischemia.
XX
XX Claim 4; SEQ ID NO 204; 132pp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsomal prostaglandin E2 synthase (mpGS-1). The
XX human mpGS-1 gene is located on chromosome 9, more specifically to
XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX mpGS-1, which specifically hybridise with the nucleic acid mpGS-1 and
XX inhibits its expression; (2) a method of inhibiting the expression of
XX mpGS-1 in cells or tissues; and (3) a method of treating an animal
XX having a disease or condition associated with mpGS-1. mpGS-1 chimeric
XX antisense oligonucleotides and antisense compounds have cytostatic,
XX antidiabetic, immunomodulatory, cardiant, neuroprotective,
XX antihypertensive, neuroprotective, nootropic, antiarthritic, vasotropic,
XX ophthalmological, immunomodulatory and cardiovascular activities, and can
XX be used as mpGS-1 inhibitors and in gene therapy. The antisense compound
XX can be used for preparing a composition for treating a disease or
XX condition associated with mpGS-1 e.g., inflammation, Alzheimer's
XX disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
XX ophthalmic, immunological, cardiovascular or neurological disorder.
XX
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 4.4e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1520 AAAAAAAAAAAGTAAA 1537
XX |||||
XX Db 20 AAAAAAAAAAAAAAAAAA 3
XX
XX RESULT 811
XX ADM14018/c
XX ID ADM14018 standard; DNA; 20 BP.
XX
XX AC ADM14018;
XX
XX 01-JUL-2004 (first entry)
XX
XX Human mpGS-1 chimeric antisense oligonucleotide SEQ ID NO.205.
XX
XX chimeric; antisense oligonucleotide; phosphorothioate; human;
XX microsomal prostaglandin E2 synthase; mpGS-1; mpGS-1 inhibitor;
XX microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
XX immunomodulatory; cardiant; neuroprotective; antiinflammatory;
XX neuroprotective; cardiotropic; antihypertensive; vasotropic; ophthalmological;
XX immunomodulatory; cardiovascular; gene therapy; inflammation;
XX Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
XX reperfusion injury; ophthalmic disorder; immunological disorder;
XX cardiovascular disorder; neurological disorder; ss.
```

```
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX FT /*tag= b
XX FT /mod_base= OTHER
XX FT /note= "phosphorothioate linkages and all cytidine
XX FT residues are 5-methylcytidines"
XX modified_base 1..5
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "2'-O-methoxyethyls"
XX FT /*tag= c
XX FT /mod_base= OTHER
XX FT /note= "2'-O-methoxyethyls"
XX
XX WO2004028458-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Gliese JK;
XX
XX WPI; 2004-305094/28.
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mpGS-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischemia.
XX
XX Claim 4; SEQ ID NO 205; 132pp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsomal prostaglandin E2 synthase (mpGS-1). The
XX human mpGS-1 gene is located on chromosome 9, more specifically to
XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX mpGS-1, which specifically hybridise with the nucleic acid mpGS-1 and
XX inhibits its expression; (2) a method of inhibiting the expression of
XX mpGS-1 in cells or tissues; and (3) a method of treating an animal
XX having a disease or condition associated with mpGS-1. mpGS-1 chimeric
XX antisense oligonucleotides and antisense compounds have cytostatic,
XX antidiabetic, immunomodulatory, cardiant, neuroprotective,
XX antihypertensive, neuroprotective, nootropic, antiarthritic, vasotropic,
XX ophthalmological, immunomodulatory and cardiovascular activities, and can
XX be used as mpGS-1 inhibitors and in gene therapy. The antisense compound
XX can be used for preparing a composition for treating a disease or
XX condition associated with mpGS-1 e.g., inflammation, Alzheimer's
XX disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
XX ophthalmic, immunological, cardiovascular or neurological disorder.
XX
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 4.4e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1520 AAAAAAAAAAAGTAAA 1537
XX |||||
XX Db 20 AAAAAAAAAAAAAAAAAA 3
XX
XX RESULT 812
XX ADM14088/c
XX ID ADM14088 standard; DNA; 20 BP.
```


XX	ADN14088 ;	
AC		
XX	01-JUL-2004 (first entry)	
DT		
XX		
DE	Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:275.	
XX		
XX	chimeric; antisense oligonucleotide; phosphorothioate; human;	
KW	microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;	
KW	microsomal prostaglandin E2 synthase inhibitor; cyclooxygenase; antidiabetic;	
KW	immunomodulator; cardiant; neuroprotective; antiinflammatory;	
KW	neuroprotective; neurotropic; antiarthritic; vasotropic; ophthalmological;	
KW	immunomodulatory; cardiovascular; gene therapy; inflammation;	
KW	Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;	
KW	reflexion injury; ophthalmic disorder; immunological disorder;	
KW	cardiovascular disorder; neurological disorder; ss.	
XX		
OS	Homo sapiens.	
OS	Synthetic.	
XX		
FH	Key	Location/Qualifiers
FT	modified_base	1..20
FT		/tag= b
FT		/mod_base= OTHER
FT		/note= "phosphorothioate linkages and all cytidine
FT		residues are 5-methylcytidines"
FT	modified_base	1..5
FT		/tag= a
FT		/mod_base= OTHER
FT		/note= "2'-O-methoxyethyls"
FT	modified_base	16..20
FT		/tag= c
FT		/mod_base= OTHER
FT		/note= "2'-O-methoxyethyls"
XX		
PN	WO2004028458-A2.	
XX		
PD	08-APR-2004.	
XX		
PF	25-SEP-2003; 2003WO-US030374.	
XX		
PR	25-SEP-2002; 2002US-0413549P.	
XX		
PA	(PHAA) PHARMACIA CORP.	
XX		
PI	Gierse JK;	
XX		
DR	WPI; 2004-305094/28.	
XX		
PT	New antisense compound, having a sequence targeted to a nucleic acid	
PT	encoding mPGES-1, useful for preparing a composition for treating e.g.,	
PT	inflammation, Alzheimer's disease, arthritis, diabetes, cancer or	
PT	ischemia.	
XX		
PS	Claim 4; SEQ ID NO 275; 132pp; English.	
XX		
CC	The present sequence represents a chimeric antisense oligonucleotide	
CC	targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The	
CC	human mPGES-1 gene is located on chromosome 9, more specifically to	
CC	9q43.3. The present invention also describes: (1) antisense compounds,	
CC	having a sequence comprising 8-30 bp targeted to a nucleic acid encoding	
CC	mPGES-1, which specifically hybridize with the nucleic acid mPGES-1 and	
CC	inhibits its expression; (2) a method of inhibiting the expression of	
CC	mPGES-1 in cells or tissues; and (3) a method of treating an animal	
CC	having a disease or condition associated with mPGES-1. mPGES-1 chimeric	
CC	antisense oligonucleotides and antisense compounds have cytoskeletal,	
CC	antidiabetic, immunomodulator, cardiant, neuroprotective,	
CC	antiinflammatory, neuroprotective, neurotropic, antiarthritic, vasotropic,	
CC	ophthalmological, immunomodulatory and cardiovascular activities, and can	
CC	be used as mPGES-1 inhibitors and in gene therapy. The antisense compound	
CC	can be used for preparing a composition for treating a disease or	
CC	condition associated with mPGES-1 e.g., inflammation, Alzheimer's	
CC	disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or	

CC	ophthalmic, immunological, cardiovascular or neurological disorder.
XX	
sq	Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
	1.1%; Score 14.8; DB 1; Length 20;
	Best Local Similarity 88.9%; Pred. No. 4.4e+02;
	Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy	1520 AAAAAAAAAAGTAAAA 1537
Db	20 AAAAAAAAAAAAAAAAAA 3
RESULT 813	
ADML4257/c	
ID	ADML4257 standard; DNA; 20 BP.
XX	
AC	ADML4257;
XX	
DT	01-JUL-2004 (first entry)
XX	
DE	Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:444.
XX	
KW	chimeric; antisense oligonucleotide; phosphorothioate; human;
KW	microsomal prostaglandin G2 synthase; mPGES-1; mPGES-1 inhibitor;
KW	microsomal prostaglandin G2 synthase inhibitor; cytostatic; antidiabetic;
KW	immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW	neuroprotective; neurotropic; antiarthritic; vasotropic; ophthalmological;
KW	immunomodulatory; cardiovascular; gene therapy; inflammation;
KW	Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW	repertusion injury; ophthalmic disorder; immunological disorder;
KW	cardiovascular disorder; neurological disorder; ss.
XX	
OS	Homo sapiens.
XX	
OS	Synthetic.
XX	
Key	Location/Qualifiers
FT	1..20
FT	/*tag= b
FT	/mod_base= OTHER
FT	/note= "phosphorothioate linkages and all cytidine
FT	residues are 5-methylcytidines"
FT	1..5
FT	/*tag= a
FT	/mod_base= OTHER
FT	/note= "2'-O-methoxyethyls"
FT	16..20
FT	/*tag= c
FT	/mod_base= OTHER
FT	/note= "2'-O-methoxyethyls"
XX	
PN	WO2004028458-A2.
XX	
DD	08-APR-2004.
XX	
PF	25-SEP-2003; 2003WO-US030374.
XX	
PR	25-SEP-2002; 2002US-0413549P.
XX	
PA	(PHAA) PHARMACIA CORP.
XX	
PI	Gierse JK;
XX	
DR	WPI; 2004-305094/28.
XX	
PT	New antisense compound, having a sequence targeted to a nucleic acid
PT	encoding mPGES-1, useful for preparing a composition for treating e.g.,
PT	inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT	ischemia.
XX	
PS	Claim 4; SEQ ID NO 444; 132pp; English.
XX	
CC	The present sequence represents a chimeric antisense oligonucleotide

CC	targeted to human microsomal prostaglandin E2 synthase (MPGES-1). The
CC	human MPGES-1 gene is located on chromosome 9, more specifically to
CC	9q44.3. The present invention also describes: (1) antisense compounds,
CC	having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC	MPGES-1, which specifically hybridise with the nucleic acid MPGES-1 and
CC	inhibits its expression; (2) a method of inhibiting the expression of
CC	MPGES-1 in cells or tissues; and (3) a method of treating an animal
CC	having a disease or condition associated with MPGES-1. MPGES-1 chimeric
CC	antisense oligonucleotides and antisense compounds have cytostatic,
CC	antidiabetic, immunomodulator, cardiact, neuroprotective,
CC	antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC	cardiovascular, immunomodulatory and cardiovascular activities, and can
CC	be used as MPGES-1 inhibitors and in gene therapy. The antisense compound
CC	can be used for preparing a composition for treating a disease or
CC	condition associated with MPGES-1 e.g., inflammation, Alzheimer's
CC	disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC	ophthalmic, immunological, cardiovascular or neurological disorder.
XX	
SQ	Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
Query Match	1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity	88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
Qy	1520 AAAAAAAAAAGTAAA 1537 20 AAAAAAAAAAAAAA 3
Db	
RESULT 814	
ADML4000/c	
ID	ADML4000 standard; DNA; 20 BP.
XX	
AC	ADML4000;
XX	
DT	01-JUL-2004 (first entry)
XX	
DE	Human MPGES-1 chimeric antisense oligonucleotide SEQ ID NO:187.
XX	
KW	chimeric; antisense oligonucleotide; phosphorothioate; human;
KW	microsomal prostaglandin E2 synthase; MPGES-1; MPGES-1 inhibitor;
KW	microsomal prostaglandin E2 synthase inhibitor; cytosaric; antidiabetic;
KW	immunomodulator; cardiact; neuroprotective; antiinflammatory;
KW	neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW	Alzheimer's disease; cardiovascular; gene therapy; inflammation;
KW	reperfusion injury; ophthalmic disorder; immunological disorder;
KW	cardiovascular disorder; neurological disorder; ss.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
Key	Location/Qualifiers
FT	modified_base 1..20
FT	/tag= b
FT	/mod_base= OTHER
FT	/note= "phosphorothioate linkages and all cytidine residues are 5-methylcytidines"
FT	modified_base 1..5
FT	/tag= a
FT	/mod_base= OTHER
FT	/note= "2'-O-methoxyethyls"
FT	modified_base 16..20
FT	/tag= c
FT	/mod_base= OTHER
FT	/note= "2'-O-methoxyethyls"
XX	
XX	
PN	WO2004028458-A2.
PD	08-APR-2004.
XX	
XX	25-SEP-2003; 2003WO-US030374.
DF	
XX	

XX		25-SEP-2002; 2002US-0413549P.
PX	(PHAA) PHARMACIA CORP.	
TX	Gierse JK;	
XX	WPI; 2004-305094/28.	
DR		
PT	New antisense compound, having a sequence targeted to a nucleic acid encoding mpGS-1, useful for preparing a composition for treating e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer or ischemia.	
PS	Claim 4; SEQ ID NO 187; 132bp; English.	
CC	The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mpGS-1). The human mpGS-1 gene is located on chromosome 9, more specifically to cc 9q34.3. The present invention also describes: (1) antisense compounds, cc having a sequence comprising 8-20 bp targeted to a nucleic acid encoding mpGS-1, which specifically hybridize with the nucleic acid mpGS-1 and CC inhibits its expression; (2) a method of inhibiting the expression of CC mpGS-1 in cells or tissues; and (3) a method of treating an animal CC having a disease or condition associated with mpGS-1. MPGS-1 chimeric antisense oligonucleotides and antisense compounds have cytostatic, CC antidiabetic, immunomodulator, cardiac, neuroprotective, anti-inflammatory, neuroprotective, nootropic, antiarthritic, vasotropic, optthalmological, immunomodulatory and cardiovascular activities, and can CC be used as mpGS-1 inhibitors and in gene therapy. The antisense compound CC can be used for preparing a composition for treating a disease or CC condition associated with mpGS-1 e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer, ischemia or reperfusion injury, or CC opthalmic, immunological, cardiovascular or neurological disorder. XX SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other; YY	
OY	Query Match 1.1%; Score 14.8; DB 1; Length 20; Best Local Similarity 88.9%; Pred.No. 4.4e+02; Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0 1520 AAAAAAAAAAAGTAAA 1537 20 AAAAAAAAAAAAAAAA 3	
DY		
RESULT 815		
ID	ADM14006/c	
AD	ADM14006 standard; DNA; 20 BP.	
XX		
XX	ADM14006;	
DT		
DE	01-JUL-2004 (first entry)	
HU	Human mpGS-1 chimeric antisense oligonucleotide SEQ ID NO:193.	
KM	chimeric; antisense oligonucleotide; phosphorothioate; human;	
KM	micosomal prostaglandin E2 synthase; mpGS-1; mpGS-1 inhibitor;	
KM	micosomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;	
KM	immunomodulatory; cardiac; neuroprotective; antiinflammatory;	
KM	neuroprotective; nootropic; antiarthitic; vasotropic; ophthalmological;	
KM	immunomodulatory; cardiovascular; gene therapy; inflammation;	
KM	Alzheimer's disease; arthritis; diabetes; cancer; ischemia;	
KM	reperfusion injury; opthalmic disorder; immunological disorder;	
KM	cardiovascular disorder; neurological disorder; ss.	
OS	Homo sapiens.	
SC	Synthetic.	
XX		
Key	Location/Qualifiers	
FT	modified_base 1..20	
FT	/+tag= b	
FT	/mod_base= OTHER	
FT	/note="phosphorothioate linkages and all cytidine"	

```
FT modified_base      residues are 5-methylcytidines"
FT                      1. .5
FT                      /*tag= a
FT                      /mod_base= OTHER
FT                      /note= "2'-O-methoxyethyls"
FT modified_base      16. .20
FT                      /*tag= c
FT                      /mod_base= OTHER
FT                      /note= "2'-O-methoxyethyls"
XX
XX WO2004028458-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Gliese JK;
XX
XX WPI; 2004-305094/28.
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischemia.
XX
XX Claim 4; SEQ ID NO 193; 132pp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX human mPGES-1 gene is located on chromosome 9, more specifically to
XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
XX inhibits its expression; (2) a method of inhibiting the expression of
XX mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX antisense oligonucleotides and antisense compounds have cytostatic,
XX antiinflammatory, immunomodulator, cardiant, neuroprotective,
XX ophthalmological, immunomodulatory and cardiovascular activities, and can
XX be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
XX can be used for preparing a composition for treating a disease or
XX condition associated with mPGES-1 e.g., inflammation, Alzheimer's
XX disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
XX ophthalmic, immunological, cardiovascular or neurological disorder.
XX
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
XX
XX Query Match      1.1%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. NO. 4.4e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX Oy      1520 AAAAAAAAAAAGTAA 1537
XX      |||||
XX      20 AAAAAAAAAAAAAAAAAA 3
XX
XX RESULT 816
XX ADM14014/c
XX ID ADM14014 standard; DNA; 20 BP.
XX
XX AC ADM14014;
XX
XX 01-JUL-2004 (first entry)
XX
XX Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:201.
XX
XX chimeric; antisense oligonucleotide; phosphorothioate; human;
XX microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
```

```
KW microsomal prostaglandin E2 synthase inhibitor; cytostatic; antidiabetic;
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; neurotropic; antiarthritis; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX Key
XX Location/Qualifiers
XX modified_base      1. .20
XX                      /*tag= b
XX                      /mod_base= OTHER
XX                      /note= "phosphorothioate linkages and all cytidine
XX                      residues are 5-methylcytidines"
XX modified_base      1. .5
XX                      /*tag= a
XX                      /mod_base= OTHER
XX                      /note= "2'-O-methoxyethyls"
XX modified_base      16. .20
XX                      /*tag= c
XX                      /mod_base= OTHER
XX                      /note= "2'-O-methoxyethyls"
XX
XX WO2004028458-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Gliese JK;
XX
XX WPI; 2004-305094/28.
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischemia.
XX
XX Claim 4; SEQ ID NO 201; 132pp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX human mPGES-1 gene is located on chromosome 9, more specifically to
XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
XX inhibits its expression; (2) a method of inhibiting the expression of
XX mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX antisense oligonucleotides and antisense compounds have cytostatic,
XX antiinflammatory, immunomodulator, cardiant, neuroprotective,
XX ophthalmological, immunomodulatory and cardiovascular activities, and can
XX be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
XX can be used for preparing a composition for treating a disease or
XX condition associated with mPGES-1 e.g., inflammation, Alzheimer's
XX disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
XX ophthalmic, immunological, cardiovascular or neurological disorder.
XX
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
XX
XX Query Match      1.1%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. NO. 4.4e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX Oy      1520 AAAAAAAAAAAGTAA 1537
```

```
Db      20 AAAAAAAAAAAAAAAAAA 3
RESULT 817
ADM14020/c
ID      ADM14020 standard; DNA; 20 BP.
XX
XX      ADM14020;
AC
XX      01-JUL-2004 (first entry)
DT
XX
DE      Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:207.
XX
KM      chimeric; antisense oligonucleotide; phosphorothioate; human;
KM      microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KM      immunomodulator; cardiant; neuroprotective; antiinflammatory;
KM      neuroprotective; cardiant; neuroprotective; vasotrophic; ophthalmological;
KM      immunomodulator; cardiant; neuroprotective; vasotrophic; ophthalmological;
KM      Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KM      reperfusion injury; ophthalmic disorder; immunological disorder;
KM      cardiovascular disorder; neurological disorder; ss.
XX
XX      Homo sapiens.
OS      Synthetic.
XX
XX      Key
XX      modified_base
XX      1..20
XX      /tag= b
XX      /mod_base= OTHER
XX      /note= "phosphorothioate linkages and all cytidine
XX      residues are 5-methylcytidines"
XX      1..5
XX      /tag= a
XX      /mod_base= OTHER
XX      /note= "2'-O-methoxyethyls"
XX      16..20
XX      /tag= c
XX      /mod_base= OTHER
XX      /note= "2'-O-methoxyethyls"
XX      WO2004028458-A2.
XX      08-APR-2004.
XX      PD
XX      PF      25-SEP-2003; 2003WO-US030374.
XX      PR      25-SEP-2002; 2002US-0413549P.
XX      PA      (PHAA ) PHARMACIA CORP.
XX      PI      Gliese JK;
XX      XX      WPI; 2004-305094/28.
XX      DR
XX      PT      New antisense compound, having a sequence targeted to a nucleic acid
XX      PT      encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX      PT      inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX      PT      ischaemia.
XX      PS      Claim 4; SEQ ID NO 207; 132bp; English.
XX
XX      The present sequence represents a chimeric antisense oligonucleotide
XX      CC      targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX      CC      human mPGES-1 gene is located on chromosome 9, more specifically to
XX      CC      9q34.3. The present invention also describes: (1) antisense compounds,
XX      CC      having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX      CC      mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
XX      CC      inhibits its expression; (2) a method of inhibiting the expression of
XX      CC      mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX      CC      having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX      CC      antisense oligonucleotides and antisense compounds have cytosstatic,
```

```
CC      anti-diabetic, immunomodulator, cardiant, neuroprotective,
CC      antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotrophic,
CC      ophthalmological, immunomodulatory and cardiovascular activities, and can
CC      be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC      can be used for preparing a composition for treating a disease or
CC      condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC      disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC      ophthalmic, immunological, cardiovascular or neurological disorder.
XX
XX      Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
SQ
Query Match      1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy      1520 AAAAAAAAAAGTAA 1537
Db      20 AAAAAAAAAAAAAAAAAA 3
RESULT 818
ADM13991/c
ID      ADM13991 standard; DNA; 20 BP.
XX
XX      ADM13991;
AC
XX      01-JUL-2004 (first entry)
DT
XX
DE      Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:178.
XX
XX      chimeric; antisense oligonucleotide; phosphorothioate; human;
XX      microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
XX      microsomal prostaglandin E2 synthase inhibitor; cytosstatic; anti-diabetic;
XX      immunomodulator; cardiant; neuroprotective; antiinflammatory;
XX      neuroprotective; nootropic; antiarthritic; vasotrophic; ophthalmological;
XX      immunomodulator; cardiant; neuroprotective; vasotrophic; ophthalmological;
XX      Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
XX      reperfusion injury; ophthalmic disorder; immunological disorder;
XX      cardiovascular disorder; neurological disorder; ss.
XX
XX      Homo sapiens.
OS      Synthetic.
XX
XX      Key
XX      modified_base
XX      1..20
XX      /tag= b
XX      /mod_base= OTHER
XX      /note= "phosphorothioate linkages and all cytidine
XX      residues are 5-methylcytidines"
XX      1..5
XX      /tag= a
XX      /mod_base= OTHER
XX      /note= "2'-O-methoxyethyls"
XX      16..20
XX      /tag= c
XX      /mod_base= OTHER
XX      /note= "2'-O-methoxyethyls"
XX      WO2004028458-A2.
XX      08-APR-2004.
XX      PD
XX      PF      25-SEP-2003; 2003WO-US030374.
XX      PR      25-SEP-2002; 2002US-0413549P.
XX      PA      (PHAA ) PHARMACIA CORP.
XX      PI      Gliese JK;
XX      XX      WPI; 2004-305094/28.
XX      DR
XX      PT      New antisense compound, having a sequence targeted to a nucleic acid
```

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PT encoding mPGES-1, useful for preparing a composition for treating e.g.,
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT ischemia.
XX
XX Claim 4; SEQ ID NO 178; 132bp; English.
XX
CC The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
CC human mPGES-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds,
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mPGES-1. mPGES-1 chimeric
CC antisense oligonucleotides and antisense compounds have cytostatic,
CC antidiabetic, immunomodulatory, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAGTAAA 1537
DB 20 AAAAAAAAAAAAAAAAAA 3
RESULT 819
ADM14003/C
ID ADM14003 standard; DNA; 20 BP.
XX
XX ADM14003;
AC
XX 01-JUL-2004 (first entry)
XX
DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:190.
XX
KW chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
XX Homo sapiens.
OS Synthetic.
XX
FH Key 1.20 Location/Qualifiers
FT 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT

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XX
XX WO2004028458-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX
XX (PAAA ) PHARMACIA CORP.
XX
XX Gierse JK;
XX
XX WPI; 2004-305094/28.
XX
PT New antisense compound, having a sequence targeted to a nucleic acid
PT encoding mPGES-1, useful for preparing a composition for treating e.g.,
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT ischemia.
XX
XX Claim 4; SEQ ID NO 190; 132bp; English.
XX
CC The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
CC human mPGES-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds,
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mPGES-1. mPGES-1 chimeric
CC antisense oligonucleotides and antisense compounds have cytostatic,
CC antidiabetic, immunomodulatory, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAGTAAA 1537
DB 20 AAAAAAAAAAAAAAAAAA 3
RESULT 820
ADM14005/C
ID ADM14005 standard; DNA; 20 BP.
XX
XX ADM14005;
AC
XX 01-JUL-2004 (first entry)
XX
DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:192.
XX
KW chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
XX Homo sapiens.
OS

```

```
OS Synthetic.
XX Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX WO2004028458-A2.
XX 08-APR-2004.
XX 25-SEP-2003; 2003WO-US030374.
XX 25-SEP-2002; 2002US-0413549P.
XX (PHAA ) PHARMACIA CORP.
XX Gliese JK;
XX WPI; 2004-305094/28.
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischemia.
XX Claim 4; SEQ ID NO 192; 132pp; English.
XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX human mPGES-1 gene is located on chromosome 9, more specifically to
XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
XX inhibits its expression; (2) a method of inhibiting the expression of
XX mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX antisense oligonucleotides and antisense compounds have cytostatic,
XX antidiabetic, immunomodulator, cardiant, neuroprotective,
XX antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
XX cardioprotective, immunomodulatory and cardiovascular activities, and can
XX be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
XX can be used for preparing a composition for treating a disease or
XX condition associated with mPGES-1 e.g., inflammation, Alzheimer's
XX disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
XX opthalmic, immunological, cardiovascular or neurological disorder.
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other:
XX
XX Query Match 1..14; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 4.4e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1520 AAAAAAAAAAGTAA 1537
XX |||||
XX 20 AAAAAAAAAAAAAAAAA 3
XX
XX RESULT 821
XX ADM14246/c
XX ID ADM14246 standard; DNA; 20 BP.
XX
XX AC ADM14246;
```

```
XX 01-JUL-2004 (first entry)
XX Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:433.
XX
XX chimeric; antisense oligonucleotide; mPGES-1; mPGES-1 inhibitor;
XX microsomal prostaglandin E2 synthase inhibitor; cytostatic; antidiabetic;
XX immunomodulator; cardiant; neuroprotective; antiinflammatory;
XX neuroprotective; nootropic; antiarthritic; vasotropic; opthalmological;
XX immunomodulatory; cardiovascular; gene therapy; inflammation;
XX Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
XX reperfusion injury; opthalmic disorder; immunological disorder;
XX cardiovascular disorder; neurological disorder; ss.
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX WO2004028458-A2.
XX 08-APR-2004.
XX 25-SEP-2003; 2003WO-US030374.
XX 25-SEP-2002; 2002US-0413549P.
XX (PHAA ) PHARMACIA CORP.
XX Gliese JK;
XX WPI; 2004-305094/28.
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischemia.
XX Claim 4; SEQ ID NO 433; 132pp; English.
XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX human mPGES-1 gene is located on chromosome 9, more specifically to
XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
XX inhibits its expression; (2) a method of inhibiting the expression of
XX mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX antisense oligonucleotides and antisense compounds have cytostatic,
XX antidiabetic, immunomodulator, cardiant, neuroprotective,
XX antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
XX cardioprotective, immunomodulatory and cardiovascular activities, and can
XX be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
XX can be used for preparing a composition for treating a disease or
XX condition associated with mPGES-1 e.g., inflammation, Alzheimer's
XX disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
XX opthalmic, immunological, cardiovascular or neurological disorder.
XX
```

```
SQ Sequence 20 BP; 0 A; 0 C; 1 G; 19 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAGTAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 822
ADM13995/C
ID ADM13995 standard; DNA; 20 BP.
XX
XX ADM13995;
XX
XX 01-JUL-2004. (first entry)
XX
XX Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:182.
XX
XX chimeric; antisense oligonucleotide; phosphorothioate; human;
XX microsome1 prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
XX microsome1 prostaglandin E2 synthase inhibitor; cyclostatic; antidiabetic;
XX immunomodulator; cardiant; neuroprotective; antiinflammatory;
XX neuroprotective; noctropic; antiarthritic; vasotropic; ophthalmological;
XX immunomodulatory; cardiovascular; gene therapy; inflammation;
XX Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
XX reperfusion injury; ophthalmic disorder; immunological disorder;
XX cardiovascular disorder; neurological disorder; ss.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX /*tag= b
XX /mod_base= OTHER
XX /note= "phosphorothioate linkages and all cytidine
XX residues are 5-methylcytidines"
XX
XX modified_base 1..5
XX /*tag= a
XX /mod_base= OTHER
XX /note= "2'-O-methoxyethyls"
XX
XX modified_base 16..20
XX /*tag= c
XX /mod_base= OTHER
XX /note= "2'-O-methoxyethyls"
XX
XX WO2004028458-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Gliese JK;
XX
XX WPI; 2004-305094/28.
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischaemia.
XX
XX Claim 4; SEQ ID NO 182; 132pp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsome1 prostaglandin E2 synthase (mPGES-1). The
XX human mPGES-1 gene is located on chromosome 9, more specifically to
```

```
CC 9q34.3. The present invention also describes: (1) antisense compounds,
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mPGES-1. mPGES-1 chimeric
CC antisense oligonucleotides and antisense compounds have cyclostatic,
CC antidiabetic, immunomodulator, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, noctropic, antiarthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
XX SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAGTAAA 1537
Db 20 AAAAAAAAAAAAAAAAAA 3

RESULT 823
ADM14011/C
ID ADM14011 standard; DNA; 20 BP.
XX
XX ADM14011;
XX
XX 01-JUL-2004 (first entry)
XX
XX Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:198.
XX
XX chimeric; antisense oligonucleotide; phosphorothioate; human;
XX microsome1 prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
XX microsome1 prostaglandin E2 synthase inhibitor; cyclostatic; antidiabetic;
XX immunomodulator; cardiant; neuroprotective; antiinflammatory;
XX neuroprotective; noctropic; antiarthritic; vasotropic; ophthalmological;
XX immunomodulatory; cardiovascular; gene therapy; inflammation;
XX Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
XX reperfusion injury; ophthalmic disorder; immunological disorder;
XX cardiovascular disorder; neurological disorder; ss.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX /*tag= b
XX /mod_base= OTHER
XX /note= "phosphorothioate linkages and all cytidine
XX residues are 5-methylcytidines"
XX
XX modified_base 1..5
XX /*tag= a
XX /mod_base= OTHER
XX /note= "2'-O-methoxyethyls"
XX
XX modified_base 16..20
XX /*tag= c
XX /mod_base= OTHER
XX /note= "2'-O-methoxyethyls"
XX
XX WO2004028458-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX
```

PA	(PMAA) PHARMACIA CORP.
XX	
PI	Glerse JK;
XX	
DR	WPI; 2004-305094/28.
XX	
PT	New antisense compound, having a sequence targeted to a nucleic acid
PT	encoding mPGES-1, useful for preparing a composition for treating e.g.,
PT	inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT	ischemia.
XX	
PS	Claim 4; SEQ ID NO 198; 132bp; English.
XX	
CC	The present sequence represents a chimeric antisense oligonucleotide
CC	targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
CC	human mPGES-1 gene is located on chromosome 9, more specifically to
CC	9q34.3. The present invention also describes: (1) antisense compounds,
CC	having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC	mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
CC	inhibits its expression; (2) a method of inhibiting the expression of
CC	mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC	having a disease or condition associated with mPGES-1. mPGES-1 chimeric
CC	antisense oligonucleotides and antisense compounds have cytostatic,
CC	antidiabetic, immunomodulator, cardiant, neuroprotective,
CC	antiinflammatory, neuroprotective, neurotropic, antiarthritic, vasotropic,
CC	ophthalmological, immunomodulatory and cardiovascular activities, and can
CC	be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC	can be used for preparing a composition for treating a disease or
CC	condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC	disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC	ophthalmic, immunological, cardiovascular or neurological disorder.
XX	
SQ	Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
	Query Match 1.1%; Score 14.8; DB 1; Length 20;
	Best Local Similarity 88.9%; Pred. No. 4,4e+02;
	Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0
QY	1520 AAAAAAAAAAGTAAAA 1537
Db	20 AAAAAAAAAAAAAAAAAA 3
RESULT 824	
ADMI4240/C	
ID	ADMI4240 standard; DNA; 20 BP.
XX	
AC	ADMI4240;
XX	
DT	
XX	01-JUL-2004 (first entry)
XX	
DE	Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:427.
XX	
KW	chimeric; antisense oligonucleotide; phosphorothioate; human;
KW	microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW	microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
KW	immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW	neuroprotective; neurotropic; antiarthritic; vasotropic; ophthalmological;
KW	immunomodulatory; cardiovascular; gene therapy; inflammation;
KW	Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW	reperfusion injury; ophthalmic disorder; immunological disorder;
KW	cardiovascular disorder; neurological disorder; ss.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
XX	
XX	Key
XX	Location/Qualifiers
FT	1..20
FT	/tag= b
FT	/mod_base= OTHER
FT	/note="phosphorothioate linkages and all cytidine
FT	residues are 5-methylcytidines"
FT	1..5
FT	modified base

[illegible]

KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key
FT modified_base
FT 1..20
FT /tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT 1..5
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT modified_base
FT 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT
FT
FT
XX
XX WO2004028458-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX
XX (PHAA) PHARMACIA CORP.
XX
XX Gierse JK;
XX
XX WPI; 2004-305094/28.
XX
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischemia.
XX
XX
XX Claim 4; SEQ ID NO 196; 132bp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX human mPGES-1 gene is located on chromosome 9, more specifically to
XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
XX inhibits its expression; (2) a method of inhibiting the expression of
XX mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX antisense oligonucleotides and antisense compounds have cytostatic,
XX antidiabetic, immunomodulator, cardiac, neuroprotective,
XX antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
XX ophthalmological, immunomodulatory and cardiovascular activities, and can
XX be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
XX can be used for preparing a composition for treating a disease or
XX condition associated with mPGES-1 e.g., inflammation, Alzheimer's
XX disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
XX ophthalmic, immunological, cardiovascular or neurological disorder.
XX
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 4.4e-02;
XX Match 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

~RESULT 826
ADMI4010/c
ID ADMI4010 standard; DNA; 20 BP.
XX
XX ADMI4010;
XX
XX 01-JUL-2004 (first entry)
XX
XX Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:197.
XX
XX chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
KW immunomodulator; cardiac; neuroprotective; antiinflammatory;
KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX
XX Key
XX modified_base
XX 1..20
XX /tag= b
XX /mod_base= OTHER
XX /note= "phosphorothioate linkages and all cytidine
XX residues are 5-methylcytidines"
XX 1..5
XX /tag= a
XX /mod_base= OTHER
XX /note= "2'-O-methoxyethyls"
XX modified_base
XX 16..20
XX /tag= c
XX /mod_base= OTHER
XX /note= "2'-O-methoxyethyls"
XX
XX
XX WO2004028458-A2.
XX
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX
XX (PHAA) PHARMACIA CORP.
XX
XX Gierse JK;
XX
XX WPI; 2004-305094/28.
XX
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischemia.
XX
XX
XX Claim 4; SEQ ID NO 197; 132bp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX human mPGES-1 gene is located on chromosome 9, more specifically to
XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
XX inhibits its expression; (2) a method of inhibiting the expression of
XX mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX antisense oligonucleotides and antisense compounds have cytostatic,
XX antidiabetic, immunomodulator, cardiac, neuroprotective,
XX antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,

CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mPGEs-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGEs-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAGTAAAA 1537
Db 20 AAAAAAAAAAAAAAAAAA 3
RESULT 827
ADM14089/c
ID ADM14089 standard; DNA; 20 BP.
XX
AC ADM14089;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human mPGEs-1 chimeric antisense oligonucleotide SEQ ID NO:276.
XX
KW chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase; mPGEs-1; mPGEs-1 inhibitor;
KW microsomal prostaglandin E2 synthase inhibitor; cyclostatic; antidiabetic;
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX
EN WO2004028458-A2.
XX
PD 08-APR-2004.
XX
PF 25-SEP-2003; 2003WO-USO30374.
XX
PR 25-SEP-2002; 2002US-0413549P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Gierse JK;
XX
DR WPI; 2004-305094/28.
XX
PT New antisense compound, having a sequence targeted to a nucleic acid
PT encoding mPGEs-1, useful for preparing a composition for treating e.g.,
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or

PT ischemia.
XX
PS Claim 4; SEQ ID NO 276; 132bp; English.
XX
CC The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microsomal prostaglandin E2 synthase (mPGEs-1). The
CC human mPGEs-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds,
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mPGEs-1, which specifically hybridise with the nucleic acid mPGEs-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mPGEs-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mPGEs-1. mPGEs-1 chimeric
CC antisense oligonucleotides and antisense compounds have cyclostatic,
CC antidiabetic, immunomodulator, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mPGEs-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGEs-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAGTAAAA 1537
Db 20 AAAAAAAAAAAAAAAAAA 3
RESULT 828
ADM14016/c
ID ADM14016 standard; DNA; 20 BP.
XX
AC ADM14016;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human mPGEs-1 chimeric antisense oligonucleotide SEQ ID NO:203.
XX
KW chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase; mPGEs-1; mPGEs-1 inhibitor;
KW microsomal prostaglandin E2 synthase inhibitor; cyclostatic; antidiabetic;
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX
EN WO2004028458-A2.

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XX 08-APR-2004.
PD
PP 25-SEP-2003; 2003WO-US030374.
XX 25-SEP-2002; 2002US-0413549P.
XX (PHAA ) PHARMACIA CORP.
PA
XX
PI Gliese JK;
XX
DR WPI; 2004-305094/28.
XX
PT New antisense compound, having a sequence targeted to a nucleic acid
PT encoding mPGES-1, useful for preparing a composition for treating e.g.,
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT ischemia.
PS
PS Claim 4; SEQ ID NO 203; 132p; English.
XX
CC The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
CC human mPGES-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds,
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mPGES-1, which specifically hybridize with the nucleic acid mPGES-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mPGES-1. mPGES-1 chimeric
CC antisense oligonucleotides and antisense compounds have cytostatic,
CC antidiabetic, immunomodulatory, cardiatic, neuroprotective,
CC antiinflammatory, neuroprotective, noctropic, antiarthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAGTAA 1537
DB 20 AAAAAAAAAAAAAAAAA 3
RESULT 829
ADMI4075/C
ID ADMI4075 standard; DNA; 20 BP.
XX
AC ADMI4075;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:262.
XX
KW chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
KW immunomodulatory; cardiatic; neuroprotective; antiinflammatory;
KW neuroprotective; noctropic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
XX Homo sapiens.
OS
XX Synthetic.
XX

```

```

FH Key Location/Qualifiers
PT modified_base 1..20
PT /*tag= b
PT /mod_base= OTHER
PT /note= "phosphorothioate linkages and all cytidine
PT residues are 5-methylcytidines"
PT modified_base 1..5
PT /*tag= a
PT /mod_base= OTHER
PT /note= "2'-O-methoxyethyls"
PT modified_base 16..20
PT /*tag= c
PT /mod_base= OTHER
PT /note= "2'-O-methoxyethyls"
PN W02004028458-A2.
XX
XX 08-APR-2004.
PD
PP 25-SEP-2003; 2003WO-US030374.
XX 25-SEP-2002; 2002US-0413549P.
XX (PHAA ) PHARMACIA CORP.
PA
XX
PI Gliese JK;
XX
DR WPI; 2004-305094/28.
XX
PT New antisense compound, having a sequence targeted to a nucleic acid
PT encoding mPGES-1, useful for preparing a composition for treating e.g.,
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT ischemia.
PS
PS Claim 4; SEQ ID NO 262; 132p; English.
XX
CC The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
CC human mPGES-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds,
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mPGES-1, which specifically hybridize with the nucleic acid mPGES-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mPGES-1. mPGES-1 chimeric
CC antisense oligonucleotides and antisense compounds have cytostatic,
CC antidiabetic, immunomodulatory, cardiatic, neuroprotective,
CC antiinflammatory, neuroprotective, noctropic, antiarthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAGTAA 1537
DB 20 AAAAAAAAAAAAAAAAA 3
RESULT 830
ADMI4189/C
ID ADMI4189 standard; DNA; 20 BP.
XX
AC ADMI4189;
XX
DT 01-JUL-2004 (first entry)
XX

```

XX Human mpGS-1 chimeric antisense oligonucleotide SEQ ID NO:376.
XX
XX chimeric; antisense oligonucleotide; phosphorothioate; human;
KM microsome1 prostaglandin E2 synthase; mpGS-1; mpGS-1 inhibitor;
KM microsome1 prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
KM immunomodulatory; cardiant; neuroprotective; antiinflammatory;
KM neuroprotective; neurotropic; antiarthritic; vasotropic; ophthalmological;
KM immunomodulatory; cardiovascular; gene therapy; inflammation;
KM Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KM reperfusion injury; ophthalmic disorder; immunological disorder;
KM cardiovascular disorder; neurological disorder; ss.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key
FH modified_base
FT 1..20
FT /tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT 1..5
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX
XX WO2004028458-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX
XX (PHAA) PHARMACIA CORP.
XX
XX Gierse JK;
PI
PI
DR WPI; 2004-305094/28.
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
PT encoding mpGS-1, useful for preparing a composition for treating e.g.,
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT ischaemia.
XX
XX
XX Claim 4; SEQ ID NO 376; 132pp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microsome1 prostaglandin E2 synthase (mpGS-1). The
CC human mpGS-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds,
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mpGS-1, which specifically hybridise with the nucleic acid mpGS-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mpGS-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mpGS-1. mpGS-1 chimeric
CC antisense oligonucleotides and antisense compounds have cytosolic,
CC antidiabetic, immunomodulatory, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, neurotropic, antiarthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mpGS-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mpGS-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Cy 1520 AAAAAAAAAAAGTAAA 1537
Db 20 AAAAAAAAAAAAAAAAAA 3
RESULT 831
ADM13996/C
ID ADM13996 standard; DNA; 20 BP.
XX
XX AC ADM13996;
XX
XX DT 01-JUL-2004 (first entry)
XX
XX DE Human mpGS-1 chimeric antisense oligonucleotide SEQ ID NO:183.
XX
XX chimeric; antisense oligonucleotide; phosphorothioate; human;
KM microsome1 prostaglandin E2 synthase; mpGS-1; mpGS-1 inhibitor;
KM microsome1 prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
KM immunomodulatory; cardiant; neuroprotective; antiinflammatory;
KM neuroprotective; neurotropic; antiarthritic; vasotropic; ophthalmological;
KM immunomodulatory; cardiovascular; gene therapy; inflammation;
KM Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KM reperfusion injury; ophthalmic disorder; immunological disorder;
KM cardiovascular disorder; neurological disorder; ss.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key
FH modified_base
FT 1..20
FT /tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT 1..5
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX
XX WO2004028458-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX
XX (PHAA) PHARMACIA CORP.
XX
XX Gierse JK;
PI
PI
DR WPI; 2004-305094/28.
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
PT encoding mpGS-1, useful for preparing a composition for treating e.g.,
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT ischaemia.
XX
XX
XX Claim 4; SEQ ID NO 183; 132pp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microsome1 prostaglandin E2 synthase (mpGS-1). The
CC human mpGS-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds,
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding

CC mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mPGES-1. mPGES-1 chimeric
CC antisense oligonucleotides and antisense compounds have cytostatic,
CC antidiabetic, immunomodulatory, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Gy 1520 AAAAAAAAAAGTAAA 1537
Db 20 AAAAAAAAAAAAAAAAAA 3
RESULT 832
ADM14001/c
ID ADM14001 standard; DNA; 20 BP.
XX
AC ADM14001;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:188.
XX
KW chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microosomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW microosomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key
FT modified_base
FT 1..20
FT Location/Qualifiers
FT /*tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX
PN WO2004028458-A2.
XX
PD 08-APR-2004.
XX
PF 25-SEP-2003; 2003WO-US030374.
XX
PR 25-SEP-2002; 2002US-0413549P.
XX
PA (PHAA) PHARMACIA CORP.
XX

PI Gierse JK;
XX
DR MPI; 2004-305094/28.
XX
PT New antisense compound, having a sequence targeted to a nucleic acid
PT encoding mPGES-1, useful for preparing a composition for treating e.g.,
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT ischemia.
XX
PS Claim 4; SEQ ID NO 188; 132pp; English.
XX
CC The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microosomal prostaglandin E2 synthase (mPGES-1). The
CC human mPGES-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds,
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mPGES-1. mPGES-1 chimeric
CC antisense oligonucleotides and antisense compounds have cytostatic,
CC antidiabetic, immunomodulator, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Gy 1520 AAAAAAAAAAGTAAA 1537
Db 20 AAAAAAAAAAAAAAAAAA 3
RESULT 833
ADM14004/c
ID ADM14004 standard; DNA; 20 BP.
XX
AC ADM14004;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:191.
XX
KW chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microosomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW microosomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key
FT modified_base
FT 1..20
FT Location/Qualifiers
FT /*tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT 1..5
FT /*tag= a
FT /mod_base= OTHER
FT

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FT modified_base /note= "2'-O-methoxyethyls"  
FT 16. .20  
FT /*tag= c  
FT /mod_base= OTHER  
FT /note= "2'-O-methoxyethyls"  
XX  
XX WO2004028458-A2.  
XX  
XX 08-APR-2004.  
XX  
XX 25-SEP-2003; 2003WO-US030374.  
XX  
XX 25-SEP-2002; 2002US-0413549P.  
XX  
XX (PHAA ) PHARMACIA CORP.  
XX  
XX Gierse JK;  
XX  
XX WPI; 2004-305094/28.  
XX  
XX  
XX New antisense compound, having a sequence targeted to a nucleic acid  
PT encoding mpGS-1, useful for preparing a composition for treating e.g.,  
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or  
PT ischemia.  
XX  
XX  
XX Claim 4; SEQ ID NO 191; 132pp; English.  
XX  
XX The present sequence represents a chimeric antisense oligonucleotide  
CC targeted to human microsomal prostaglandin E2 synthase (mpGS-1). The  
CC human mpGS-1 gene is located on chromosome 9, more specifically to  
CC 9q34.3. The present invention also describes: (1) antisense compounds,  
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding  
CC mpGS-1, which specifically hybridize with the nucleic acid mpGS-1 and  
CC inhibits its expression; (2) a method of inhibiting the expression of  
CC mpGS-1 in cells or tissues; and (3) a method of treating an animal  
CC having a disease or condition associated with mpGS-1. mpGS-1 chimeric  
CC antisense oligonucleotides and antisense compounds have cytostatic,  
CC antidiabetic, immunomodulatory, cardiant, neuroprotective,  
CC antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,  
CC ophthalmological, immunomodulatory and cardiovascular activities, and can  
CC be used as mpGS-1 inhibitors and in gene therapy. The antisense compound  
CC can be used for preparing a composition for treating a disease or  
CC condition associated with mpGS-1 e.g., inflammation, Alzheimer's  
CC disease, arthritis, diabetes, cancer, ischemia or reperfusion injury, or  
CC ophthalmic, immunological, cardiovascular or neurological disorder.  
XX  
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;  
SQ  
Query Match 1.1%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 4.4e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 1520 AAAAAAAAAAAGTAA 1537  
Db 20 AAAAAAAAAAAAAAAAAA 3  
RESULT 834  
ADMI4012/c  
ID ADMI4012 standard; DNA; 20 BP.  
XX  
XX ADMI4012;  
XX  
XX 01-JUL-2004 (first entry)  
XX  
XX Human mpGS-1 chimeric antisense oligonucleotide SEQ ID NO:199.  
DE  
XX  
XX chimeric; antisense oligonucleotide; phosphorothioate; human;  
KW microsomal prostaglandin E2 synthase; mpGS-1; mpGS-1 inhibitor;  
KW microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;  
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;  
KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;  
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
```

```
KW Alzheimer's disease; arthritis; diabetes; cancer; ischemia;  
KW reperfusion injury; ophthalmic disorder; immunological disorder;  
KW cardiovascular disorder; neurological disorder; ss.  
XX  
XX Homo sapiens.  
OS  
OS Synthetic.  
XX  
XX  
XX Key Location/Qualifiers  
FH modified_base 1. .20  
FT /*tag= b  
FT /mod_base= OTHER  
FT /note= "phosphorothioate linkages and all cytidine  
FT residues are 5-methylcytidines"  
FT  
FT modified_base 1. .5  
FT /*tag= a  
FT /mod_base= OTHER  
FT /note= "2'-O-methoxyethyls"  
FT modified_base 16. .20  
FT /*tag= c  
FT /mod_base= OTHER  
FT /note= "2'-O-methoxyethyls"  
PN WO2004028458-A2.  
PD 08-APR-2004.  
XX  
XX 25-SEP-2003; 2003WO-US030374.  
XX  
XX 25-SEP-2002; 2002US-0413549P.  
XX  
XX (PHAA ) PHARMACIA CORP.  
XX  
XX Gierse JK;  
XX  
XX WPI; 2004-305094/28.  
XX  
XX  
XX New antisense compound, having a sequence targeted to a nucleic acid  
PT encoding mpGS-1, useful for preparing a composition for treating e.g.,  
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or  
PT ischemia.  
XX  
XX  
XX Claim 4; SEQ ID NO 199; 132pp; English.  
XX  
XX The present sequence represents a chimeric antisense oligonucleotide  
CC targeted to human microsomal prostaglandin E2 synthase (mpGS-1). The  
CC human mpGS-1 gene is located on chromosome 9, more specifically to  
CC 9q34.3. The present invention also describes: (1) antisense compounds,  
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding  
CC mpGS-1, which specifically hybridize with the nucleic acid mpGS-1 and  
CC inhibits its expression; (2) a method of inhibiting the expression of  
CC mpGS-1 in cells or tissues; and (3) a method of treating an animal  
CC having a disease or condition associated with mpGS-1. mpGS-1 chimeric  
CC antisense oligonucleotides and antisense compounds have cytostatic,  
CC antidiabetic, immunomodulator, cardiant, neuroprotective,  
CC antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,  
CC ophthalmological, immunomodulatory and cardiovascular activities, and can  
CC be used as mpGS-1 inhibitors and in gene therapy. The antisense compound  
CC can be used for preparing a composition for treating a disease or  
CC condition associated with mpGS-1 e.g., inflammation, Alzheimer's  
CC disease, arthritis, diabetes, cancer, ischemia or reperfusion injury, or  
CC ophthalmic, immunological, cardiovascular or neurological disorder.  
XX  
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;  
SQ  
Query Match 1.1%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 4.4e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 1520 AAAAAAAAAAAGTAA 1537  
Db 20 AAAAAAAAAAAAAAAAAA 3
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RESULT 835
ADM14467/C
ID ADM14467 standard; DNA; 20 BP.
XX
AC ADM14467;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:654.
XX
KW chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin H2 synthase; mPGES-1; mPGES-1 inhibitor;
KW microsomal prostaglandin H2 synthase inhibitor; cytosolic; antidiabetic;
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; neurotrophic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; opththalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX
WO2004028458-A2.
XX
PD 08-APR-2004.
XX
PF 25-SEP-2003; 2003WO-US030374.
XX
PR 25-SEP-2002; 2002US-0413549P.
XX
PA (PHAA ) PHARMACIA CORP.
XX
PI Gierse JK;
XX
DR WPI; 2004-305094/28.
XX
PT New antisense compound, having a sequence targeted to a nucleic acid
PT encoding mPGES-1, useful for preparing a composition for treating e.g.,
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT ischemia.
XX
PS Claim 4; SEQ ID NO 654; 132p; English.
XX
CC The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microsomal prostaglandin H2 synthase (mPGES-1). The
CC human mPGES-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds,
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mPGES-1. mPGES-1 chimeric
CC antisense oligonucleotides and antisense compounds have cytostatic,
CC antidiabetic, immunomodulator, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, neurotropic, antiarthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
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CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC opththalmic, immunological, cardiovascular or neurological disorder.
XX
SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 14.6; DB 1; Length 20;
Best Local Similarity 86.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1520 AAAAAAAAAAGTAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1
XX
RESULT 836
ADM14015/C
ID ADM14015 standard; DNA; 20 BP.
XX
AC ADM14015;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:202.
XX
KW chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin H2 synthase; mPGES-1; mPGES-1 inhibitor;
KW microsomal prostaglandin H2 synthase inhibitor; cytosolic; antidiabetic;
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; neurotrophic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; opththalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX
WO2004028458-A2.
XX
PD 08-APR-2004.
XX
PF 25-SEP-2003; 2003WO-US030374.
XX
PR 25-SEP-2002; 2002US-0413549P.
XX
PA (PHAA ) PHARMACIA CORP.
XX
PI Gierse JK;
XX
DR WPI; 2004-305094/28.
XX
PT New antisense compound, having a sequence targeted to a nucleic acid
PT encoding mPGES-1, useful for preparing a composition for treating e.g.,
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT ischemia.
XX
```

PS Claim 4; SEQ ID NO 202; 132pp; English.
XX
CC The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
CC human mPGES-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mPGES-1. mPGES-1 chimeric
CC antisense oligonucleotides and antisense compounds have cytostatic,
CC antidiabetic, immunomodulatory, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAGTAAA 1537
Db 20 AAAAAAAAAAAAAAAAAA 3
RESULT 837
ADM14021/c
ID ADM14021 standard; DNA; 20 BP.
XX
AC ADM14021;
DT 01-JUL-2004 (first entry)
XX
DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:208.
XX
KW chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW microsomal prostaglandin E2 synthase inhibitor; cytosstatic; antidiabetic;
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT 1..5
FT /*tag= a
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FT /note= "2'-O-methoxyethyls"
FT 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX
XX WO2004028458-A2.
XX
XX 08-APR-2004. PD

XX
PF 25-SEP-2003; 2003WO-US030374.
XX
PR 25-SEP-2002; 2002US-0413549P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Gierse JK;
XX
DR WPI; 2004-305094/28.
XX
PT New antisense compound, having a sequence targeted to a nucleic acid
PT encoding mPGES-1, useful for preparing a composition for treating e.g.,
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT ischaemia.
XX
PS Claim 4; SEQ ID NO 208; 132pp; English.
XX
CC The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
CC human mPGES-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds,
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mPGES-1. mPGES-1 chimeric
CC antisense oligonucleotides and antisense compounds have cytostatic,
CC antidiabetic, immunomodulator, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAGTAAA 1537
Db 20 AAAAAAAAAAAAAAAAAA 3
RESULT 838
ADM14388/c
ID ADM14388 standard; DNA; 20 BP.
XX
AC ADM14388;
DT 01-JUL-2004 (first entry)
XX
DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:575.
XX
KW chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW microsomal prostaglandin E2 synthase inhibitor; cytosstatic; antidiabetic;
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
XX
XX


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FT FT /*tag= b
FT FT /mod_base= OTHER
FT FT /note= "phosphorothioate linkages and all cytidine
FT FT residues are 5-methylcytidines"
FT FT
FT FT modified_base
FT FT 1..5
FT FT /*tag= a
FT FT /mod_base= OTHER
FT FT /note= "2'-O-methoxyethyls"
FT FT 16..20
FT FT /*tag= c
FT FT /mod_base= OTHER
FT FT /note= "2'-O-methoxyethyls"
PN PN WO2004028458-A2.
PD PD 08-APR-2004.
PP PP 25-SEP-2003; 2003WO-US030374.
PR PR 25-SEP-2002; 2002US-0413549P.
PA PA (PHMA ) PHARMACIA CORP.
PI PI Gierse JK;
PX PX WPI; 2004-305094/28.
DR DR
XX XX
XX XX New antisense compound, having a sequence targeted to a nucleic acid
XX XX encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX XX ischemia.
PS PS Claim 4; SEQ ID NO 575; 132pp; English.
XX XX
XX XX The present sequence represents a chimeric antisense oligonucleotide
XX XX targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX XX human mPGES-1 gene is located on chromosome 9, more specifically to
XX XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX XX mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
XX XX inhibits its expression; (2) a method of inhibiting the expression of
XX XX mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX XX having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX XX antisense oligonucleotides and antisense compounds have cytostatic,
XX XX antidiabetic, immunomodulator, cardiant, neuroprotective,
XX XX antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
XX XX CC antiinflammatory, immunomodulatory and cardiovascular activities, and can
XX XX CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
XX XX CC can be used for preparing a composition for treating a disease or
XX XX CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's
XX XX CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
XX XX CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX XX
XX XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
SQ SQ
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAGTAAA 1537
Db 20 AAAAAAAAAAAAAAAAAA 3
RESULT 839
ADM14013/C
ID ADM14013 standard; DNA; 20 BP.
XX
XX ADM14013;
XX
XX 01-JUL-2004 (first entry)
XX
XX Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:200.
```

```
XX XX
XX XX chimeric; antisense oligonucleotide; phosphorothioate; human;
XX XX microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
XX XX microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
XX XX immunomodulator; cardiant; neuroprotective; antiinflammatory;
XX XX neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
XX XX immunomodulatory; cardiovascular; gene therapy; inflammation;
XX XX Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
XX XX reperfusion injury; ophthalmic disorder; immunological disorder;
XX XX cardiovascular disorder; neurological disorder; ss.
XX XX
XX XX Homo sapiens.
OS OS Synthetic.
XX XX
XX XX Key
XX XX modified_base
XX XX 1..20
XX XX /*tag= b
XX XX /mod_base= OTHER
XX XX /note= "phosphorothioate linkages and all cytidine
XX XX residues are 5-methylcytidines"
XX XX 1..5
XX XX /*tag= a
XX XX /mod_base= OTHER
XX XX /note= "2'-O-methoxyethyls"
XX XX 16..20
XX XX /*tag= c
XX XX /mod_base= OTHER
XX XX /note= "2'-O-methoxyethyls"
XX XX
XX XX WO2004028458-A2.
XX XX
XX XX 08-APR-2004.
XX XX
XX XX 25-SEP-2003; 2003WO-US030374.
XX XX
XX XX 25-SEP-2002; 2002US-0413549P.
XX XX
XX XX (PHMA ) PHARMACIA CORP.
XX XX
XX XX Gierse JK;
XX XX WPI; 2004-305094/28.
XX XX
XX XX New antisense compound, having a sequence targeted to a nucleic acid
XX XX encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX XX ischemia.
PS PS Claim 4; SEQ ID NO 200; 132pp; English.
XX XX
XX XX The present sequence represents a chimeric antisense oligonucleotide
XX XX targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX XX human mPGES-1 gene is located on chromosome 9, more specifically to
XX XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX XX mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
XX XX inhibits its expression; (2) a method of inhibiting the expression of
XX XX mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX XX having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX XX antisense oligonucleotides and antisense compounds have cytostatic,
XX XX antidiabetic, immunomodulator, cardiant, neuroprotective,
XX XX antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
XX XX CC antiinflammatory, immunomodulatory and cardiovascular activities, and can
XX XX CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
XX XX CC can be used for preparing a composition for treating a disease or
XX XX CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's
XX XX CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
XX XX CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX XX
XX XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
SQ SQ
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
```

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Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 1520 AAAAAAAAAAAGTAAA 1537
    |||||
Db 20 AAAAAAAAAAAAAAAAAA 3

RESULT 840
ADM14019/c
XX ADM14019 standard; DNA; 20 BP.
XX
XX ADM14019;
XX
XX 01-JUL-2004 (first entry)
XX
XX Human mpGS-1 chimeric antisense oligonucleotide SEQ ID NO:206.
XX
XX chimeric; antisense oligonucleotide; phosphorothioate; human;
XX microsome1 prostaglandin E2 synthase; mpGS-1; mpGS-1 inhibitor;
XX microsome1 prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
XX immunomodulatory; cardiant; neuroprotective; antiinflammatory;
XX neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
XX immunomodulatory; cardiovascular; gene therapy; inflammation;
XX Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
XX reperfusion injury; opthalamic disorder; immunological disorder;
XX cardiovascular disorder; neurological disorder; ss.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX Key
XX Location/Qualifiers
XX modified_base
XX 1..20
XX /tag= b
XX /mod_base= OTHER
XX /note= "phosphorothioate linkages and all cytidine
XX residues are 5-methylcytidines"
XX 1..5
XX /tag= a
XX /mod_base= OTHER
XX /note= "2'-O-methoxyethyls"
XX 16..20
XX /tag= c
XX /mod_base= OTHER
XX /note= "2'-O-methoxyethyls"
XX
XX WO2004028458-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Gierse JK;
XX PI
XX WPI; 2004-305094/28.
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mpGS-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischaemia.
XX
XX Claim 4; SEQ ID NO 206; 132pp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsome1 prostaglandin E2 synthase (mpGS-1). The
XX human mpGS-1 gene is located on chromosome 9, more specifically to
XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX mpGS-1, which specifically hybridize with the nucleic acid mpGS-1 and
XX inhibits its expression; (2) a method of inhibiting the expression of
```

```
CC mpGS-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mpGS-1. mpGS-1 chimeric
CC antisense oligonucleotides and antisense compounds have cytosolic,
CC antidiabetic, immunomodulatory, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mpGS-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mpGS-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC opthalamic, immunological, cardiovascular or neurological disorder.
XX
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 4.4e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 1520 AAAAAAAAAAAGTAAA 1537
    |||||
Db 20 AAAAAAAAAAAAAAAAAA 3

RESULT 841
ADM14087/c
XX ADM14087 standard; DNA; 20 BP.
XX
XX ADM14087;
XX
XX 01-JUL-2004 (first entry)
XX
XX Human mpGS-1 chimeric antisense oligonucleotide SEQ ID NO:274.
XX
XX chimeric; antisense oligonucleotide; phosphorothioate; human;
XX microsome1 prostaglandin E2 synthase; mpGS-1; mpGS-1 inhibitor;
XX microsome1 prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
XX immunomodulatory; cardiant; neuroprotective; antiinflammatory;
XX neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
XX immunomodulatory; cardiovascular; gene therapy; inflammation;
XX Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
XX reperfusion injury; opthalamic disorder; immunological disorder;
XX cardiovascular disorder; neurological disorder; ss.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX Key
XX Location/Qualifiers
XX modified_base
XX 1..20
XX /tag= b
XX /mod_base= OTHER
XX /note= "phosphorothioate linkages and all cytidine
XX residues are 5-methylcytidines"
XX 1..5
XX /tag= a
XX /mod_base= OTHER
XX /note= "2'-O-methoxyethyls"
XX 16..20
XX /tag= c
XX /mod_base= OTHER
XX /note= "2'-O-methoxyethyls"
XX
XX WO2004028458-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Gierse JK;
XX PI
```

```
DR WPI; 2004-305094/28.
XX
PT New antisense compound, having a sequence targeted to a nucleic acid
PT encoding mPGES-1, useful for preparing a composition for treating e.g.,
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT ischemia.
XX
PS Claim 4; SEQ ID NO 274; 132pp; English.
XX
CC The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
CC human mPGES-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds,
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mPGES-1. mPGES-1 chimeric
CC antisense oligonucleotides and antisense compounds have cytostatic,
CC antiinflammatory, neuroprotective, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, neurotropic, antiaarthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAGTAAAG 1537
DB 20 AAAAAAAAAAAAAAAAAA 3
RESULT 842
ADM14300/c
ID ADM14300 standard; DNA; 20 BP.
XX
AC ADM14300;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:487.
XX
KW chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
KW immunomodulatory; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; neurotropic; antiaarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
OS Homo sapiens.
XX
FH Key
FT Location/Qualifiers
FT 1..20
FT /tag= b
FT /mod bases= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT 1..5
FT /*tag= a
FT /mod bases= OTHER
FT /note= "2'-O-methoxyethyls"
FT modified_base
FT 16..20
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PT /*tag= c
FT /mod bases= OTHER
FT /note= "2'-O-methoxyethyls"
XX
XX W02004028458-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Gierse JK;
XX
XX WPI; 2004-305094/28.
XX
PT New antisense compound, having a sequence targeted to a nucleic acid
PT encoding mPGES-1, useful for preparing a composition for treating e.g.,
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT ischemia.
XX
PS Claim 4; SEQ ID NO 487; 132pp; English.
XX
CC The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
CC human mPGES-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds,
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mPGES-1. mPGES-1 chimeric
CC antisense oligonucleotides and antisense compounds have cytostatic,
CC antiinflammatory, immunomodulatory, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, neurotropic, antiaarthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAGTAAAG 1537
DB 20 AAAAAAAAAAAAAAAAAA 3
RESULT 843
ADM13993/c
ID ADM13993 standard; DNA; 20 BP.
XX
AC ADM13993;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:180.
XX
KW chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
KW immunomodulatory; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; neurotropic; antiaarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
```

KW cardiovascular disorder; neurological disorder; ss.
XX Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
PN WO2004028458-A2.
PD 08-APR-2004.
PP 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX
XX (PHAA) PHARMACIA CORP.
XX
XX Gliese UK;
XX
XX WPI; 2004-305094/28.
XX
PT New antisense compound, having a sequence targeted to a nucleic acid
PT encoding mPGES-1, useful for preparing a composition for treating e.g.,
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT ischemia.
XX
XX
PS Claim 4; SEQ ID NO 180; 132pp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX human mPGES-1 gene is located on chromosome 9, more specifically to
XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX mPGES-1, which specifically hybridize with the nucleic acid mPGES-1 and
XX inhibits its expression; (2) a method of inhibiting the expression of
XX mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX antisense oligonucleotides and antisense compounds have cytostatic,
XX antidiabetic, immunomodulatory, cardiant, neuroprotective,
XX antiinflammatory, neuroprotective, nocotropic, antiarthritic, vasotropic,
XX ophthalmological, immunomodulatory and cardiovascular activities, and can
XX be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
XX can be used for preparing a composition for treating a disease or
XX condition associated with mPGES-1 e.g., inflammation, Alzheimer's
XX disease, arthritis, diabetes, cancer, ischemia or reperfusion injury, or
XX ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAGTAA 1537
DB 20 AAAAAAAAAAAAAAAAA 3
RESULT 844
ADM13998/c

ID ADM13998 standard; DNA; 20 BP.
XX
XX AC
XX ADM13998;
XX
XX
XX 01-JUL-2004 (first entry)
DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:185.
XX
XX chimeric; antisense oligonucleotide; phosphorothioate; human;
XX microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
XX microsomal prostaglandin E2 synthase inhibitor; cytostatic; antidiabetic;
XX immunomodulatory; cardiant; neuroprotective; antiinflammatory;
XX neuroprotective; nocotropic; antiarthritic; vasotropic; ophthalmological;
XX immunomodulatory; cardiovascular; gene therapy; inflammation;
XX Alzheimer's disease; arthritis; diabetes; cancer; ischemia;
XX reperfusion injury; ophthalmic disorder; immunological disorder;
XX cardiovascular disorder; neurological disorder; ss.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
PN WO2004028458-A2.
PD 08-APR-2004.
PP 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX
XX (PHAA) PHARMACIA CORP.
XX
XX Gliese UK;
XX
XX WPI; 2004-305094/28.
XX
PT New antisense compound, having a sequence targeted to a nucleic acid
PT encoding mPGES-1, useful for preparing a composition for treating e.g.,
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT ischemia.
XX
XX
PS Claim 4; SEQ ID NO 185; 132pp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX human mPGES-1 gene is located on chromosome 9, more specifically to
XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX mPGES-1, which specifically hybridize with the nucleic acid mPGES-1 and
XX inhibits its expression; (2) a method of inhibiting the expression of
XX mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX antisense oligonucleotides and antisense compounds have cytostatic,
XX antidiabetic, immunomodulatory, cardiant, neuroprotective,
XX antiinflammatory, neuroprotective, nocotropic, antiarthritic, vasotropic,
XX ophthalmological, immunomodulatory and cardiovascular activities, and can
XX be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
XX can be used for preparing a composition for treating a disease or
XX condition associated with mPGES-1 e.g., inflammation, Alzheimer's

CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAGTAAA 1537
Db 20 AAAAAAAAAAAAAAAAAA 3
RESULT 845
ADM14007/C
ID ADM14007 standard; DNA; 20 BP.
XX
AC ADM14007;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human mPGEs-1 chimeric antisense oligonucleotide SEQ ID NO:194.
XX
KW chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase inhibitor; cyclostatic; antidiabetic;
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; nocotropic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FT Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX
PN WO2004028458-A2.
XX
PD 08-APR-2004.
XX
PF 25-SEP-2003; 2003WO-US030374.
XX
PR 25-SEP-2002; 2002US-0413549P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Glaxo JK;
XX
DR WP1; 2004-305094/28.
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
PT encoding mPGEs-1, useful for preparing a composition for treating e.g.,
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT ischaemia.
XX
PS Claim 4; SEQ ID NO 194; 132pp; English.
XX

CC The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microsomal prostaglandin E2 synthase (mPGEs-1). The
CC human mPGEs-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds;
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mPGEs-1, which specifically hybridise with the nucleic acid mPGEs-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mPGEs-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mPGEs-1. mPGEs-1 chimeric
CC antisense oligonucleotides and antisense compounds have cyclostatic,
CC antidiabetic, immunomodulator, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, nocotropic, antiarthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mPGEs-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGEs-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAGTAAA 1537
Db 20 AAAAAAAAAAAAAAAAAA 3
RESULT 846
ADM14124/C
ID ADM14124 standard; DNA; 20 BP.
XX
AC ADM14124;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human mPGEs-1 chimeric antisense oligonucleotide SEQ ID NO:311.
XX
KW chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase; mPGEs-1 inhibitor;
KW microsomal prostaglandin E2 synthase inhibitor; cyclostatic; antidiabetic;
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; nocotropic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FT Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX
PN WO2004028458-A2.
XX
PD 08-APR-2004.
XX
PF 25-SEP-2003; 2003WO-US030374.
XX

```
XX 25-SEP-2002; 2002US-0413549P.
XX (PHAA ) PHARMACIA CORP.
XX
XX Gliese JK;
XX
XX WPI; 2004-305094/28.
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischemia.
XX
XX Claim 4; SEQ ID NO 311; 132bp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX human mPGES-1 gene is located on chromosome 9, more specifically to
XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX mPGES-1, which specifically hybridize with the nucleic acid mPGES-1 and
XX inhibits its expression; (2) a method of inhibiting the expression of
XX mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX antisense oligonucleotides and antisense compounds have cytostatic,
XX antidiabetic, immunomodulatory, cardiant, neuroprotective,
XX antiinflammatory, neuroprotective, neurotropic, antiarthritic, vasotropic,
XX ophthalmological, immunomodulatory and cardiovascular activities, and can
XX be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
XX can be used for preparing a composition for treating a disease or
XX condition associated with mPGES-1 e.g., inflammation, Alzheimer's
XX disease, arthritis, diabetes, cancer, ischemia or reperfusion injury, or
XX ophthalmic, immunological, cardiovascular or neurological disorder.
XX
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 4.4e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1520 AAAAAAAAAAGTAAAA 1537
XX ||||||||| |||
XX 20 AAAAAAAAAAAAAAAAAA 3
XX
XX RESULT 847
XX ADM14216/C
XX ID ADM14216 standard; DNA; 20 BP.
XX
XX ADM14216;
XX
XX 01-JUL-2004 (first entry)
XX
XX Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:403.
XX
XX chimeric; antisense oligonucleotide; phosphorothioate; human;
XX microsomal prostaglandin E2 synthase; mPGES-1; inhibitor;
XX immunomodulatory; cardiant; neuroprotective; antiinflammatory;
XX neurotropic; nootropic; antiarthritic; vasotropic; ophthalmological;
XX immunomodulatory; cardiovascular; gene therapy; inflammation;
XX Alzheimer's disease; arthritis; diabetes; cancer; ischemia;
XX reperfusion injury; ophthalmic disorder; immunological disorder;
XX cardiovascular disorder; neurological disorder; ss.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX Key location/Qualifiers
XX modified_base 1..20
XX /*tag= b
XX /mod_base= OTHER
XX
XX FT
```

```
FT /note="phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT FT
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT FT
XX /note="2'-O-methoxyethyls"
XX /note="2'-O-methoxyethyls"
XX
XX NO2004028458-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Gliese JK;
XX
XX WPI; 2004-305094/28.
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischemia.
XX
XX Claim 4; SEQ ID NO 403; 132bp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX human mPGES-1 gene is located on chromosome 9, more specifically to
XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX mPGES-1, which specifically hybridize with the nucleic acid mPGES-1 and
XX inhibits its expression; (2) a method of inhibiting the expression of
XX mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX antisense oligonucleotides and antisense compounds have cytostatic,
XX antidiabetic, immunomodulatory, cardiant, neuroprotective,
XX antiinflammatory, neuroprotective, neurotropic, antiarthritic, vasotropic,
XX ophthalmological, immunomodulatory and cardiovascular activities, and can
XX be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
XX can be used for preparing a composition for treating a disease or
XX condition associated with mPGES-1 e.g., inflammation, Alzheimer's
XX disease, arthritis, diabetes, cancer, ischemia or reperfusion injury, or
XX ophthalmic, immunological, cardiovascular or neurological disorder.
XX
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 4.4e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1520 AAAAAAAAAAGTAAAA 1537
XX ||||||||| |||
XX 20 AAAAAAAAAAAAAAAAAA 3
XX
XX RESULT 848
XX ADO46424/C
XX ID ADO46424 standard; DNA; 20 BP.
XX
XX ADO46424;
XX
XX 15-JUL-2004 (first entry)
XX
XX Human oligonucleotide #1790.
XX
XX Human; ss; interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5;
XX
XX FT
```

KW CCRI1, CCR3; Botaxin-1; RANTES, MCP4, CD23; ICAM; VCAM; tryptase a;
KW tryptase b; PDE4 A; PDE4 B; PDE4 C; PDE4 D; respiratory disease;
KW lung disease; hyper-responsiveness; adenosine; adenosine A receptor;
KW asthma; lung allergy; inflammation; inflammatory disease;
KW airway inflammation; allergy; impeded respiration; cystic fibrosis; CF;
KW chronic obstructive pulmonary disease; COPD; allergic rhinitis;
KW acute respiratory distress syndrome; pulmonary hypertension;
KW lung inflammation; bronchitis; airway obstruction; bronchoconstriction.
XX Homo sapiens.
XX US2004049022-A1.
XX 11-MAR-2004.
XX 25-JUL-2003; 2003US-00627930.
XX 23-APR-2002; 2002WO-US013135.
XX 23-APR-2002; 2002WO-US013143.
XX (NYCE/) NYCE J W.
XX (SAND/) SANDRASAGRA A.
XX (TANG/) TANG L.
XX (AGUI/) AGUILAR D.
XX (MILL/) MILLER S.
XX (SHAH/) SHAHABUDDIN S.
XX (LJHH/) LI H.
XX (CONG/) CONG H.
XX NYCE JW, Sandrasagra A, Tang L, Aguilar D, Miller S;
XX Shahabuddin S, Lu H, Cong H;
XX WPI; 2004-293804/27.
XX Novel single or multiple target oligonucleotide anti-sense to e.g.
XX initiation codon, intron of respiratory disease-relevant gene e.g. CCR1,
XX RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g.
XX asthma.
XX Claim 2; SEQ ID NO 1791; 174bp; English.
XX The invention relates to oligonucleotides anti-sense to an initiation
XX codon, coding region, 5' or 3' intron-exon junction, intron or region
XX with 2-10 nucleotides of the 5'-end or 3'-end of a nucleic acid target
XX chosen from a gene encoding interleukin (IL)-4 receptor, interleukin (IL)
XX -5 receptor, CCR1, CCR3, Botaxin-1, RANTES, MCP4, CD23, ICAM, VCAM,
XX tryptase a, tryptase b, PDE4 A, PDE4 B, PDE4 C or PDE4 D. The invention
XX also relates to a method of screening a candidate compound that binds to
XX one or more nucleic acid target(s) or expressed product(s), for the
XX prevention and/or treatment of a respiratory or lung disease. The
XX oligonucleotides are useful for reducing or inhibiting expression of a
XX gene or mRNA encoding interleukin-4 receptor, interleukin-5 receptor,
XX CCR1, CCR3, Botaxin-1, RANTES, MCP4, CD23, ICAM, VCAM, tryptase a,
XX tryptase b, PDE4 A, PDE4 B, PDE4 C, or PDE4 D. The oligonucleotides are
XX useful for preventing or treating a respiratory or lung disease. The
XX respiratory or lung disease is associated with hyper-responsiveness to
XX and/or increased levels of, adenosine and/or levels of adenosine A
XX receptor(s), and/or asthma and/or lung allergies associated with
XX inflammation or an inflammatory disease. The respiratory or lung disease
XX is chosen from airway inflammation, allergy, asthma, impeded respiration,
XX cystic fibrosis (CF), chronic obstructive pulmonary disease (COPD),
XX allergic rhinitis, acute respiratory distress syndrome, pulmonary
XX hypertension, lung inflammation, bronchitis, airway obstruction or
XX bronchoconstriction. This sequence represents an oligonucleotide of the
XX invention.
XX Sequence 20 BP; 0 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537

DB 19 AAAAAAAAAAAAAAAAAA 2
RESULT 849
AD003711
ID AD003711 standard; DNA; 20 BP.
AC AD003711;
XX 29-JUL-2004 (first entry)
XX SERS-based analyte detection oligonucleotide seqid 31.
XX Raman label; specific binding member; surface-enhanced Raman scattering;
XX SERS; 88.
XX Synthetic.
XX US2004086897-A1.
XX 06-MAY-2004.
XX 07-MAY-2003; 2003US-00431341.
XX 07-MAY-2002; 2002US-0378538P.
XX 28-MAY-2002; 2002US-0383630P.
XX 14-JUN-2002; 2002US-00172428.
XX (MIRK/) MIRKIN C A.
XX (CAOY/) CAO Y.
XX (JINR/) JIN R.
XX Mirkin CA, Cao Y, Jin R;
XX WPI; 2004-418413/39.
XX Reagent, useful for detecting target analyte e.g., nucleic acid,
XX comprising particle having bound to at least one Raman label, which can
XX be activated to provide surface-enhanced Raman scattering effect, and
XX specific binding member.
XX Disclosure; SEQ ID NO 31; 55bp; English.
XX The invention describes a reagent (I) comprising a particle bound to at
XX least one Raman label and a specific binding member, where the Raman
XX label can be activated to provide a surface-enhanced Raman scattering
XX (SERS) effect or comprising a specific binding member having two or more
XX different Raman labels bound to it. Also described are: a test kit (II),
XX comprising (I) in one container and a silver, gold or copper Raman
XX enhancer stain in another container; and a fibre optic detection device
XX (III), having a bundle of optical fibres terminating with ends of the
XX optical fibre, where a several of the optical fibres have (I) located at
XX the ends of the optical fibre. (I) is useful for: detecting for the
XX presence or absence of one or more target analytes in a sample, the
XX target analytes having at least two binding sites; detecting the presence
XX or absence of one or more target nucleic acid in a sample, the sequence
XX of the nucleic acid having at least two portions; and for screening one
XX or more molecules to determine whether the molecule is a ligand to one or
XX more specific receptors. This sequence represents an oligonucleotide
XX associated with the SERS-based detection analyte detection method.
XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
DB 1 AAAAAAAAAAAAAAAAAA 18

```

RESULT 850
ADP78301/c
XX ADP78301 standard; DNA; 20 BP.
XX
AC ADP78301;
XX
DT 12-AUG-2004 (first entry)
XX
DE Chimeric phosphorothioate oligonucleotide #2100.
XX
KM GFAT; Antidiabetic; Cardiant;
XX Glutamine-fructose-6-phosphate amidotransferase; diabetes; ischemia;
XX repertusion; ss.
XX
OS Synthetic.
XX
FT Key
FT modified_base 1..4 Location/Qualifiers
FT /+tag= a
FT /mod_base= other
FT /note= "2-methoxyethyl wing"
FT modified_base 17..20
FT /+tag= b
FT /mod_base= other
FT /note= "2-methoxyethyl wing"
XX
XX WO2004035763-A2.
XX
PD 29-APR-2004.
XX
PF 02-OCT-2003; 2003WO-US033332.
XX
XX 17-OCT-2002; 2002US-0419268P.
XX
PA (PHAA ) PHARMACIA CORP.
XX
PI Broeschat KO, Crosby SD;
XX
DR WPI; 2004-348453/32.
XX
XX
XX New compounds, particularly antisense oligonucleotides targeted to a
XX nucleic acid encoding glutamine-fructose-6-phosphate amidotransferase
XX (GFAT), for treating diabetes, a cardiovascular or neurologic disorder,
XX ischemia/repertusion injury.
XX
XX Claim 4; SEQ ID NO 2100; 175pp; English.
XX
XX The present invention relates to a compound which specifically hybridizes
XX with a nucleic acid molecule encoding GFAT, and inhibits the expression
XX of GFAT. Specifically claimed are antisense oligonucleotides capable of
XX modulating the expression of GFAT, and which comprise any of the 3063
XX sequences of 20 base pairs, given in the specification. The compound,
XX composition and methods are useful for treating a disease or condition
XX associated with GFAT, such as a disease or condition, e.g. diabetes, a
XX cardiovascular or neurological disorder, ischemia/repertusion injury.
XX They are also useful in research and diagnostics for modulating the
XX expression of GFAT. The present sequence represents a chimeric
XX phosphorothioate oligonucleotide with 2'-MOB wings and a deoxy gap, these
XX oligonucleotides inhibit human GFAT expression.
XX
SQ Sequence 20 BP; 11 A; 1 C; 2 G; 6 T; 0 U; 0 Other;

```

```

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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```

QY 1252 TTTTGTGTTTAAATCAGA 1269
XX |||||
XX 20 TTTGTGTTTAAATCAAA 3

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RESULT 851
ADP10746

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```

ID ADP10746 standard; DNA; 20 BP.
XX
AC ADP10746;
XX
DT 12-AUG-2004 (first entry)
XX
DE Set 1 left PCR primer for marker probe #91.
XX
XX transplant rejection; immune system; rheumatoid arthritis; lupus;
XX inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss; primer.
XX
OS Homo sapiens.
XX
XX WO2004042346-A2.
XX
PD 21-MAY-2004.
XX
PF 24-APR-2003; 2003WO-US012946.
XX
XX 24-APR-2002; 2002US-00131831.
XX 20-DEC-2002; 2002US-00325899.
XX
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
XX
PI Mehlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
PI Rosenberg S;
XX
DR WPI; 2004-400724/37.
XX
XX
XX Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
XX pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
XX rejection, in an individual, comprises detecting the expression level of
XX the genes.
XX
XX Claim 58; SEQ ID NO 755; 1762pp; English.
XX
XX
XX The present invention relates to diagnosing or monitoring transplant
XX rejection, e.g. cardiac or kidney transplant rejection, in an individual
XX comprising detecting the expression level of one or more genes. The
XX methods, system and kits are useful in diagnosing or monitoring
XX transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
XX islet, lung, bone marrow or stem cell transplant rejection.
XX xenotransplant rejection or mechanical organ replacement rejection, in an
XX individual. The method is also useful in assessing the immune status of
XX an individual. The methods are also useful in diagnosing and monitoring
XX diseases that involve the immune system, e.g. rheumatoid arthritis,
XX lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
XX viral, bacterial or fungal infection. The present sequence represents a
XX primer for a 50 mer oligonucleotide marker for diagnosis and monitoring
XX of allograft rejection and other disorders.
XX
SQ Sequence 20 BP; 0 A; 3 C; 8 G; 9 T; 0 U; 0 Other;

```

```

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 545 TGTGTGCTGTGTGCGTG 562
XX |||||
XX 1 TGTGTGCTGTGTGCGTG 18

```

```

RESULT 852
ADP20152
ID ADP20152 standard; DNA; 20 BP.
XX
AC ADP20152;
XX
DT 26-AUG-2004 (first entry)
XX
DE Nucleic acid detection method linking oligonucleotide #66.
XX
XX Nucleic acid detection; nanoparticle-oligonucleotide conjugate;
XX
XX

```



```
KW genetic disease; bacterial infection; viral infection; forensic;
KW DNA sequencing; paternity testing; linking oligonucleotide; ss.
XX
OS Synthetic.
XX
PN US2004110220-A1.
XX
PD 10-JUN-2004.
XX
PF 18-NOV-2003; 2003US-00716829.
XX
PR 29-JUL-1996; 96US-0031809P.
PR 21-JUL-1997; 97WO-US012783.
PR 29-JAN-1999; 99US-00240755.
PR 25-JUN-1999; 99US-00344667.
PR 13-JAN-2000; 2000US-0176409P.
PR 26-APR-2000; 2000US-0200161P.
PR 26-JUN-2000; 2000US-00603830.
PR 26-JUN-2000; 2000US-0213906P.
PR 12-JAN-2001; 2001US-00760500.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI Mitkin CA, Letsinger RL, Mucic RC, Storchhoff JJ, Elghamian R;
PI Tacon TA, Garimella V, Li Z;
XX
DR WPI; 2004-440357/41.
XX
PT Nanoparticles useful for detection and separation of nucleic acids e.g.
PT genes associated with disease, in a diagnostic assay, comprise several
PT oligonucleotides attached to them.
XX
PS Example 24; SEQ ID NO 70; 142pp; English.
XX
CC The invention relates to a method of detecting a nucleic acid with at
CC least two portions by providing a type of nanoparticle-oligonucleotide
CC conjugate, contacting the nucleic acid and nanoparticles to allow
CC hybridisation of the oligonucleotides with the two or more portions of
CC the nucleic acid and observing a detectable change brought about by
CC hybridisation. The oligonucleotides have a sequence complementary to the
CC sequence of at least two portions of the nucleic acid. Hybridisation of
CC the oligonucleotides on the nanoparticles with the nucleic acid results
CC in a detectable change. The method is used for detection and separation
CC of nucleic acids (e.g. viral DNA, a gene associated with a disease,
CC bacterial DNA, fungal DNA, synthetic DNA, structurally-modified DNA, DNA
CC from biological sources or PCR products) for diagnosis of various
CC diseases (such as genetic diseases, bacterial infections and viral
CC infections) and for forensics, DNA sequencing, paternity testing and
CC monitoring gene therapy. This sequence represents a linking
CC oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAGTAAA 1537
DB 1 AAAAAAAAAAAAAAAAAA 18
RESULT 853
ADP20137
ID ADP20137 standard; DNA; 20 BP.
XX
AC ADP20137;
XX
DT 26-AUG-2004 (first entry)
DE Nucleic acid detection method linking oligonucleotide #54.
XX
KW Nucleic acid detection; nanoparticle-oligonucleotide conjugate;
```

```
KW genetic disease; bacterial infection; viral infection; forensic;
KW DNA sequencing; paternity testing; linking oligonucleotide; ss.
XX
OS Synthetic.
XX
PN US2004110220-A1.
XX
PD 10-JUN-2004.
XX
PF 18-NOV-2003; 2003US-00716829.
XX
PR 29-JUL-1996; 96US-0031809P.
PR 21-JUL-1997; 97WO-US012783.
PR 29-JAN-1999; 99US-00240755.
PR 25-JUN-1999; 99US-00344667.
PR 13-JAN-2000; 2000US-0176409P.
PR 26-APR-2000; 2000US-0200161P.
PR 26-JUN-2000; 2000US-00603830.
PR 26-JUN-2000; 2000US-0213906P.
PR 12-JAN-2001; 2001US-00760500.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI Mitkin CA, Letsinger RL, Mucic RC, Storchhoff JJ, Elghamian R;
PI Tacon TA, Garimella V, Li Z;
XX
DR WPI; 2004-440357/41.
XX
PT Nanoparticles useful for detection and separation of nucleic acids e.g.
PT genes associated with disease, in a diagnostic assay, comprise several
PT oligonucleotides attached to them.
XX
PS Example 18; SEQ ID NO 55; 142pp; English.
XX
CC The invention relates to a method of detecting a nucleic acid with at
CC least two portions by providing a type of nanoparticle-oligonucleotide
CC conjugate, contacting the nucleic acid and nanoparticles to allow
CC hybridisation of the oligonucleotides with the two or more portions of
CC the nucleic acid and observing a detectable change brought about by
CC hybridisation. The oligonucleotides have a sequence complementary to the
CC sequence of at least two portions of the nucleic acid. Hybridisation of
CC the oligonucleotides on the nanoparticles with the nucleic acid results
CC in a detectable change. The method is used for detection and separation
CC of nucleic acids (e.g. viral DNA, a gene associated with a disease,
CC bacterial DNA, fungal DNA, synthetic DNA, structurally-modified DNA, DNA
CC from biological sources or PCR products) for diagnosis of various
CC diseases (such as genetic diseases, bacterial infections and viral
CC infections) and for forensics, DNA sequencing, paternity testing and
CC monitoring gene therapy. This sequence represents a linking
CC oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAGTAAA 1537
DB 1 AAAAAAAAAAAAAAAAAA 18
RESULT 854
ADP69379/C
ID ADP69379 standard; DNA; 20 BP.
XX
AC ADP69379;
XX
DT 09-SEP-2004 (first entry)
DE Human mltONEBT-specific antisense oligonucleotide #273.
XX
KW human; antisense oligonucleotide; mitochondrial membrane;
```

```
KM insulin sensitizing antidiabetic thiazolidinediones; mitonERT; diabetes;
KM immunological disorder; cardiovascular disorder; including hypertension;
KM neurological disorders; ischaemia; reperfusion; ss;
KM 2'-methoxyethyl gapmer; 2'-MOE gapmer; phosphorothioate backbone.
OS Homo sapiens.
XX
XX WO2004053060-A2.
XX
XX 24-JUN-2004.
XX
XX 25-NOV-2003; 2003WO-US037621.
XX
XX 06-DEC-2002; 2002US-0431529P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Colca JR;
XX
XX WPI; 2004-468836/44.
XX
XX New antisense oligonucleotides encoding mitonERT, useful for modulating
PT mitonERT expression or for treating diseases associated with mitonERT,
PT e.g. diabetes, immunological disorders or cardiovascular disorders.
XX
XX Claim 4; SEQ ID NO 273; 226pp; English.
XX
XX The invention comprises antisense oligonucleotides that are targeted to
CC the nucleic acids encoding a family of human proteins from mitochondrial
CC membranes, which bind insulin sensitizing, antidiabetic
CC thiazolidinediones (referred to as: mitonERT). The antisense
CC oligonucleotides of the invention are useful for modulating mitonERT
CC expression and for treating diseases or conditions associated with
CC mitonERT, such as: diabetes, immunological disorders, cardiovascular
CC disorders including hypertension, neurological disorders, and
CC ischaemia/reperfusion injuries. The present DNA sequence represents a
CC mitonERT-specific antisense oligonucleotide of the invention. NOTE: The
CC present sequence is a 2'-methoxyethyl (2'-MOE) gapmer with a
CC phosphorothioate backbone.
XX
XX Sequence 20 BP; 3 A; 0 C; 1 G; 16 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1514 TTAATTAAAAAAA 1531
Db 19 TTAACAACAAAAAAA 2
RESULT 855
ADP69506/C
ID ADP69506 standard; DNA; 20 BP.
XX
XX ADP69506;
XX
XX 09-SEP-2004 (first entry)
XX
XX Human mitonERT-specific antisense oligonucleotide #400.
XX
XX human; antisense oligonucleotide; mitochondrial membrane;
XX insulin sensitizing antidiabetic thiazolidinediones; mitonERT; diabetes;
XX immunological disorder; cardiovascular disorder; including hypertension;
XX neurological disorders; ischaemia; reperfusion; ss;
XX 2'-methoxyethyl gapmer; 2'-MOE gapmer; phosphorothioate backbone.
OS Homo sapiens.
XX
XX WO2004053060-A2.
XX
XX 24-JUN-2004.
XX
```

```
PF 25-NOV-2003; 2003WO-US037621.
XX
XX 06-DEC-2002; 2002US-0431529P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Colca JR;
XX
XX WPI; 2004-468836/44.
XX
XX New antisense oligonucleotides encoding mitonERT, useful for modulating
PT mitonERT expression or for treating diseases associated with mitonERT,
PT e.g. diabetes, immunological disorders or cardiovascular disorders.
XX
XX Claim 4; SEQ ID NO 400; 226pp; English.
XX
XX The invention comprises antisense oligonucleotides that are targeted to
CC the nucleic acids encoding a family of human proteins from mitochondrial
CC membranes, which bind insulin sensitizing, antidiabetic
CC thiazolidinediones (referred to as: mitonERT). The antisense
CC oligonucleotides of the invention are useful for modulating mitonERT
CC expression and for treating diseases or conditions associated with
CC mitonERT, such as: diabetes, immunological disorders, cardiovascular
CC disorders including hypertension, neurological disorders, and
CC ischaemia/reperfusion injuries. The present DNA sequence represents a
CC mitonERT-specific antisense oligonucleotide of the invention. NOTE: The
CC present sequence is a 2'-methoxyethyl (2'-MOE) gapmer with a
CC phosphorothioate backbone.
XX
XX Sequence 20 BP; 3 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1514 TTAATTAAAAAAA 1531
Db 18 TTAACAACAAAAAAA 1
RESULT 856
ADQ80728/C
ID ADQ80728 standard; DNA; 20 BP.
XX
XX ADQ80728;
XX
XX 23-SEP-2004 (first entry)
XX
XX Porcine TSSCS intron 1 DN-primer.
XX
XX Anorectic; Antidiabetic; Muscular; Gene Therapy; Cpg island;
XX IGF2 gene intron 3; muscle mass; fat deposition; test number; obesity;
XX muscle deficiency; diabetes; PCR; primer; ss; pig.
XX
XX Sus scrofa.
XX
XX EP1437418-A1.
XX
XX 14-JUL-2004.
XX
XX 10-JAN-2003; 2003EP-00075091.
XX
XX 10-JAN-2003; 2003EP-00075091.
XX
XX (UYLT-) UNIV LIEGE.
XX (MELI-) MELICA HB.
XX (GENT-) GENTEC BV.
XX
XX Andersson L, Andersson G, Georges M, Buys N;
XX
XX WPI; 2004-501307/48.
XX
XX Selecting an animal for desired genotypic or potential phenotypic
PT
```


RESULT 858
ADP99302/c
ADP99302 standard; DNA; 20 BP.
AC ADP99302;
XX
DT 23-SEP-2004 (first entry)
XX
DE Stem cell factor, SCF, universal PCR primer #2.
XX
KM SCF, stem cell factor; gene therapy: haematopoietic progenitor cell;
KM aplastic anaemia; paroxysmal nocturnal haemoglobinuria; myelofibrosis;
KM myelodysplasia; osteopetrosis; metastatic carcinoma; acute leukaemia;
KM multiple myeloma; Hodgkin's disease; lymphoma; Gaucher's disease;
KM Niemann-Pick disease; Letterer-Siwe disease;
KM refractory erythroidlastic anaemia; Di Guglielmo syndrome;
KM congestive splenomegaly; Kala awar; sarcoidosis;
KM primary splenic pancytopenia; miliary tuberculosis;
KM disseminated fungus disease; fulminating septicæmia; malaria;
KM vitamin B12 deficiency; folate deficiency; pyridoxine deficiency;
KM Diamond Blackfan anaemia; hypopigmentation disorder; plebaldism;
KM vitiligo; neurological damage; infertility; intestinal damage;
KM irradiation; chemotherapy; AIDS; haematopoietic recovery;
KM acute blood loss; neoplasm; cancer; ss; PCR; primer.
XX
XX Mammalia.
XX OS
XX US6759215-B1.
XX PN
XX 06-JUL-2004.
XX PD
XX PF 07-AUG-2000; 2000US-00635251.
XX
XX 16-OCT-1989; 89US-00422383.
XX PR 11-JUN-1990; 90US-00537198.
XX PR 24-AUG-1990; 90US-00573616.
XX PR 01-OCT-1990; 90US-00589701.
XX PR 10-APR-1991; 91US-00684535.
XX PR 25-NOV-1992; 92US-00982255.
XX PR 21-DEC-1993; 93US-00172329.
XX PR 24-MAY-1995; 95US-00449182.
XX
XX (AMGE-) AMGEN INC.
XX PA
XX Zebo XM, Boseelman RA, Suggs SV, Martin FH;
XX PI
XX WPI; 2004-497128/47.
XX
XX PT Preparing a human stem cell factor (SCF) polypeptide, useful for treating
XX PT hematopoietic disorders, e.g., aplastic anemia, comprises growing host
XX PT cells transfected or transfected with DNA encoding a human SCF.
XX
XX Example 3; SEQ ID NO 32; 210pp; English.

CC of protein synthesis, in genetic therapy in humans and other mammals, and
CC in developing transgenic mammalian species which may serve as eukaryotic
CC hosts for production of SCF and SCF products in quantity. The SCF is
CC useful for treating haematopoietic disorders, e.g., aplastic anaemia,
CC paroxysmal nocturnal haemoglobinuria, myelofibrosis, myelocleorosis,
CC osteopetrosis, metastatic carcinoma, acute leukaemia, multiple myeloma,
CC Hodgkin's disease, lymphoma, Gaucher's disease, Niemann-Pick disease,
CC Letterer-Siwe disease, refractory erythroidlastic anaemia, Di Guglielmo
CC syndrome, congestive splenomegaly, Kala awar, sarcoidosis, primary
CC splenic pancytopenia, miliary tuberculosis, disseminated fungus disease,
CC fulminating septicæmia, malaria, vitamin B 12 and folate deficiency,
CC pyridoxine deficiency, Diamond Blackfan anaemia, and hypopigmentation
CC disorders such as plebaldism and vitiligo. The SCF are also useful for
CC treating neurological damage, infertility states, intestinal damage
CC resulting from irradiation or chemotherapy, and AIDS. SCF is also useful
CC for enhancing haematopoietic recovery after acute blood loss and as a
CC boost to the immune system for fighting neoplasia (cancer). The present
CC sequence is a universal SCF PCR primer used in the isolation of SCF DNA.
XX
XX Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAAGTAAA 1537
DB 18 AAAAAAAAAAAAAAAAAA 1
RESULT 859
AAQ75707/c
ID AAQ75707 standard; DNA; 21 BP.
XX
XX AC AAQ75707;
XX
XX DT 04-AUG-1995 (first entry)
XX
XX DE Reverse transcription primer used in cDNA analysis technique.
XX
XX KM Analysis; gene expression: reverse transcription; primer; cDNA;
XX KM aggregate; restriction enzyme; ss.
XX
XX OS Synthetic.
XX OS
XX JP06303997-A.
XX PN
XX 01-NOV-1994.
XX PD
XX 16-APR-1993; 93JP-00112515.
XX PF
XX 16-APR-1993; 93JP-00112515.
XX PR
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX PA
XX WPI; 1995-018287/03.
XX DR
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PT
XX PS Disclosure; Page 7; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESCO files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 4.2e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1519 TAAAAAAAAGTAAA 1536
 |||||
 DB 18 TAAAAAAAAGTAAA 1

RESULT 860

AAQ33789
 ID AAQ33789 standard; DNA; 21 BP.

XX AAQ33789;

XX 25-MAR-2003 (revised)

DT 02-FEB-1993 (first entry)

XX Microsatellite sequence from clone TGLA2.

XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;

XX genetic mapping; trait; amplification; ss.

XX Boe taurus.

XX MO9213102-A1.

XX 06-AUG-1992.

XX 15-JAN-1992; 92WO-US000340.

XX 15-JAN-1991; 91US-00642342.

XX (GENM-) GENMARK.

XX Georges M. Massey JM;

XX WPI; 1992-284684/34.

XX Polymorphic bovine DNA markers - used in genetic identification, gene

XX mapping, and selective breeding.

XX Table 7; Page 245; 517pp; English.

XX The sequence is that of a bovine microsatellite sequence obtd. by

XX screening a library of bovine MboI DNA fragments of between 250 and 500

XX bp with an (AC)₁₅ and a (TC)₁₅ oligonucleotide probe. One out of 50

XX clones cross-hybridised. Assuming independent distribution of

XX microsatellites and MboI sites, the frequency of (T6)_n > 9 microsatellites

XX in the bovine genome is estimated at >100, 000. The sequence information

XX for ca. 230 such bovine microsatellites is summarised in the

XX specification and indexed herein (see below). The sequences upstream and

XX downstream of the microsatellite sequence were used to generate the

XX required PCR primers for in vitro amplification of the corresp.

XX microsatellite (using the program OPTIPRIM). The microsatellites may be

XX used to identify individuals, for parentage testing, and in the genetic

XX mapping of economic trait loci, or genes involved the determinism of

XX economically important traits esp. in cattle, to allow selective

XX breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN

XX field.)

XX Sequence 21 BP; 0 A; 1 C; 10 G; 10 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 21;

Best Local Similarity 88.9%; Pred. No. 4.2e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 545 TGTGGTCCGTGCTGCTG 562

DB 3 TGTGTGCTGCTGCTG 20

RESULT 861

AAQ75702/C
 ID AAQ75702 standard; DNA; 21 BP.

XX AAQ75702;

XX 04-AUG-1995 (first entry)

XX Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;

XX aggregate; restriction enzyme; ss.

XX Synthetic.

XX JP06303997-A.

XX 01-NOV-1994.

XX 16-APR-1993; 93JP-00112515.

XX 16-APR-1993; 93JP-00112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed

XX by digestion with restriction enzymes.

XX Disclosure; Page 7; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of

XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of

XX labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)

XX and using the aggregate of mRNAs as the template for each reverse

XX transcription primer; (b) digesting each of the prepared aggregates of

XX the double-stranded cDNAs with restriction enzyme and; (c)

XX electrophoresing the digested aggregate of cDNAs in separate lanes. The

XX method can be used to analyse gene expression rapidly and easily

XX Sequence 21 BP; 1 A; 3 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 21;

Best Local Similarity 88.9%; Pred. No. 4.2e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1519 TAAAAAAAAGTAAA 1536

DB 18 TAAAAAAAAGTAAA 1

AAQ75671/C

AAQ75671 standard; DNA; 21 BP.

AAQ75671;

04-AUG-1995 (first entry)

Reverse transcription primer used in cDNA analysis technique.

Analysis; gene expression; reverse transcription; primer; cDNA;

aggregate; restriction enzyme; ss.

Synthetic.

JP06303997-A.

01-NOV-1994.

16-APR-1993; 93JP-00112515.

16-APR-1993; 93JP-00112515.

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XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
PA WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESBQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1519 TAAAAAAAAAAAGTAAA 1536
DB 18 TAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 863
XX AAQ75675/c
XX ID AAQ75675 standard; DNA; 21 BP.
XX
XX AAQ75675;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESBQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
SQ

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XX Query Match 1.1%; Score 14.8; DB 1; Length 21;
XX Best Local Similarity 88.9%; Pred. No. 4.2e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1519 TAAAAAAAAAAAGTAAA 1536
DB 18 TAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 864
XX AAQ75674/c
XX ID AAQ75674 standard; DNA; 21 BP.
XX
XX AAQ75674;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESBQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1519 TAAAAAAAAAAAGTAAA 1536
DB 18 TAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 865
XX AAQ75687/c
XX ID AAQ75687 standard; DNA; 21 BP.
XX
XX AAQ75687;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX

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XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 7; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 21;
XX Best Local Similarity 88.9%; Pred. No. 4.2e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1519 TAAAAAAAAAAGTAAA 1536
Db 18 TAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 866
XX AAQ75718/c
XX ID AAQ75718 standard; DNA; 21 BP.
XX AC AAQ75718;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 8; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
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CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 21;
XX Best Local Similarity 88.9%; Pred. No. 4.2e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1519 TAAAAAAAAAAGTAAA 1536
Db 18 TAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 867
XX AAQ75690/c
XX ID AAQ75690 standard; DNA; 21 BP.
XX AC AAQ75690;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 7; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 21;
XX Best Local Similarity 88.9%; Pred. No. 4.2e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1519 TAAAAAAAAAAGTAAA 1536
Db 18 TAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 868
XX AAQ75678/c
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ID AAQ75678 standard; DNA; 21 BP.
XX
XX AAQ75678;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KM Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESBQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily.
XX
XX Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1519 TAAAAAAAAGTAAA 1536
DB 18 TAAAAAAAAGTAAA 1
RESULT 869
AAQ75688/c
ID AAQ75688 standard; DNA; 21 BP.
XX
XX AAQ75688;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX

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PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESBQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily.
XX
XX Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1519 TAAAAAAAAGTAAA 1536
DB 18 TAAAAAAAAGTAAA 1
RESULT 870
AAQ75715/c
ID AAQ75715 standard; DNA; 21 BP.
XX
XX AAQ75715;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 8; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESBQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily.
XX
XX Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 14.8; DB 1; Length 21;

```


Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1519 TAAAAAAAAAAGTAAA 1536

Db 18 TAAAAAAAAAAAAAAAAA 1

RESULT 871

AAQ75686/C
ID AAQ75686 standard; DNA; 21 BP.

XX AAQ75686;

DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;

KW aggregate; restriction enzyme; ss.

OS Synthetic.

PN JP06303997-A.

XX 01-NOV-1994.

PD 16-APR-1993; 93JP-00112515.

PF 16-APR-1993; 93JP-00112515.

PR 16-APR-1993; 93JP-00112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

DR Analysis of cDNA and gene expression - by amplification of mRNA followed

PT by digestion with restriction enzymes.

XX Disclosure; Page 7; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of

CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of

CC labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)

CC and using the aggregate of mRNAs as the template for each reverse

CC transcription primer; (b) digesting each of the prepared aggregates of

CC the double-stranded cDNAs with restriction enzyme and; (c)

CC electrophoresing the digested aggregate of cDNAs in separate lanes. The

XX method can be used to analyse gene expression rapidly and easily

SO Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 21;

Best Local Similarity 88.9%; Pred. No. 4.2e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1519 TAAAAAAAAAAGTAAA 1536

Db 18 TAAAAAAAAAAAAAAAAA 1

RESULT 872

AAQ75689/C
ID AAQ75689 standard; DNA; 21 BP.

XX AAQ75689;

DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;

KW aggregate; restriction enzyme; ss.

OS Synthetic.

PN JP06303997-A.

XX 01-NOV-1994.

PD 16-APR-1993; 93JP-00112515.

PF 16-APR-1993; 93JP-00112515.

PR 16-APR-1993; 93JP-00112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

DR Analysis of cDNA and gene expression - by amplification of mRNA followed

PT by digestion with restriction enzymes.

XX Disclosure; Page 7; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of

CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of

OS Synthetic.

PN JP06303997-A.

XX 01-NOV-1994.

PD 16-APR-1993; 93JP-00112515.

PF 16-APR-1993; 93JP-00112515.

PR 16-APR-1993; 93JP-00112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

DR Analysis of cDNA and gene expression - by amplification of mRNA followed

PT by digestion with restriction enzymes.

XX Disclosure; Page 7; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of

CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of

CC labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)

CC and using the aggregate of mRNAs as the template for each reverse

CC transcription primer; (b) digesting each of the prepared aggregates of

CC the double-stranded cDNAs with restriction enzyme and; (c)

CC electrophoresing the digested aggregate of cDNAs in separate lanes. The

XX method can be used to analyse gene expression rapidly and easily

SO Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 21;

Best Local Similarity 88.9%; Pred. No. 4.2e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1519 TAAAAAAAAAAGTAAA 1536

Db 18 TAAAAAAAAAAAAAAAAA 1

RESULT 873

AAQ75703/C
ID AAQ75703 standard; DNA; 21 BP.

XX AAQ75703;

DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;

KW aggregate; restriction enzyme; ss.

OS Synthetic.

PN JP06303997-A.

XX 01-NOV-1994.

PD 16-APR-1993; 93JP-00112515.

PF 16-APR-1993; 93JP-00112515.

PR 16-APR-1993; 93JP-00112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

DR Analysis of cDNA and gene expression - by amplification of mRNA followed

PT by digestion with restriction enzymes.

XX Disclosure; Page 7; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of

CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of

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CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 0 C; 3 G; 17 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1519 TAAAAAAAAAAGTAAA 1536
Db 18 TAAAAAAAAAAAAAAAAA 1
RESULT 874
AAQ75705/c
ID AAQ75705 standard; DNA; 21 BP.
XX
AC AAQ75705;
XX
XX 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX
XX Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1519 TAAAAAAAAAAGTAAA 1536
Db 18 TAAAAAAAAAAAAAAAAA 1
RESULT 875
AAQ75672/c
ID AAQ75672 standard; DNA; 21 BP.
```

```
XX
XX AAQ75672;
XX
XX 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX
XX Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1519 TAAAAAAAAAAGTAAA 1536
Db 18 TAAAAAAAAAAAAAAAAA 1
RESULT 876
AAQ75706/c
ID AAQ75706 standard; DNA; 21 BP.
XX
XX AAQ75706;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
```

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XX      WPI; 1995-018287/03.
DR
XX      Analysis of cDNA and gene expression - by amplification of mRNA followed
PT      by digestion with restriction enzymes.
XX
XX      Disclosure; Page 7; 11pp; Japanese.
XX
CC      A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC      double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC      labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
CC      and using the aggregate of mRNAs as the template for each reverse
CC      transcription primer; (b) digesting each of the prepared aggregates of
CC      the double-stranded cDNAs with restriction enzyme and; (c)
CC      electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC      method can be used to analyse gene expression rapidly and easily
XX
XX      Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;
SQ
XX      Query Match      1.1%; Score 14.8; DB 1; Length 21;
XX      Best Local Similarity 88.9%; Pred. No. 4.2e+02;
XX      Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY      1519 TAAAAAAAAAAAGTAAA 1536
DB      |||||
      18 TAAAAAAAAAAAAAAAAAAAA 1

RESULT 877
AAQ75685/c
ID      AAQ75685 standard; DNA; 21 BP.
AC
XX      AAQ75685;
AC
XX      04-AUG-1995 (first entry)
DT
XX      Reverse transcription primer used in cDNA analysis technique.
DE
XX      Analysis; gene expression; reverse transcription; primer; cDNA;
KW      aggregate; restriction enzyme; ss.
XX
XX      Synthetic.
OS
XX      JP06303997-A.
PN
XX      01-NOV-1994.
PD
XX      16-APR-1993; 93JP-00112515.
PF
XX      16-APR-1993; 93JP-00112515.
PR
XX      16-APR-1993; 93JP-00112515.
PA      (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR      WPI; 1995-018287/03.
XX
PT      Analysis of cDNA and gene expression - by amplification of mRNA followed
PT      by digestion with restriction enzymes.
XX
XX      Disclosure; Page 7; 11pp; Japanese.
XX
CC      A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC      double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC      labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
CC      and using the aggregate of mRNAs as the template for each reverse
CC      transcription primer; (b) digesting each of the prepared aggregates of
CC      the double-stranded cDNAs with restriction enzyme and; (c)
CC      electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC      method can be used to analyse gene expression rapidly and easily
XX
XX      Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 U; 0 Other;
SQ
XX      Query Match      1.1%; Score 14.8; DB 1; Length 21;
XX      Best Local Similarity 88.9%; Pred. No. 4.2e+02;
XX      Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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XX      Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY      1519 TAAAAAAAAAAAGTAAA 1536
DB      |||||
      18 TAAAAAAAAAAAAAAAAAAAA 1

RESULT 878
AAQ75699/c
ID      AAQ75699 standard; DNA; 21 BP.
AC
XX      AAQ75699;
AC
XX      04-AUG-1995 (first entry)
DT
XX      Reverse transcription primer used in cDNA analysis technique.
DE
XX      Analysis; gene expression; reverse transcription; primer; cDNA;
KW      aggregate; restriction enzyme; ss.
XX
XX      Synthetic.
OS
XX      JP06303997-A.
PN
XX      01-NOV-1994.
PD
XX      16-APR-1993; 93JP-00112515.
PF
XX      16-APR-1993; 93JP-00112515.
PR
XX      16-APR-1993; 93JP-00112515.
PA      (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR      WPI; 1995-018287/03.
XX
PT      Analysis of cDNA and gene expression - by amplification of mRNA followed
PT      by digestion with restriction enzymes.
XX
XX      Disclosure; Page 7; 11pp; Japanese.
XX
CC      A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC      double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC      labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
CC      and using the aggregate of mRNAs as the template for each reverse
CC      transcription primer; (b) digesting each of the prepared aggregates of
CC      the double-stranded cDNAs with restriction enzyme and; (c)
CC      electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC      method can be used to analyse gene expression rapidly and easily
XX
XX      Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;
SQ
XX      Query Match      1.1%; Score 14.8; DB 1; Length 21;
XX      Best Local Similarity 88.9%; Pred. No. 4.2e+02;
XX      Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY      1519 TAAAAAAAAAAAGTAAA 1536
DB      |||||
      18 TAAAAAAAAAAAAAAAAAAAA 1

RESULT 879
AAQ75704/c
ID      AAQ75704 standard; DNA; 21 BP.
AC
XX      AAQ75704;
AC
XX      04-AUG-1995 (first entry)
DT
XX      Reverse transcription primer used in cDNA analysis technique.
DE
XX      Analysis; gene expression; reverse transcription; primer; cDNA;
KW      aggregate; restriction enzyme; ss.
XX
XX      Synthetic.
OS

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XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESBQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily.
XX
XX Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 21;
XX Best Local Similarity 88.9%; Pred. No. 4.2e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1519 TAAAAAAAAGTAA 1536
XX |||||
XX 18 TAAAAAAAAGTAA 1
XX
XX RESULT 880
XX AAQ75708/c
XX ID AAQ75708 standard; DNA; 21 BP.
XX
XX AC AAQ75708;
XX
XX DT 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX OS Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESBQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily.
XX
XX Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 U; 0 Other;
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CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily.
XX
XX Sequence 21 BP; 3 A; 0 C; 1 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 21;
XX Best Local Similarity 88.9%; Pred. No. 4.2e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1519 TAAAAAAAAGTAA 1536
XX |||||
XX 18 TAAAAAAAAGTAA 1
XX
XX RESULT 881
XX AAQ75717/c
XX ID AAQ75717 standard; DNA; 21 BP.
XX
XX AC AAQ75717;
XX
XX DT 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX OS Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 8; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESBQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily.
XX
XX Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 21;
XX Best Local Similarity 88.9%; Pred. No. 4.2e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1519 TAAAAAAAAGTAA 1536
XX |||||
XX 18 TAAAAAAAAGTAA 1
XX
XX RESULT 882
XX AAQ75673/c
XX ID AAQ75673 standard; DNA; 21 BP.
XX
```

AC AAQ75673;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENES0 files AAQ75547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1519 TAAAAAAAAAAGTAAA 1536
DB 18 TAAAAAAAAAAAAAAAAA 1
XX
RESULT 883
AAQ75677/c
ID AAQ75677 standard; DNA; 21 BP.
XX
AC AAQ75677;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX

DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENES0 files AAQ75547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1519 TAAAAAAAAAAGTAAA 1536
DB 18 TAAAAAAAAAAAAAAAAA 1
XX
RESULT 884
AAQ75683/c
ID AAQ75683 standard; DNA; 21 BP.
XX
AC AAQ75683;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENES0 files AAQ75547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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OY      1519 TAAAAAAGTAAA 1536
      |||||
      18 TAAAAAAGTAAA 1
Db

RESULT 885
AAQ75710/C
ID AAQ75710 standard; DNA; 21 BP.
XX
XX AAQ75710;
AC
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
XX Synthetic.
OS
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY      1519 TAAAAAAGTAAA 1536
      |||||
      18 TAAAAAAGTAAA 1
Db

RESULT 886
AAQ75701/C
ID AAQ75701 standard; DNA; 21 BP.
XX
XX AAQ75701;
AC
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
XX Synthetic.
OS
XX

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PN      JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY      1519 TAAAAAAGTAAA 1536
      |||||
      18 TAAAAAAGTAAA 1
Db

RESULT 887
AAQ75709/C
ID AAQ75709 standard; DNA; 21 BP.
XX
XX AAQ75709;
AC
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
XX Synthetic.
OS
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse

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CC transcripction primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1519 TAAAAAAAAAAGTAAA 1536
Db 18 TAAAAAAAAAAAAAAAAA 1
RESULT 889
AAQ0391 ID AAQ0391 standard; DNA; 21 BP.
XX
AC AAQ0391;
XX
DT 08-JAN-1996 (first entry)
XX
DE CP-1 (synthetic DNA probe with 3'ribonucleoside terminal #2).
XX
KM CP-1; HLA; dca; 3' ribonucleoside; self-addressable electronic device;
KM SMD; hybridisation; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 21 /*tag= a
FT /note= "3' ribonucleoside terminal"
XX
XX WO9512808-A1.
XX
XX PD 11-MAY-1995.
XX
XX PF 26-OCT-1994; 94WO-US012270.
XX
XX PR 01-NOV-1993; 93US-00146504.
XX
XX PA (NANO-) NANOGEN INC.
XX
XX PI Heller MJ, Tu E;
XX
XX PS Example 1; Page 40; 86pp; English.
XX
XX The sequences represented by, AAQ0390-90401 are synthetic DNA probes
XX containing 3' ribonucleoside terminl. The sequences shown in AAQ0402-15
XX are synthetic DNA probes with 5' amino terminl. These sequences were
XX specific for the polymorphisms of HLA gene dca. The sequences were used
XX in the device of the invention. This is a self-addressable electronic
XX device (SMD) that can be used to carry out multi-step and multiplex
XX reactions, such as nucleic acid hybridisations. The advantages of this
XX method are that these reactions can be carried out with complete and
XX precise electronic control, and that the rate, specificity and
XX sensitivity of these reactions are greatly improved at micro-locations
XX
SQ Sequence 21 BP; 20 A; 0 C; 0 G; 0 T; 1 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1520 AAAAAAAAAAAGTAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 18
RESULT 889
AA10743 ID AA10743 standard; RNA; 21 BP.
XX
AC AA10743;
XX
DT 09-SEP-1996 (first entry)
XX
DE Oligonucleotide probe, CP-1.
XX
KM Electronically self-addressable device; ED; electrode; current source;
KM attachment layer; permeable; counterion; genetic typing; probe;
KM detection; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 21 /*tag= a
FT /note= "3'-ribonucleoside terminus"
XX
XX WO9601836-A1.
XX
XX PD 25-JAN-1996.
XX
XX PF 05-JUL-1995; 95WO-US008570.
XX
XX PR 07-JUL-1994; 94US-00271882.
XX
XX PA (NANO-) NANOGEN INC.
XX
XX PI Heller MJ, Tu E, Evans GA, Sosnowski RG;
XX
XX PS WPI; 1996-097582/10.
XX
XX PF Electronically self-addressable device - used for electronic control of,
XX e.g. nucleic acid hybridisation.
XX
XX PS Example 1; Page 60; 155pp; English.
XX
XX The sequences given in AA10742-67 are synthetic oligonucleotides which
XX are used in the construction of the electronically self-addressable
XX device (ED) of the invention. The ED comprises a substrate, an electrode
XX or opt. a number of electrodes supported by the substrate, a current
XX source operatively connected to the electrode and an attachment layer
XX adjacent to the electrode which is permeable to a counterion but not
XX permeable to a molecule capable of insulating or binding to the
XX electrode. The attachment layer is capable of attaching a macromolecule.
XX The ED is used for genetic typing and comprises a number of
XX electronically addressable locations each comprising an electrode, and a
XX binding entity, such as one of these probes, attached to each of the
XX locations capable of detecting the presence of a genetic sequence
XX
SQ Sequence 21 BP; 20 A; 0 C; 0 G; 0 T; 1 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAAGTAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 18
RESULT 890
AAV35395 ID AAV35395 standard; DNA; 21 BP.
XX

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```

AC  AAV35395;
XX
XX  13-OCT-1998 (first entry)
XX
XX  HIV-1 gag protein DNA primer #8.
DE
XX  Hypervariable region; ENV protein; vaccinia virus; gag gene; retrovirus;
XX  vaccines; infection; protection; primer; ss.
XX
XX  Synthetic.
OS
XX  WO9822596-A1.
XX
XX  28-MAY-1998.
XX
XX  19-NOV-1997; 97WO-JP004216.
XX
XX  19-NOV-1996; 96JP-00323412.
XX
XX  (NINA-) JAPAN NAT INST INFECTIOUS DISEASES.
XX  (JAPG) NIPPON ZEON KK.
XX
XX  Kojima A, Kurata T, Yasuda A;
XX
XX  WPI; 1998-312481/27.
XX
XX  Recombinant vaccinia virus containing fusion H1B gag gene - for
XX  production in host cells of gag protein for use as vaccine.
XX
XX  Example 1; Page 66; 84pp; Japanese.
XX
XX  AAV35388-V35414 are primers used in a method which results in a
XX  recombinant vaccinia virus comprising of a gag gene from a retrovirus
XX  such as HIV-1 or HIV-2, fused to a DNA fragment containing an epitope
XX  region (30-300 bases in length) of a retroviral gene other than the gag
XX  gene. The gag gene may be altered so as to produce a gag protein modified
XX  from the natural sequence by the addition, deletion or substitution of at
XX  least 1 amino acid residue. The fusion gene is inserted into a region of
XX  a vaccinia virus not essential to its propagation, to give a recombinant
XX  vaccinia virus vector which is used to transform a host cell (such as
XX  HeLa, Vero, VEF, rabbit kidney RK13 or human myeloma TK-143 cells). Upon
XX  culturing the host cell produces particulate structures containing the
XX  fusion gag protein. The recombinant vaccinia virus or the fusion gag
XX  protein particles may be used in the production of vaccines for
XX  protecting against infection with retroviruses such as HIV
XX
XX  Sequence 21 BP; 19 A; 2 C; 0 G; 0 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred.No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAGTAAA 1537
DB 3 AAAAAAAAAAAAAAAAAA 20

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XX  Homo sapiens.
XX
XX  WO9841648-A2.
XX
XX  24-SEP-1998.
XX
XX  19-MAR-1998; 98WO-US005419.
XX
XX  20-MAR-1997; 97US-0041057P.
XX
XX  (VART-) VARIAGENICS INC.
XX
XX  Housman D, Ledley FD, Stanton VP;
XX
XX  WPI; 1998-521232/44.
XX
XX  Identifying target genes for allele-specific drugs - used for diagnosis,
XX  prevention and treatment of, e.g. cancers, atherosclerotic plaque,
XX  dysplastic lesions, endometriosis or graft versus host disease.
XX
XX  Disclosure; Fig 7; 605pp; English.
XX
XX  This invention describes a novel method for identifying an inhibitor
XX  potentially useful for treatment of cancer, where the inhibitor is active
XX  on a gene vital for cell growth or viability, and where the gene is
XX  subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
XX  used for preventing the development of cancer in a patient having a
XX  precancerous condition, by administering to the patient a first allele
XX  specific inhibitor (ASI) targeted to an allele of a first essential gene
XX  present in cells of the precancerous condition, where the normal somatic
XX  cells of the patient are heterozygous for the first gene, the inhibitor
XX  is active on at least one but less than all allelic forms of the gene
XX  present in a population and targets only one allelic form present in the
XX  normal somatic cells, and the first gene. The products and methods can be
XX  used in the diagnosis, prevention and treatment of LOH disorders, e.g.
XX  cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
XX  lesions, benign tumours, endometriosis, polycystic kidney disease, and
XX  graft versus host disease. The method can also be used to remove
XX  malignant cells from bone marrow transplants. AA25812-226825 represent
XX  human polymorphic sites described in the method of the invention
XX
XX  Sequence 21 BP; 12 A; 2 C; 0 G; 7 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred.No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1514 TTAATTAAAAA 1531
DB 4 TTTTAAAAA 21

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XX 24-SEP-1998.
PD 19-MAR-1998; 98WO-US005419.
XX 19-MAR-1998; 98WO-US005419.
XX 20-MAR-1997; 97US-0041057P.
XX (VARI-) VARIAGENICS INC.
XX Houseman D, Ledley PD, Stanton VP;
XX WPI; 1998-521232/44.
XX
XX Identifying target genes for allele-specific drugs - used for diagnosis,
XX prevention and treatment of, e.g. cancers, atherosclerotic plaque,
XX dysplastic lesions, endometriosis or graft versus host disease.
XX
XX Disclosure; Fig 7; 605pp; English.
XX
XX This invention describes a novel method for identifying an inhibitor
XX potentially useful for treatment of cancer, where the inhibitor is active
XX on a gene vital for cell growth or viability, and where the gene is
XX subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
XX used for preventing the development of cancer in a patient having a
XX precancerous condition, by administering to the patient a first allele
XX specific inhibitor (ASI) targeted to an allele of a first essential gene
XX present in cells of the precancerous condition, where the normal somatic
XX cells of the patient are heterozygous for the first gene, the inhibitor
XX is active on at least one but less than all allelic forms of the gene
XX present in a population and targets only one allelic form present in the
XX normal somatic cells, and the first gene. The products and methods can be
XX used in the diagnosis, prevention and treatment of LOH disorders, e.g.
XX cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
XX lesions, benign tumors, endometriosis, polycystic kidney disease, and
XX graft versus host disease. The method can also be used to remove
XX malignant cells from bone marrow transplants. AA225812-426825 represent
XX human polymorphic sites described in the method of the invention
XX
XX Sequence 21 BP; 2 A; 6 C; 12 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 21;
XX Best Local Similarity 88.9%; Pred. No. 4.2e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX Oy 422 GAGTGGCGGCTGCCGCCG 439
XX ||| ||||| |||||
XX 3 GAGGCGCGCGCGCGCGCGC 20
XX
XX RESULT 893
XX AA81302
XX ID AA81302 standard; DNA; 21 BP.
XX
XX AA81302;
XX
XX 20-AUG-1999 (first entry)
XX
XX 3' ribonucleoside oligonucleotide probe CP-1.
XX
XX Microelectronic device; multi-step reaction; microscopic format;
XX ion-permeable permeation layer; electrode; electrical control; transport;
XX attachment; binding; DNA/RNA hybrid; probe; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX FT mlec_RNA 21
XX FT /*tag= a
XX
XX MO9929711-A1.
XX
XX 17-JUN-1999.
XX
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```
PF 01-DEC-1998; 98WO-US025475.
XX 05-DEC-1997; 97US-00986065.
XX (NANO-) NANOGEN INC.
XX
XX Sosnowski RG, Butler WF, Tu E, Nerenberg MT, Heller MJ, Edman CF;
XX WPI; 1999-385567/32.
XX
XX New microelectronic device designed to carry out and control multi-step
XX and multiplex molecular biological reactions in microscopic format.
XX
XX Example 1; Page 89; 179pp; English.
XX
XX The specification describes a self-addressable, self-assembling
XX microelectronic device which is designed to actively carry out and
XX control multi-step and multiplex molecular biological reactions in
XX microscopic formats. A key aspect of this invention is played by the ion
XX permeable permeation layer which overlies the electrode. This permeation
XX layer allows attachment of nucleic acids to permit immobilization but
XX also separates the attached oligonucleotides and hybridized target DNA
XX sequences from the highly reactive electrochemical environment generated
XX immediately at the electrode surface. The microelectronic device is
XX designed and fabricated to actively carry out and control reactions such
XX as nucleic acid hybridizations, antibody/antigen reactions, sample
XX preparation, diagnostics and biopolymer synthesis. The device can
XX electronically control the transport and attachment of specific binding
XX entities, such as nucleic acids and polypeptides, to specific micro-
XX locations. The device can subsequently control the transport and reaction
XX of analytes or reactants at the addressed specific micro-locations. The
XX device is able to concentrate analytes and reactants, remove non-
XX specifically bound molecules, provide stringency control for DNA
XX hybridization reactions and improve the detection of analytes. The
XX present sequence represents a probe used to exemplify the invention
XX
XX Sequence 21 BP; 20 A; 0 C; 0 G; 0 T; 1 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 21;
XX Best Local Similarity 88.9%; Pred. No. 4.2e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX Oy 1520 AAAAAAAAAAAGTAA 1537
XX ||||| |||||
XX 1 AAAAAAAAAAAAAAAAAA 18
XX
XX RESULT 894
XX AA71751/C
XX ID AA71751 standard; DNA; 21 BP.
XX
XX AA71751;
XX
XX 15-MAR-1999 (first entry)
XX
XX Human V3 loop HIV receptor p30/PHAP1 sense PCR primer.
XX
XX HIV receptor; V3 loop; human immunodeficiency virus; retrovirus;
XX p30 protein; PHAP1; infection; therapy; PCR; primer; ss.
XX
XX Synthetic.
XX
XX Homo sapiens.
XX
XX MO9840480-A1.
XX
XX 17-SEP-1998.
XX
XX 12-MAR-1998; 98WO-EP001409.
XX
XX 12-MAR-1997; 97US-0040969P.
XX
XX (INSP ) INST PASTEUR.
XX (CNRS ) CENT NAT RECH SCI.
XX
```

PS Disclosure; Page 62; 195pp; English.

XX The invention identifies a genetic locus ASTH1, associated with asthma,

CC mapped to human chromosome 11p. ASTH1 and ASTHJ are genes present

CC within the locus, located close to each other on human chromosome 11p,

CC and have similar patterns of expression, and common sequence motifs. The

CC ASTH1 genes and fragments, encoded protein, genomic regulatory regions

CC and anti-ASTH1 antibodies are useful in the identification of individuals

CC predisposed to development of asthma, and for the modulation of gene

CC activity in vivo for prophylactic and therapeutic purposes. The ASTH1

CC protein is useful as an immunogen to raise specific antibodies, in drug

CC screening for compositions that mimic or modulate ASTH1 activity or

CC expression, including altered forms of ASTH1 protein, and as a

CC therapeutic. Sequences AA218366-218509 represent polymorphisms in the

CC ASTH1 and ASTHJ genes

XX

SQ Sequence 21 BP; 0 A; 9 C; 1 G; 10 T; 0 U; 1 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 21;

Best Local Similarity 80.0%; Pred. No. 4.2e+02;

Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1225 CTCCTAGCTTTCAGCTTCCTC 1244

1 CTCCTTCTCTTTCCTTCCTC 20

Db

RESULT 896

AAAX26973/c

ID AAX26973 standard; cDNA; 21 BP.

XX

AC AAX26973;

XX

DT 25-JUN-1999 (first entry)

XX

DE Primer used to reverse transcribe mammaglobin RNA.

XX

KW Human; mammary-specific protein; mammaglobin; antigen; vaccine;

KW mammaglobin-expressing cancer; breast cancer;

KW autologous tumor lymphocyte; diagnosis; marker; primer; 88.

XX

OS Synthetic.

XX

PN WO9914230-A1.

PD

PD 25-MAR-1999.

XX

PF 18-SEP-1998; 98WO-US017991.

XX

PR 18-SEP-1997; 97US-00933149.

XX

PA (UNIW) UNIV WASHINGTON.

PA

PA Watson MA, Fleming TP;

PI

PI WPI; 1999-244021.20.

XX

XX Mammaglobin, secreted protein overexpressed in breast cancer.

XX

XX

XX Example 2; Page 55; 60pp; English.

PS

PS The present primer was used to reverse transcribe RNA encoding a human

CC mammary-specific protein, designated mammaglobin. The specification

CC describes a protein comprising a mammaglobin antigen that is recognized

CC by B and/or Tc cells specific for the natural, secreted and glycosylated

CC form of mammaglobin polypeptide. This protein, or recombinant vectors

CC that express it, are used in vaccines for treating mammaglobin-

CC expressing cancers, specifically of the breast. Such cancers can also be

CC treated using autologous tumor lymphocytes activated ex vivo with an

CC mammaglobin antigen, then returned to the patient. Expression of

CC mammaglobin is elevated in 27% of stage I primary breast cancers, so it

XX represents a marker useful for diagnosis of this disease

XX

```

SQ Sequence 21 BP, 0 A, 0 C, 0 G, 21 T, 0 U, 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAGTAAA 1537
Db 21 AAAAAAAAAAAAAAAAAA 4
XX

RESULT 897
AAZ44350/C
ID AAZ44350 standard; DNA; 21 BP.
XX
AC AAZ44350;
XX
DT 04-APR-2000 (first entry)
XX
DE Protein kinase inhibiting primer #12.
XX
KM Antimicrobial; cytostatic; immunosuppressive; protein kinase;
KM prophylactic; therapy; treatment; cancer; autoimmune disease;
KM pathogenic microorganism; primer; ss.
XX
OS Unidentified.
XX
PN US5998596-A.
XX
PD 07-DEC-1999.
XX
PF 04-APR-1995; 95US-00416214.
XX
PR 04-APR-1995; 95US-00416214.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Bergan R, Neckers L;
XX
WPI; 2000-104623/09.
XX
PT Oligonucleotides inhibiting protein kinase, useful for treating diseases
PT such as cancer and autoimmune disease.
XX
PS Example 6; Col 27-28; 26pp; English.
XX
CC This invention describes novel purified aptameric oligonucleotides which
CC have antimicrobial, cytostatic and immunosuppressive activity. The
CC oligonucleotides are useful for binding to and preventing or inhibiting
CC the biological function of a protein kinase or a target molecule and for
CC detecting the presence or absence of a target molecule in biological
CC samples. The oligonucleotides are also useful for prophylactic and
CC therapeutic treatment of diseases such as cancer, autoimmune diseases and
CC diseases caused by pathogenic microorganisms. This sequence represents a
CC primer used in the method of the invention
XX
SQ Sequence 21 BP, 0 A, 0 C, 0 G, 21 T, 0 U, 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAGTAAA 1537
Db 21 AAAAAAAAAAAAAAAAAA 4
XX

RESULT 898
AAA80318
ID AAA80318 standard; DNA; 21 BP.
XX
AC AAA80318;
XX

DT 22-NOV-2000 (first entry)
XX
DE Human ASTH1J 5' region polymorphic site, SEQ ID NO:66.
XX
KM ASTH1 locus; ASTH1I; ASTH1J; human; chromosome 11p; asthma;
KM bronchial hyperreactivity; ets family; transcription factor;
KM splice variant; genetic predisposition; polymorphism; antibody;
KM drug screening; prophylaxis; therapy; diagnosis;
KM single nucleotide polymorphism; SNP; ss.
XX
OS Homo sapiens.
XX
PN US6087485-A.
XX
PD 11-JUL-2000.
XX
PF 21-JAN-1998; 98US-00009913.
XX
PR 21-JAN-1997; 97US-0035663P.
XX
PR 01-JUL-1997; 97US-0051432P.
XX
PA (AXYS-) AXYS PHARM INC.
XX
PI Galvin M, Miller A, North M, Cardon L, Buckler A;
PI Brooks-Wilson AR, Carey AH;
XX
WPI; 2000-505109/45.
XX
XX
XX New nucleic acids other than naturally occurring chromosomes encoding
PT ASTH1 protein, for e.g., screening compositions that modulate expression
PT or function of ASTH1 proteins or as diagnostics for genetic
PT predisposition to asthma.
XX
PS Example; Col 41-42; 13pp; English.
XX
CC The invention relates to the ASTH1 locus on the short arm of human
CC chromosome (11p). This locus comprises the ASTH1I and ASTH1J genes, which
CC are associated with a genetic predisposition to asthma and bronchial
CC hyperreactivity. The ASTH1I and ASTH1J genes are oriented in opposite
CC directions with the ASTH1 locus, and have similar patterns of expression
CC and common sequence motifs. They are both expressed in trachea, lung and
CC several other tissues. ASTH1I and ASTH1J are novel members of the ets
CC family of transcription factors, which have been implicated in the
CC activation of a variety of genes including the TCRA gene and cytokine
CC genes known to be important in the aetiology of asthma. Both ASTH1I and
CC ASTH1J mRNAs are alternatively spliced. Alternative splicing of
CC transcripts has no effect on the open reading frame of ASTH1J, as the
CC exons involved are all 5' to the start codon in exon b. In contrast,
CC alternative splicing of ASTH1I transcripts results in 3 different ASTH1I
CC isoforms. The invention also encompasses mouse asth1 protein. The ASTH1
CC nucleic acids are useful as diagnostics for identifying a hereditary
CC predisposition to asthma, as probes for identifying ASTH1 related genes,
CC for identifying expression of the gene in a biological specimen, and for
CC generating genetically modified non-human animals or site specific gene
CC modifications in cell lines. The encoded ASTH1 proteins are useful as
CC immunogens to raise specific antibodies; in drug screening for
CC compositions that mimic or modulate activity or expression of ASTH1I
CC and/or ASTH1J (including altered forms of these proteins); and as a
CC therapeutic. The ASTH1 genes or fragments thereof, encoded proteins,
CC ASTH1 genomic regulatory regions, and anti-ASTH1I and anti-ASTH1J
CC antibodies are useful in the identification of individuals predisposed to
CC development of asthma, and for modulation of gene activity in vivo for
CC prophylactic and therapeutic purposes. The intact ASTH1I or ASTH1J
CC proteins or active fragments thereof may be used to modulate or reduce
CC bronchial hyperreactivity. Sequences AAA80260-A80261 and AAA80264-A80416
CC represent polymorphic sites within the ASTH1J or ASTH1I genes
XX
SQ Sequence 21 BP, 0 A, 9 C, 1 G, 10 T, 0 U, 1 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 80.0%; Pred. No. 4.2e+02;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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```

QY      1225 CTCTAGCTCTTAGCTTCCTC 1244
      |||||:|||||
Db      1  CTCTTCTCTCTYGCCTCCTC 20

RESULT 899
AA#99707/c
ID      AAF99707 standard; DNA; 21 BP.
AC      AAF99707;
XX
XX      12-JUN-2001 (first entry)
XX
XX      Immunostimulatory nucleic acid #823.
XX
XX      Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
XX      immunostimulatory; tumour; viral infection; bacterial infection;
XX      fungal infection; parasitic infection; cancer; asthma;
XX      infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
XX      Synthetic.
XX
XX      WO200122972-A2.
XX
XX      05-APR-2001.
XX
XX      25-SEP-2000; 2000WO-US026383.
XX
XX      25-SEP-1999; 99US-0156113P.
XX      27-SEP-1999; 99US-0156135P.
XX      23-AUG-2000; 2000US-0227436P.
XX
XX      (IOWA ) UNIV IOWA RES FOUND.
XX      (COLE-) COLEY PHARM GMBH.
XX
XX      Krieg AM, Schetter C, Vollmer J;
XX
XX      WPI; 2001-273485/28.
XX
XX      Vaccinating against tumor, infectious diseases, allergies and asthma
XX      using immunostimulatory Py-rich and TG nucleic acids.
XX
XX      Claim 101; Page 56; 338pp; English.
XX
XX      The present invention relates to a method for stimulating an immune
XX      response. The method comprises administering an immunostimulatory nucleic
XX      acid to a non-rodent subject in sufficient quantity to stimulate an
XX      immune response. The present sequence is one such immunostimulatory
XX      nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
XX      (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
XX      against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
XX      and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
XX      haemophilus, campylobacter, clostridium, Escherichia coli and/or
XX      streptococcus), fungal antigens and/or parasitic antigens. The method is
XX      also useful for preventing cancer, asthma, infectious disease, allergy or
XX      immune deficiency. The present sequence can also be used to redirect a
XX      Th1 to a Th1 immune response and to activate immune cells. Note: the
XX      present sequence may have a phosphorothioate backbone
XX
XX      Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;
XX
Query Match      1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      1520 AAAAAAAAAAAGTAAAA 1537
      |||||:|||||
Db      21 AAAAAAAAAAAAAAAAAAAAA 4

RESULT 900
AA#42480/c
ID      AA#42480 standard; DNA; 21 BP.

```

```

XX      AA#42480;
XX
XX      01-OCT-2001 (first entry)
XX
XX      Oligonucleotide used to produce branched chain compounds.
XX
XX      Branched chain compound; nucleic acid synthesis; primer extension;
XX      reverse transcription; nucleic acid hybridization;
XX      nucleic acid amplification; ss.
XX
XX      Synthetic.
XX
XX      Key      Location/Qualifiers
XX      modified_base 1
XX      FT      /*tag= a
XX      FT      /note= "NH2-C6 attached"
XX      FT      modified_base 4
XX      FT      /*tag= b
XX      FT      /note= "NH2-C6 attached"
XX      FT      misc_feature 6..7
XX      FT      /*tag= c
XX      FT      /note= "branch present"
XX
XX      EP111068-A1.
XX
XX      27-JUN-2001.
XX
XX      21-DEC-1999; 99EP-00125484.
XX
XX      21-DEC-1999; 99EP-00125484.
XX
XX      (LION-) LION BIOSCIENCE AG.
XX      (VBCG-) VBC GENOMICS GMBH.
XX
XX      Schmidt W, Hiller R, Huber M, Mueller M;
XX
XX      WPI; 2001-466959/51.
XX
XX      Branched compounds useful in e.g. nucleic acid synthesis reaction
XX      comprises nucleic acid moieties optionally extended by a polymerase.
XX
XX      Example 1; Page 10; 31pp; English.
XX
XX      The specification describes branched compounds containing nucleic acid
XX      moieties optionally extended by a polymerase. The branched chain
XX      compounds of the invention are used in nucleic acid synthesis reaction,
XX      primer extension reaction, reverse transcription reaction of RNA into
XX      cDNA, nucleic acid hybridization experiment (for identifying sequence of a
XX      nucleic acid), and nucleic acid amplification experiment (for analysing
XX      the expression pattern of genes). The compounds are also used in solid-
XX      phase enzymatic reactions. The present sequence was used in the course of
XX      the invention to produce branched chain compounds
XX
XX      Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;
XX
Query Match      1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      1520 AAAAAAAAAAAGTAAAA 1537
      |||||:|||||
Db      21 AAAAAAAAAAAAAAAAAAAAA 4

RESULT 901
AB#78428/c
ID      AB#78428 standard; DNA; 21 BP.
AC      AB#78428;
XX
XX      13-DEC-2002 (first entry)
XX

```

DE Angiogenesis inhibitory oligonucleotide #912.
XX
XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KM tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KM diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KM corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KM rubosis; Osler-Weber Syndrome; myocardial angiogenesis;
KM plaque neovascularisation; telangiectasia; haemophilic joint;
KM angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KM scleroderma; hypertrophic scar.
XX
OS Synthetic.
XX
XX WO200253141-A2.
XX
XX 11-JUN-2002.
XX
XX 14-DEC-2001; 2001WO-US048458.
XX
XX 14-DEC-2000; 2000US-0255534P.
XX
XX (COLE-) COLEY PHARM GROUP INC.
XX
XX Bratzler RL;
XX
XX WPI; 2002-566690/60.
XX
XX Inhibiting angiogenesis in a subject, involves administering at least one
PT antiangiogenic nucleic acid molecule to the subject.
XX
XX Claim 2; Page 35; 276pp; English.
XX
XX The invention relates to inhibiting angiogenesis in a subject, comprising
CC administering at least one antiangiogenic nucleic acid molecule. Also
CC including a kit comprising a first container housing the antiangiogenic
CC nucleic acids, and instructions for administering them to a subject
CC having a condition characterised by unwanted angiogenesis. The method is
CC useful for inhibiting angiogenesis associated with solid tumour growth,
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC rubosis, Osler-Weber Syndrome, myocardial angiogenesis, plaque
CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC acid of the invention
XX
SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 21;
XX Best Local Similarity 88.9%; Pred. No. 4.2e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
OY 1520 AAAAAAAAAAATAAAA 1537
XX ||||| |||||
DB 21 AAAAAAAAAAAAAAAAAA 4
XX
RESULT 902
ABL39404/C
ID ABL39404 standard; DNA; 21 BP.
XX
XX ABL39404;
XX
XX 16-APR-2002 (first entry)
XX
XX Immunostimulatory nucleic acid SEQ ID NO: 840.
XX
XX Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
KM angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.
XX
XX Synthetic.
XX

FH Key Location/Qualifiers
FT modified_base 1: 21
FT /*tag= a
FT /mod_base= OTHER
FT /note= "phosphorothioate backbone"
XX
XX WO200197843-A2.
XX
XX 27-DEC-2001.
XX
XX 22-JUN-2001; 2001WO-US020154.
XX
XX 22-JUN-2000; 2000US-0213346P.
XX
XX (IOWA) UNIV IOWA RES FOUND.
XX
XX Weiner G, Hartmann G;
XX
XX WPI; 2002-154611/20.
XX
XX
XX Treating or preventing cancer, such as basal cell carcinoma, comprises
PT administering immunostimulatory nucleic acids that induce expression of
PT cell surface antigens and antibodies to a subject having or at risk of
PT developing cancer.
XX
XX Disclosure; Page 309; 312pp; English.
XX
XX The present invention relates to methods for treating or preventing
CC cancer, involving administering to a subject having or at risk of
CC developing cancer immunostimulatory nucleic acids that induce expression
CC of cell surface antigens and antibodies. The methods are useful for
CC treating or preventing cancer such as basal cell carcinoma, bladder
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC breast cancer, cervical cancer, colon and rectum cancer, connective
CC tissue cancer, esophageal cancer, eye cancer, kidney cancer, larynx
CC cancer, leukemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC present sequence is an immunostimulatory oligonucleotide described in the
CC exemplification of the invention
XX
SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 21;
XX Best Local Similarity 88.9%; Pred. No. 4.2e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
OY 1520 AAAAAAAAAAATAAAA 1537
XX ||||| |||||
DB 21 AAAAAAAAAAAAAAAAAA 4
XX
RESULT 903
ABS97830/C
ID ABS97830 standard; DNA; 21 BP.
XX
XX ABS97830;
XX
XX 23-DEC-2002 (first entry)
XX
XX Human NADPH quinone oxidoreductase 2 (NQO2) polymorphic sequence #38.
XX
XX Human; de; cytochrome P450 A1; CYP450A1; UGT2B4; MDR1;
KM cytochrome P450 A2; CYP450A2; cytochrome P450 02E; CYP45002E1; LTF;
KM adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR1I2;
KM aryl hydrocarbon receptor nuclear translocator; ARNT; catepsin S; CTS;
KM cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
KM epoxide hydrolase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
KM glutathione-S-transferase 12; GSTI2; histamine-N-methyl transferase; NNMT;
KM HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;
KM NADPH quinone oxidoreductase 2; NQO2; sulfotransferase thermolabile; STM;
KM UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
KM

KM UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;
KM multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
KM multidrug resistance associated protein 3; cancer; prostate;
KM acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR4; CHMR5;
KM altered drug metabolism; cardiovascular function; colorectal tumour;
KM central nervous system; pulmonary; immunological; SNP;
KM single nucleotide polymorphism.
XX
OS Homo sapiens.
XX
PN M0200257410-A2.
XX
PD 25-JUL-2002.
XX
PF 28-NOV-2001; 2001WO-US044838.
XX
PR 28-NOV-2000; 2000US-00724389.
XX
PA (DNAS-) DNA SCI LAB INC.
XX
PI Guida M, Hall J;
XX
PS WPI; 2002-698522/75.
XX
DR Isolated nucleic acid molecules having polymorphisms in known human genes
XX PT e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers
XX for locating, identifying and characterizing the genes responsible for
XX disorder-related traits.
XX
XX Example 16; Page 130; 714pp; English.
XX
CC This invention relates to the sequence of an isolated nucleic acid
CC molecule comprising at least one base variation from that of a known
CC human cytochrome p450 A1 (CYP450A1), cytochrome p450 A2 (CYP450A2),
CC cytochrome p450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADBR1),
CC aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
CC (ARNT), cathepsin S (CTSS), cyclooxygenase 2 (COX2), diazepam binding
CC inhibitor (DBI), epoxide hydrolase 2 (EPHX2), 5-lipoxygenase activating
CC protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl
CC transferase (HNMT), (kallikrein 2) KLK2, nicotineamide-N-methyl
CC transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),
CC sulfoltransferase thermolabile (STW), UDP-glucuronosyl transferase 2B4
CC (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
CC transferase (UGT2B15), urokinase receptor (uPA), multidrug resistance 1
CC (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
CC (MRP3), orphan nuclear receptor (NR1I2), or acetylcholine muscarinic
CC receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
CC The polymorphisms in the human genes cited in the invention are useful as
CC genetic linkage markers for locating and characterizing the genes that
CC are responsible for specific traits within the genome and eventually
CC identifying the genes responsible for a variety of disorder-related
CC traits as a result of their e.g., overexpression, constitutive
CC expression, mutation or underexpression, which may be used in diagnosing
CC and/or treating the disorders. The nucleic acid molecules comprising the
CC polymorphic sequences contained in CYP450A1, CYP450A2, CYP4502E1,
CC ARNT, EPHX2, GST12, NNMT, NQO2, NR1I2, STW, UGT2B4, UGT2B7, UGT2B15, AHR,
CC MDR1 and/or MDR3 are useful for screening individuals for altered drug
CC metabolism. The polymorphic sequences contained in CYP450A1, CYP450A2,
CC AHR, MDR1 and/or MDR3 may also be used to screen individuals for
CC susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
CC used to screen for altered cardiovascular function, in COX2 for altered
CC susceptibility to colorectal tumours, in DBI or CHMR1 for altered central
CC nervous system function, in FLAP and HNMT for altered pulmonary,
CC immunological or haematological function, in KLK2 for altered serine
CC protease activity in the prostate, in CHMR3, CHMR4 or CHMR5 for altered central
CC and peripheral nervous system function. The present sequence represents a
CC polymorphic DNA sequence of the invention
XX
SQ Sequence 21 BP; 10 A; 9 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 545 TGTGGTGGCTGTGGCTGG 562
DB 19 TGTGTGTGCTGTGTGTGG 2

RESULT 904
AAD51323/c
ID AAD51323 standard; DNA; 21 BP.
XX
AC AAD51323;
XX
DT 16-APR-2003 (first entry)
XX
DE Regular oligo dt primer used to illustrate the method of the invention.

XX
KM Laminitis; viral disease; vaccine; bacterial disease; primer; epistaxis;
KM gastritis; gastric ulcer; respiratory ailment; fracture; joint disease;
KM musculoskeletal damage; ss.
XX
OS Unidentified.
XX
PN M0200290579-A1.
XX
PD 14-NOV-2002.
XX
PF 03-MAY-2002; 2002WO-AU000553.
XX
PR 04-MAY-2001; 2001AU-00004809.
XX
PR 29-JUN-2001; 2001US-00896941.
XX
PA (GENO-) GENOMICS RES PARTNERS PTY LTD.

XX
PI Brandon RB;
XX
PS WPI; 2003-120558/11.
XX
DR Assessing condition e.g. athletic ability, stage of disease, presence of
XX PT drugs, response to exercise, response to vaccines, therapies, nutritional
XX states, of performance animal involves analyzing nucleic acid expression.
XX
XX Disclosure; Page 46; 87pp; English.

XX
CC The invention relates to a method for assessing a condition of a
CC performance animal. The method involves determining in sample abundance
CC of expressed target nucleic acid; transmitting digital signal to
CC remote diagnostic server; processing digital sample signal at remotely
CC located database to correlate digital signal with digital information and
CC returning report of particular condition of animal. The method is useful
CC for assessing a condition of a performance animal preferably human, dog
CC or camel. The condition can be an athletic ability and a condition that
CC enhances, hinders, impedes or does not change an expected ability of the
CC performance animal, and also normal, pre-clinical, overt progress and/or
CC stage of disease, undiagnosed or unclassified conditions, presence of
CC drugs, response to exercise, response to vaccines, therapies, nutritional
CC states and response to environmental conditions. Diseases assessed by the
CC invention include laminitis, lameness, viral or bacterial disease,
CC gastritis, gastric ulcers, respiratory ailments, fractures, epistaxis,
CC musculoskeletal damage or disorders and joint diseases. The present
CC sequence is a primer used to illustrate the method of the invention
XX
SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
DB 21 AAAAAAAAAAAAAAAAAA 4

RESULT 905
ACH03246/C
ID ACH03246 standard; DNA; 21 BP.
XX
AC ACH03246;
XX
DT 25-SEP-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #881.
XX
KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW anticulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
OS Synthetic.
XX
PN US2003050268-A1.
XX
PD 13-MAR-2003.
XX
PE 29-MAR-2002; 2002US-00112653.
XX
PR 29-MAR-2001; 2001US-0279642P.
XX
PA (KRIE/) KRIEG A M.
PA (BERG/) BERG D J.
XX
PI Kriegl AM, Berg DJ;
XX
DR WPI; 2003-521815/49.
XX
PT Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT disease by administering an immunostimulatory nucleic acid.
XX
PS Disclosure; Page 33; 229pp; English.
XX
CC The invention describes a method of treating non-allergic inflammatory
CC disease comprising administering to a subject having or at risk of
CC developing a non-allergic inflammatory disease an immunostimulatory
CC nucleic acid for prevention or treatment of the disease. The method is
CC useful for treating non-allergic inflammatory diseases, such as
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC This sequence represents an immunostimulatory nucleic acid
XX
SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred.No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAAGTAAAA 1537
DB 21 AAAAAAAAAA 4
XX
RESULT 906
ADB37209/C
ID ADB37209 standard; DNA; 21 BP.
XX
AC ADB37209;
XX
DT 04-DEC-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #823.
XX
KW db; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW hypo-responsive subject; immunostimulatory.
XX
OS Synthetic.
XX

PN US2003087848-A1.
XX
PD 08-MAY-2003.
XX
PF 02-FEB-2001; 2001US-00776479.
XX
PR 03-FEB-2000; 2000US-0179991P.
XX
PA (BRAT/) BRATZLER R L.
PA (PERE/) PETERSEN D M.
PA (FOUR/) FOURON Y.
XX
PI Bratzler RL, Petersen DM, Fouron Y;
XX
DR WPI; 2003-657977/62.
XX
PT Treating and/or preventing allergy or asthma using an immunostimulatory
PT nucleic acid alone or in combination with an asthma/allergy medicament.
XX
PS Disclosure; Page 17; 221pp; English.
XX
CC The invention relates to a method of treating or preventing allergy or
CC asthma which comprises administering to a subject a poly-G nucleic acid
CC in an aerosol formulation. The methods and compositions of the present
CC invention are useful for diagnosing and/or treating asthma and allergy
CC especially in a hypo-responsive subject. The present sequence represents
CC an immunostimulatory nucleic acid of the invention.
XX
SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred.No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAAGTAAAA 1537
DB 21 AAAAAAAAAA 4
XX
RESULT 907
ADK01309/C
ID ADK01309 standard; DNA; 21 BP.
XX
AC ADK01309;
XX
DT 06-MAY-2004 (first entry)
XX
DE Rat DNA microarray capture oligonucleotide #29.
XX
KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KW blood; nerve; germ cell; food additive; food supplement.
XX
OS Rattus sp.
XX
PN DE10208794-A1.
XX
PD 04-SEP-2003.
XX
PE 28-FEB-2002; 2002DE-01008794.
XX
PR 28-FEB-2002; 2002DE-01008794.
XX
PA (DEGS) DEGUSSA BIOACTIVES GMBH.
XX
PI Boekenkamp D, Dieck HT, Hoppe H;
XX
DR WPI; 2003-714082/68.
XX
PT Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.
XX
PS Example; Page 5; 8pp; German.

XX This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC reading out, where the nucleic acids are selectively bound using capture
CC agents that are (a) immobilised on the surface of a solid matrix and (b)
CC comprise variable and non-variable regions. The capture oligonucleotides
CC have a 5'-invariable anchor region, the complement of which is present at
CC least once in each nucleic acid and a 3'-variable, discriminatory region
CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
CC The method is used (i) for analysis of patterns, especially in mucosal,
CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC additives or supplements, especially minerals, trace elements, organic
CC mixtures. The method provides rapid, inexpensive and reproducible
CC representation of differences in pools of nucleic acids from cells. It
CC allows imaging of the complete pattern of all nucleic acids in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.

XX Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 908
ADK01318/c
ID ADK01318 standard; DNA; 21 BP.

XX ADK01318;

DT 06-MAY-2004 (first entry)

DE Rat DNA microarray capture oligonucleotide #38.

XX ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KM blood; nerve; germ cell; food additive; food supplement.

XX Rattus sp.

OS DE10208794-A1.

PN 04-SEP-2003.

XX 28-FEB-2002; 2002DE-01008794.

PR 28-FEB-2002; 2002DE-01008794.

XX (DEGS) DEGUSA BIOACTIVES GMBH.

XX Boekenkamp D, Dieck HT, Hoppe H;

XX WPI; 2003-714082/68.

XX Sorting single-stranded nucleic acid, useful for analyzing expression

PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.

PS Example; Page 5; Bpp; German.

XX This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC reading out, where the nucleic acids are selectively bound using capture
CC agents that are (a) immobilised on the surface of a solid matrix and (b)
CC comprise variable and non-variable regions. The capture oligonucleotides
CC have a 5'-invariable anchor region, the complement of which is present at
CC least once in each nucleic acid and a 3'-variable, discriminatory region
CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
CC The method is used (i) for analysis of patterns, especially in mucosal,
CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC additives or supplements, especially minerals, trace elements, organic
CC mixtures. The method provides rapid, inexpensive and reproducible
CC representation of differences in pools of nucleic acids from cells. It
CC allows imaging of the complete pattern of all nucleic acids in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.

XX Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 909
ADK01323/c
ID ADK01323 standard; DNA; 21 BP.

XX ADK01323;

DT 06-MAY-2004 (first entry)

DE Rat DNA microarray capture oligonucleotide #43.

XX ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KM blood; nerve; germ cell; food additive; food supplement.

XX Rattus sp.

OS DE10208794-A1.

PN 04-SEP-2003.

XX 28-FEB-2002; 2002DE-01008794.

PR 28-FEB-2002; 2002DE-01008794.

XX (DEGS) DEGUSA BIOACTIVES GMBH.

XX Boekenkamp D, Dieck HT, Hoppe H;

XX WPI; 2003-714082/68.

XX Sorting single-stranded nucleic acid, useful for analyzing expression
 PT patterns and screening active agents, uses capture agent with variable
 PT and constant regions.

XX Example; Page 5; 8pp; German.

XX This invention describes a novel method for sorting single-stranded
 CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
 CC reading out, where the nucleic acids are selectively bound using capture
 CC agents that are (a) immobilised on the surface of a solid matrix and (b)
 CC comprise variable and non-variable regions. The capture oligonucleotides
 CC have a 5'-invariable anchor region, the complement of which is present at
 CC least once in each nucleic acid and a 3'-variable, discriminatory region
 CC that comprises all possible combinations of up to 10 nucleotides to allow
 CC binding of particular sorts of single stranded nucleic acids. The capture
 CC agents are particularly locked nucleic acids (LNA) and the anchor region
 CC comprises a sequence of 10-50, particularly 15-25, T residues. The
 CC capture oligonucleotides are biotinylated and immobilised on a surface by
 CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
 CC metal, resin, gel, crystalline material and/or membrane, having semi-
 CC conducting properties and especially in the form of a chip. Its surface
 CC is particularly a layer of (bio)molecular filaments and binding of single
 CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
 CC physical, stimulated by an electrical field or through a molecular sieve.
 CC The method is used (i) for analysis of patterns, especially in mucosal,
 CC hair root, blood, nerve or germ cells and (ii) for determining the
 CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
 CC additives or supplements, especially minerals, trace elements, salts and
 CC mixtures. The method provides rapid, inexpensive and reproducible
 CC representation of differences in pools of nucleic acids from cells. It
 CC allows imaging of the complete pattern of all nucleic acid in a cell, and
 CC can detect very small differences in the nucleic acid pool. Since the
 CC method is based on comparison of nucleic acid pools, not individual
 CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
 CC capture probes used in the method of the invention.

XX Sequence 21 BP; 0 A; 3 C; 0 G; 18 T; 0 U; 0 Other;

XX Query Match 1.1%; Score 14.8; DB 1; Length 21;
 XX Best Local Similarity 88.9%; Pred. No. 4.2e+02;
 XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537

Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 910
 ADK01344/C
 ID ADK01344 standard; DNA; 21 BP.

XX AC ADK01344;

XX DT 06-MAY-2004 (first entry)

DE Rat DNA microarray capture oligonucleotide #64.

KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
 KM blood; nerve; germ cell; food additive; food supplement.

XX OS Rattus sp.

XX PN DE10208794-A1.

XX PD 04-SEP-2003.

XX PF 28-FEB-2002; 2002DE-01008794.

XX PR 28-FEB-2002; 2002DE-01008794.

XX (DEGS) DEGUSSA BIOACTIVES GMBH.

XX bi Boekenkamp D, Dieck HT, Hoppe H;

XX WPI; 2003-714082/68.

XX Sorting single-stranded nucleic acid, useful for analyzing expression
 PT patterns and screening active agents, uses capture agent with variable
 PT and constant regions.

XX Example; Page 6; 8pp; German.

XX This invention describes a novel method for sorting single-stranded
 CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
 CC reading out, where the nucleic acids are selectively bound using capture
 CC agents that are (a) immobilised on the surface of a solid matrix and (b)
 CC comprise variable and non-variable regions. The capture oligonucleotides
 CC have a 5'-invariable anchor region, the complement of which is present at
 CC least once in each nucleic acid and a 3'-variable, discriminatory region
 CC that comprises all possible combinations of up to 10 nucleotides to allow
 CC binding of particular sorts of single stranded nucleic acids. The capture
 CC agents are particularly locked nucleic acids (LNA) and the anchor region
 CC comprises a sequence of 10-50, particularly 15-25, T residues. The
 CC capture oligonucleotides are biotinylated and immobilised on a surface by
 CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
 CC metal, resin, gel, crystalline material and/or membrane, having semi-
 CC conducting properties and especially in the form of a chip. Its surface
 CC is particularly a layer of (bio)molecular filaments and binding of single
 CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
 CC physical, stimulated by an electrical field or through a molecular sieve.
 CC The method is used (i) for analysis of patterns, especially in mucosal,
 CC hair root, blood, nerve or germ cells and (ii) for determining the
 CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
 CC additives or supplements, especially minerals, trace elements, organic
 CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
 CC mixtures. The method provides rapid, inexpensive and reproducible
 CC representation of differences in pools of nucleic acids from cells. It
 CC allows imaging of the complete pattern of all nucleic acid in a cell, and
 CC can detect very small differences in the nucleic acid pool. Since the
 CC method is based on comparison of nucleic acid pools, not individual
 CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
 CC capture probes used in the method of the invention.

XX Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;

XX Query Match 1.1%; Score 14.8; DB 1; Length 21;
 XX Best Local Similarity 88.9%; Pred. No. 4.2e+02;
 XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537

Db 21 AAAAAAAAAAAAAAAAAA 4

RESULT 911
 ADK01340/C
 ID ADK01340 standard; DNA; 21 BP.

XX AC ADK01340;

XX DT 06-MAY-2004 (first entry)

DE Rat DNA microarray capture oligonucleotide #60.

KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
 KM blood; nerve; germ cell; food additive; food supplement.

XX OS Rattus sp.

XX PN DE10208794-A1.

XX PD 04-SEP-2003.

```
XX 28-FEB-2002; 2002DE-01008794.
PF
XX
XX 28-FEB-2002; 2002DE-01008794.
PR
XX
XX (DEGS ) DEGUSSA BIOACTIVES GMBH.
PA
XX
XX Boekenkamp D, Dieck HT, Hoppe H;
PI
XX WPI; 2003-714082/68.
DR
XX
XX Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.
XX
XX Example; Page 6; 8pp; German.
XX
CC This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC reading out, where the nucleic acids are selectively bound using capture
CC agents that are (a) immobilised on the surface of a solid matrix and (b)
CC comprise variable and non-variable regions. The capture oligonucleotides
CC have a 5'-invariable anchor region, the complement of which is present at
CC least once in each nucleic acid and a 3'-variable, discriminatory region
CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
CC The method is used (i) for analysis of patterns, especially in mucosal,
CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC additives or supplements, especially minerals, trace elements, organic
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC mixtures. The method provides rapid, inexpensive and reproducible
CC representation of differences in pools of nucleic acids from cells. It
CC allows imaging of the complete pattern of all nucleic acid in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.
XX
XX Sequence 21 BP; 0 A; 1 C; 0 G; 20 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAAGTAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2
RESULT 912
ADK01319/c
ID ADK01319 standard; DNA; 21 BP.
XX
XX ADK01319;
AC
XX
XX 06-MAY-2004 (first entry)
DT
XX
XX Rat DNA microarray capture oligonucleotide #39.
DE
XX
XX se; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KM blood; nerve; germ cell; food additive; food supplement.
XX
XX Rattus sp.
OS
```

```
XX DE10208794-A1.
XX
XX
XX 04-SEP-2003.
PD
XX
XX 28-FEB-2002; 2002DE-01008794.
PF
XX
XX 28-FEB-2002; 2002DE-01008794.
PR
XX
XX (DEGS ) DEGUSSA BIOACTIVES GMBH.
PA
XX
XX Boekenkamp D, Dieck HT, Hoppe H;
PI
XX WPI; 2003-714082/68.
DR
XX
XX Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.
XX
XX Example; Page 5; 8pp; German.
XX
CC This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC reading out, where the nucleic acids are selectively bound using capture
CC agents that are (a) immobilised on the surface of a solid matrix and (b)
CC comprise variable and non-variable regions. The capture oligonucleotides
CC have a 5'-invariable anchor region, the complement of which is present at
CC least once in each nucleic acid and a 3'-variable, discriminatory region
CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
CC The method is used (i) for analysis of patterns, especially in mucosal,
CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC additives or supplements, especially minerals, trace elements, organic
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC mixtures. The method provides rapid, inexpensive and reproducible
CC representation of differences in pools of nucleic acids from cells. It
CC allows imaging of the complete pattern of all nucleic acid in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.
XX
XX Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAAGTAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1
RESULT 913
ADK01328/c
ID ADK01328 standard; DNA; 21 BP.
XX
XX ADK01328;
AC
XX
XX 06-MAY-2004 (first entry)
DT
XX
XX Rat DNA microarray capture oligonucleotide #48.
DE
XX
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ID ADK01302 standard; DNA; 21 BP.
XX
XX ADK01302;
XX
DT 06-MAY-2004 (first entry)
XX
DE Rat DNA microarray capture oligonucleotide #22.
XX
XX ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KM blood; nerve; germ cell; food additive; food supplement.
XX
XX Rattus sp.
XX
XX DE10208794-A1.
XX
XX 04-SEP-2003.
XX
XX 28-FEB-2002; 2002DE-01008794.
XX
XX 28-FEB-2002; 2002DE-01008794.
XX
XX (DEGSA ) DEGUSA BIOACTIVES GMBH.
XX
XX Boekenkamp D, Dieck HT, Hoppe H;
XX
XX WPI; 2003-714082/68.
XX
PT Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.
XX
XX Example; Page 5; 8pp; German.
XX
CC This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC reading out, where the nucleic acids are selectively bound using capture
CC agents that are (a) immobilised on the surface of a solid matrix and (b)
CC comprise variable and non-variable regions. The capture oligonucleotides
CC have a 5'-invariable anchor region, the complement of which is present at
CC least once in each nucleic acid and a 3'-variable, discriminatory region
CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
CC The method is used (i) for analysis of patterns, especially in mucosal,
CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC additives or supplements, especially minerals, trace elements, organic
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC mixtures. The method provides rapid, inexpensive and reproducible
CC representation of differences in pools of nucleic acids from cells. It
CC allows imaging of the complete pattern of all nucleic acid in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.
XX
SQ Sequence 21 BP; 0 A; 0 C; 3 G; 18 T; 0 U; 0 Other;
```

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Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
0Y 1520 AAAAAAAAAAAGTAA 1537
18 AAAAAAAAAAAAAAAAA 1
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RESULT 916
ADK01317/c
ID ADK01317 standard; DNA; 21 BP.
XX
XX ADK01317;
XX
DT 06-MAY-2004 (first entry)
XX
DE Rat DNA microarray capture oligonucleotide #37.
XX
XX ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KM blood; nerve; germ cell; food additive; food supplement.
XX
XX Rattus sp.
XX
XX DE10208794-A1.
XX
XX 04-SEP-2003.
XX
XX 28-FEB-2002; 2002DE-01008794.
XX
XX 28-FEB-2002; 2002DE-01008794.
XX
XX (DEGSA ) DEGUSA BIOACTIVES GMBH.
XX
XX Boekenkamp D, Dieck HT, Hoppe H;
XX
XX WPI; 2003-714082/68.
XX
PT Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.
XX
XX Example; Page 5; 8pp; German.
XX
CC This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC reading out, where the nucleic acids are selectively bound using capture
CC agents that are (a) immobilised on the surface of a solid matrix and (b)
CC comprise variable and non-variable regions. The capture oligonucleotides
CC have a 5'-invariable anchor region, the complement of which is present at
CC least once in each nucleic acid and a 3'-variable, discriminatory region
CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
CC The method is used (i) for analysis of patterns, especially in mucosal,
CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC additives or supplements, especially minerals, trace elements, organic
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC mixtures. The method provides rapid, inexpensive and reproducible
CC representation of differences in pools of nucleic acids from cells. It
CC allows imaging of the complete pattern of all nucleic acid in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.
XX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
```

```
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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OY      1520 AAAAAAAAAAGTAAAA 1537
DB      18 AAAAAAAAAAAAAAAAAA 1

RESULT 917
ID      ADK01334 standard; DNA; 21 BP.
XX      ADK01334;
AC      ADK01334;
XX      06-MAY-2004 (first entry)
DT
XX      Rat DNA microarray capture oligonucleotide #54.
DE
XX      ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KW      blood; nerve; germ cell; food additive; food supplement.
XX      Rattus sp.
OS      DE10208794-A1.
XX      04-SEP-2003.
PD      28-FEB-2002; 2002DE-01008794.
XX      28-FEB-2002; 2002DE-01008794.
PR      28-FEB-2002; 2002DE-01008794.
XX      (DEGS ) DEGUSSA BIOACTIVES GMBH.
PA      Boekenkamp D, Dieck HT, Hoppe H;
XX      WPI; 2003-714082/68.
DR
XX      Sorting single-stranded nucleic acid, useful for analyzing expression
PT      patterns and screening active agents, uses capture agent with variable
PT      and constant regions.
XX
PS      Example; Page 5; 8pp; German.
XX
CC      This invention describes a novel method for sorting single-stranded
CC      nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC      reading out, where the nucleic acids are selectively bound using capture
CC      agents that are (a) immobilised on the surface of a solid matrix and (b)
CC      comprise variable and non-variable regions. The capture oligonucleotides
CC      have a 5'-invariable anchor region, the complement of which is present at
CC      least once in each nucleic acid and a 3'-variable, discriminatory region
CC      that comprises all possible combinations of up to 10 nucleotides to allow
CC      binding of particular sorts of single stranded nucleic acids. The capture
CC      agents are particularly locked nucleic acids (LNA) and the anchor region
CC      comprises a sequence of 10-50, particularly 15-25, T residues. The
CC      capture oligonucleotides are biotinylated and immobilised on a surface by
CC      interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC      metal, resin, gel, crystalline material and/or membrane, having semi-
CC      conducting properties and especially in the form of a chip. Its surface
CC      is particularly a layer of (bio)molecular filaments and binding of single
CC      stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC      physical, stimulated by an electrical field or through a molecular sieve.
CC      The method is used (i) for analysis of patterns, especially in mucosal,
CC      hair root, blood, nerve or germ cells and (ii) for determining the
CC      activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC      additives or supplements, especially minerals, trace elements, organic
CC      acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC      mixtures. The method provides rapid, inexpensive and reproducible
CC      representation of differences in pools of nucleic acids from cells. It
CC      allows imaging of the complete pattern of all nucleic acids in a cell, and
CC      can detect very small differences in the nucleic acid pool. Since the
CC      method is based on comparison of nucleic acid pools, not individual
CC      genes, matrix mislabelisation is possible. ADK01281-ADK01344 represent
CC      capture probes used in the method of the invention.
XX      Sequence 21 BP; 0 A; 0 C; 2 G; 19 T; 0 U; 0 Other;
SQ

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Query Match      1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      1520 AAAAAAAAAAGTAAAA 1537
DB      19 AAAAAAAAAAAAAAAAAA 2

RESULT 918
ID      ADK01303 standard; DNA; 21 BP.
XX      ADK01303;
AC      ADK01303;
XX      06-MAY-2004 (first entry)
DT
XX      Rat DNA microarray capture oligonucleotide #23.
DE
XX      ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KW      blood; nerve; germ cell; food additive; food supplement.
XX      Rattus sp.
OS      DE10208794-A1.
XX      04-SEP-2003.
PD      28-FEB-2002; 2002DE-01008794.
XX      28-FEB-2002; 2002DE-01008794.
PR      28-FEB-2002; 2002DE-01008794.
XX      (DEGS ) DEGUSSA BIOACTIVES GMBH.
PA      Boekenkamp D, Dieck HT, Hoppe H;
XX      WPI; 2003-714082/68.
DR
XX      Sorting single-stranded nucleic acid, useful for analyzing expression
PT      patterns and screening active agents, uses capture agent with variable
PT      and constant regions.
XX
PS      Example; Page 5; 8pp; German.
XX
CC      This invention describes a novel method for sorting single-stranded
CC      nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC      reading out, where the nucleic acids are selectively bound using capture
CC      agents that are (a) immobilised on the surface of a solid matrix and (b)
CC      comprise variable and non-variable regions. The capture oligonucleotides
CC      have a 5'-invariable anchor region, the complement of which is present at
CC      least once in each nucleic acid and a 3'-variable, discriminatory region
CC      that comprises all possible combinations of up to 10 nucleotides to allow
CC      binding of particular sorts of single stranded nucleic acids. The capture
CC      agents are particularly locked nucleic acids (LNA) and the anchor region
CC      comprises a sequence of 10-50, particularly 15-25, T residues. The
CC      capture oligonucleotides are biotinylated and immobilised on a surface by
CC      interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC      metal, resin, gel, crystalline material and/or membrane, having semi-
CC      conducting properties and especially in the form of a chip. Its surface
CC      is particularly a layer of (bio)molecular filaments and binding of single
CC      stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC      physical, stimulated by an electrical field or through a molecular sieve.
CC      The method is used (i) for analysis of patterns, especially in mucosal,
CC      hair root, blood, nerve or germ cells and (ii) for determining the
CC      activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC      additives or supplements, especially minerals, trace elements, organic
CC      acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC      mixtures. The method provides rapid, inexpensive and reproducible
CC      representation of differences in pools of nucleic acids from cells. It
CC      allows imaging of the complete pattern of all nucleic acids in a cell, and
CC      can detect very small differences in the nucleic acid pool. Since the
CC      method is based on comparison of nucleic acid pools, not individual

```

CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.

XX Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 21;

Best Local Similarity 88.9%; Pred. No. 4.2e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 919
ADK01327/c
ID ADK01327 standard; DNA; 21 BP.

XX AC ADK01327;

XX DT 06-MAY-2004 (first entry)

XX DE Rat DNA microarray capture oligonucleotide #47.

XX KM ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;

XX KM blood; nerve; germ cell; food additive; food supplement.

XX OS Rattus sp.

XX PN DE10208794-A1.

XX PD 04-SEP-2003.

XX PF 28-FEB-2002; 2002DE-01008794.

XX PR 28-FEB-2002; 2002DE-01008794.

XX PA (DEGSS) DEGSSA BIOACTIVES GMBH.

XX PI Boekenkamp D, Dieck HT, Hoppe H;

XX DR WPI; 2003-714082/68.

PT Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.

XX PS Example; Page 5; Bpp; German.

XX This invention describes a novel method for sorting single-stranded
XX nucleic acids by isolation and hybridisation of nucleic acid pools, then

XX reading out, where the nucleic acids are selectively bound using capture
XX agents that are (a) immobilised on the surface of a solid matrix and (b)

XX comprise variable and non-variable regions. The capture oligonucleotides
XX have a 5'-invariable anchor region, the complement of which is present at

XX least once in each nucleic acid and a 3'-variable, discriminatory region
XX that comprises all possible combinations of up to 10 nucleotides to allow

XX binding of particular sorts of single stranded nucleic acids. The capture
XX agents are particularly locked nucleic acids (LNA) and the anchor region

XX comprises a sequence of 10-50, particularly 15-25, T residues. The
XX capture oligonucleotides are biotinylated and immobilised on a surface by

XX interaction with streptavidin. The matrix is of plastic, ceramic, glass,
XX metal, resin, gel, crystalline material and/or membrane, having semi-

XX conducting properties and especially in the form of a chip. Its surface
XX is particularly a layer of (bio)molecular filaments and binding of single

XX stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
XX physical, stimulated by an electrical field or through a molecular sieve.

XX The method is used (i) for analysis of patterns, especially in mucosal,
XX hair root, blood, nerve or germ cells and (ii) for determining the

XX activity of pharmaceuticals and/or nutritional compounds, e.g. food
XX additives or supplements, especially minerals, trace elements, organic

XX acids (amino, carboxylic or fatty acid) or their derivatives, salts and
XX mixtures. The method provides rapid, inexpensive and reproducible

CC representation of differences in pools of nucleic acids from cells. It
CC allows imaging of the complete pattern of all nucleic acid in a cell, and

CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual

CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.

XX Sequence 21 BP; 0 A; 2 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 21;

Best Local Similarity 88.9%; Pred. No. 4.2e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 920
ADK01338/c
ID ADK01338 standard; DNA; 21 BP.

XX AC ADK01338;

XX DT 06-MAY-2004 (first entry)

XX DE Rat DNA microarray capture oligonucleotide #58.

XX KM ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;

XX KM blood; nerve; germ cell; food additive; food supplement.

XX OS Rattus sp.

XX PN DE10208794-A1.

XX PD 04-SEP-2003.

XX PF 28-FEB-2002; 2002DE-01008794.

XX PR 28-FEB-2002; 2002DE-01008794.

XX PA (DEGSS) DEGSSA BIOACTIVES GMBH.

XX PI Boekenkamp D, Dieck HT, Hoppe H;

XX DR WPI; 2003-714082/68.

PT Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.

XX PS Example; Page 6; Bpp; German.

XX This invention describes a novel method for sorting single-stranded
XX nucleic acids by isolation and hybridisation of nucleic acid pools, then

XX reading out, where the nucleic acids are selectively bound using capture
XX agents that are (a) immobilised on the surface of a solid matrix and (b)

XX comprise variable and non-variable regions. The capture oligonucleotides
XX have a 5'-invariable anchor region, the complement of which is present at

XX least once in each nucleic acid and a 3'-variable, discriminatory region
XX that comprises all possible combinations of up to 10 nucleotides to allow

XX binding of particular sorts of single stranded nucleic acids. The capture
XX agents are particularly locked nucleic acids (LNA) and the anchor region

XX comprises a sequence of 10-50, particularly 15-25, T residues. The
XX capture oligonucleotides are biotinylated and immobilised on a surface by

XX interaction with streptavidin. The matrix is of plastic, ceramic, glass,
XX metal, resin, gel, crystalline material and/or membrane, having semi-

XX conducting properties and especially in the form of a chip. Its surface
XX is particularly a layer of (bio)molecular filaments and binding of single

XX stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
XX physical, stimulated by an electrical field or through a molecular sieve.

XX The method is used (i) for analysis of patterns, especially in mucosal,
XX hair root, blood, nerve or germ cells and (ii) for determining the

CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC additives or supplements, especially minerals, trace elements, organic
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC mixtures. The method provides rapid, inexpensive and reproducible
CC representation of differences in pools of nucleic acids from cells. It
CC allows imaging of the complete pattern of all nucleic acid in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.
XX
SQ Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 86.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAGTAAA 1537
DB 19 AAAAAAAAAAAAAAAAAA 2
RESULT 921
ADK01307/C
ID ADK01307 standard; DNA; 21 BP.
XX
AC ADK01307;
XX
DT 06-MAY-2004 (first entry)
XX
DE Rat DNA microarray capture oligonucleotide #27.
XX
KM ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KM blood; nerve; germ cell; food additive; food supplement.
XX
OS Rattus sp.
XX
PN DE10208794-A1.
PD 04-SEP-2003.
XX
PF 28-FEB-2002; 2002DE-01008794.
XX
PR 28-FEB-2002; 2002DE-01008794.
XX
PA (DEGS) DEGUSSA BIOACTIVES GMBH.
XX
PI Boekenkamp D, Dieck HT, Hoppe H;
XX
DR WPI; 2003-714082/68.
XX
PT Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.
XX
PS Example; Page 5; 8pp; German.
XX
CC This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC reading out, where the nucleic acids are selectively bound using capture
CC agents that are (a) immobilised on the surface of a solid matrix and (b)
CC comprise variable and non-variable regions. The capture oligonucleotides
CC have a 5'-invariable anchor region, the complement of which is present at
CC least once in each nucleic acid and a 3'-variable, discriminatory region
CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single

CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
CC The method is used (i) for analysis of patterns, especially in mucosal,
CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC additives or supplements, especially minerals, trace elements, organic
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC mixtures. The method provides rapid, inexpensive and reproducible
CC representation of differences in pools of nucleic acids from cells. It
CC allows imaging of the complete pattern of all nucleic acid in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.
XX
SQ Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAGTAAA 1537
DB 18 AAAAAAAAAAAAAAAAAA 1
RESULT 922
ADK01320/C
ID ADK01320 standard; DNA; 21 BP.
XX
AC ADK01320;
XX
DT 06-MAY-2004 (first entry)
XX
DE Rat DNA microarray capture oligonucleotide #40.
XX
KM ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KM blood; nerve; germ cell; food additive; food supplement.
XX
OS Rattus sp.
XX
PN DE10208794-A1.
PD 04-SEP-2003.
XX
PF 28-FEB-2002; 2002DE-01008794.
XX
PR 28-FEB-2002; 2002DE-01008794.
XX
PA (DEGS) DEGUSSA BIOACTIVES GMBH.
XX
PI Boekenkamp D, Dieck HT, Hoppe H;
XX
DR WPI; 2003-714082/68.
XX
PT Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.
XX
PS Example; Page 5; 8pp; German.
XX
CC This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC reading out, where the nucleic acids are selectively bound using capture
CC agents that are (a) immobilised on the surface of a solid matrix and (b)
CC comprise variable and non-variable regions. The capture oligonucleotides
CC have a 5'-invariable anchor region, the complement of which is present at
CC least once in each nucleic acid and a 3'-variable, discriminatory region
CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by

CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
CC The method is used (i) for analysis of patterns, especially in mucosal,
CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC additives or supplements, especially minerals, trace elements, organic
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC mixtures. The method provides rapid, inexpensive and reproducible
CC representation of differences in pools of nucleic acids from cells. It
CC allows imaging of the complete pattern of all nucleic acid in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.

XX Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 21;

Best Local Similarity 88.9%; Pred. No. 4.2e+02; Mismatches 2; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAAGTAAAA 1537

DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 923

ADK01304/c

ID ADK01304 standard; DNA; 21 BP.

AC ADK01304;

DT 06-MAY-2004 (first entry)

DE Rat DNA microarray capture oligonucleotide #24.

KM 8g; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;

KM blood; nerve; germ cell; food additive; food supplement.

OS Rattus sp.

PN DE10208794-A1.

XX 04-SEP-2003.

XX 28-FEB-2002; 2002DE-01008794.

XX 28-FEB-2002; 2002DE-01008794.

XX (DEGS) DEGUSSA BIOACTIVES GMBH.

XX Boekenkamp D, Dieck HT, Hoppe H;

XX WPI; 2003-714082/68.

PT Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.

XX Example; Page 5; 8pp; German.

XX This invention describes a novel method for sorting single-stranded

CC nucleic acids by isolation and hybridisation of nucleic acid pools, then

CC reading out, where the nucleic acids are selectively bound using capture

CC agents that are (a) immobilised on the surface of a solid matrix and (b)

CC comprise variable and non-variable regions. The capture oligonucleotides

CC have a 5'-invariable anchor region, the complement of which is present at

CC least once in each nucleic acid and a 3'-variable, discriminatory region

CC that comprises all possible combinations of up to 10 nucleotides to allow

CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
CC The method is used (i) for analysis of patterns, especially in mucosal,
CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC additives or supplements, especially minerals, trace elements, organic
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC mixtures. The method provides rapid, inexpensive and reproducible
CC representation of differences in pools of nucleic acids from cells. It
CC allows imaging of the complete pattern of all nucleic acid in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.

XX Sequence 21 BP; 0 A; 0 C; 2 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 21;

Best Local Similarity 88.9%; Pred. No. 4.2e+02; Mismatches 2; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAAGTAAAA 1537

DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 924

ADK01306/c

ID ADK01306 standard; DNA; 21 BP.

AC ADK01306;

DT 06-MAY-2004 (first entry)

DE Rat DNA microarray capture oligonucleotide #26.

KM 8g; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;

KM blood; nerve; germ cell; food additive; food supplement.

OS Rattus sp.

XX 04-SEP-2003.

XX 28-FEB-2002; 2002DE-01008794.

XX 28-FEB-2002; 2002DE-01008794.

XX (DEGS) DEGUSSA BIOACTIVES GMBH.

XX Boekenkamp D, Dieck HT, Hoppe H;

XX WPI; 2003-714082/68.

PT Sorting single-stranded nucleic acid, useful for analyzing expression

PT patterns and screening active agents, uses capture agent with variable

PT and constant regions.

XX Example; Page 5; 8pp; German.

CC This invention describes a novel method for sorting single-stranded

CC nucleic acids by isolation and hybridisation of nucleic acid pools, then

CC reading out, where the nucleic acids are selectively bound using capture

CC agents that are (a) immobilised on the surface of a solid matrix and (b)

CC comprise variable and non-variable regions. The capture oligonucleotides
CC have a 5'-invariable anchor region, the complement of which is present at
CC least once in each nucleic acid and a 3'-variable, discriminatory region
CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
CC The method is used (i) for analysis of patterns, especially in mucosal,
CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC additives or supplements, especially minerals, trace elements, organic
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC mixtures. The method provides rapid, inexpensive and reproducible
CC representation of differences in pools of nucleic acids from cells. It
CC allows imaging of the complete pattern of all nucleic acid in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.

XX Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537

Db |||||
18 AAAAAAAAAAAAAAAAAA 1

RESULT 925
ADK01325/C

ID ADK01325 standard; DNA; 21 BP.

XX AC ADK01325;

XX DT 06-MAY-2004 (first entry)

XX DE Rat DNA microarray capture oligonucleotide #45.

XX KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;

XX KM blood; nerve; germ cell; food additive; food supplement.

XX OS Rattus sp.

XX PN DE10208794-A1.

XX PD 04-SEP-2003.

XX PF 28-FEB-2002; 2002DE-01008794.

XX PR 28-FEB-2002; 2002DE-01008794.

XX PA (DEGS) DEGUSSA BIOACTIVES GMBH.

XX PI Boekenkamp D, Dieck HT, Hoppe H;

XX DR WPI; 2003-714082/68.

XX PT Sorting single-stranded nucleic acid, useful for analyzing expression
XX patterns and screening active agents, uses capture agent with variable
XX and constant regions.

XX Example; Page 5; 8pp; German.

CC This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC reading out, where the nucleic acids are selectively bound using capture
CC agents that are (a) immobilised on the surface of a solid matrix and (b)
CC comprise variable and non-variable regions. The capture oligonucleotides
CC have a 5'-invariable anchor region, the complement of which is present at
CC least once in each nucleic acid and a 3'-variable, discriminatory region
CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
CC The method is used (i) for analysis of patterns, especially in mucosal,
CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC additives or supplements, especially minerals, trace elements, organic
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC mixtures. The method provides rapid, inexpensive and reproducible
CC representation of differences in pools of nucleic acids from cells. It
CC allows imaging of the complete pattern of all nucleic acid in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.

XX Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537

Db |||||
18 AAAAAAAAAAAAAAAAAA 1

RESULT 926
ADK01339/C

ID ADK01339 standard; DNA; 21 BP.

XX AC ADK01339;

XX DT 06-MAY-2004 (first entry)

XX DE Rat DNA microarray capture oligonucleotide #59.

XX KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;

XX KM blood; nerve; germ cell; food additive; food supplement.

XX OS Rattus sp.

XX PN DE10208794-A1.

XX PD 04-SEP-2003.

XX PF 28-FEB-2002; 2002DE-01008794.

XX PR 28-FEB-2002; 2002DE-01008794.

XX PA (DEGS) DEGUSSA BIOACTIVES GMBH.

XX PI Boekenkamp D, Dieck HT, Hoppe H;

XX DR WPI; 2003-714082/68.

XX PT Sorting single-stranded nucleic acid, useful for analyzing expression
XX patterns and screening active agents, uses capture agent with variable

PT and constant regions.
 XX
 PS Example; Page 6; Bpp; German.
 XX
 CC This invention describes a novel method for sorting single-stranded
 CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
 CC reading out, where the nucleic acids are selectively bound using capture
 CC agents that are (a) immobilised on the surface of a solid matrix and (b)
 CC comprise variable and non-variable regions. The capture oligonucleotides
 CC have a 5'-invariable anchor region, the complement of which is present at
 CC least once in each nucleic acid and a 3'-variable, discriminatory region
 CC that comprises all possible combinations of up to 10 nucleotides to allow
 CC binding of particular sorts of single stranded nucleic acids. The capture
 CC agents are particularly locked nucleic acids (LNA) and the anchor region
 CC comprises a sequence of 10-50, particularly 15-25, T residues. The
 CC capture oligonucleotides are biotinylated and immobilised on a surface by
 CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
 CC metal, resin, gel, crystalline material and/or membrane, having semi-
 CC conducting properties and especially in the form of a chip. Its surface
 CC is particularly a layer of (bio)molecular filaments and binding of single
 CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
 CC physical, stimulated by an electrical field or through a molecular sieve.
 CC The method is used (i) for analysis of patterns, especially in mucosal,
 CC hair root, blood, nerve or germ cells and (ii) for determining the
 CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
 CC additives or supplements, especially minerals, trace elements, organic
 CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
 CC mixtures. The method provides rapid, inexpensive and reproducible
 CC representation of differences in pools of nucleic acids from cells. It
 CC allows imaging of the complete pattern of all nucleic acid in a cell, and
 CC can detect very small differences in the nucleic acid pool. Since the
 CC method is based on comparison of nucleic acid pools, not individual
 CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
 CC capture probes used in the method of the invention.
 CC
 XX
 SQ Sequence 21 BP; 0 A; 2 C; 0 G; 19 T; 0 U; 0 Other;
 Query Match 1.1%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 4.2e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 1520 AAAAAAAAAAGTAAAA 1537
 |||||
 Db 19 AAAAAAAAAAAAAAAAAA 2
 RESULT 927
 ADK01343/c
 ID ADK01343 standard; DNA; 21 BP.
 XX
 AC ADK01343;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Rat DNA microarray capture oligonucleotide #63.
 XX
 KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
 KM blood; nerve; germ cell; food additive; food supplement.
 XX
 OS Rattus sp.
 XX
 PN DE10208794-A1.
 XX
 PD 04-SEP-2003.
 PF 28-FEB-2002; 2002DE-01008794.
 PR 28-FEB-2002; 2002DE-01008794.
 XX
 PA (DEGS) DEGUSSA BIOACTIVES GMBH.
 XX
 PI Boekenkamp D, Dieck HT, Hoppe H;
 XX

DR WPI; 2003-714082/68.
 XX
 PT Sorting single-stranded nucleic acid, useful for analyzing expression
 PT patterns and screening active agents, uses capture agent with variable
 PT and constant regions.
 XX
 PS Example; Page 6; Bpp; German.
 XX
 CC This invention describes a novel method for sorting single-stranded
 CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
 CC reading out, where the nucleic acids are selectively bound using capture
 CC agents that are (a) immobilised on the surface of a solid matrix and (b)
 CC comprise variable and non-variable regions. The capture oligonucleotides
 CC have a 5'-invariable anchor region, the complement of which is present at
 CC least once in each nucleic acid and a 3'-variable, discriminatory region
 CC that comprises all possible combinations of up to 10 nucleotides to allow
 CC binding of particular sorts of single stranded nucleic acids. The capture
 CC agents are particularly locked nucleic acids (LNA) and the anchor region
 CC comprises a sequence of 10-50, particularly 15-25, T residues. The
 CC capture oligonucleotides are biotinylated and immobilised on a surface by
 CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
 CC metal, resin, gel, crystalline material and/or membrane, having semi-
 CC conducting properties and especially in the form of a chip. Its surface
 CC is particularly a layer of (bio)molecular filaments and binding of single
 CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
 CC physical, stimulated by an electrical field or through a molecular sieve.
 CC The method is used (i) for analysis of patterns, especially in mucosal,
 CC hair root, blood, nerve or germ cells and (ii) for determining the
 CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
 CC additives or supplements, especially minerals, trace elements, organic
 CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
 CC mixtures. The method provides rapid, inexpensive and reproducible
 CC representation of differences in pools of nucleic acids from cells. It
 CC allows imaging of the complete pattern of all nucleic acid in a cell, and
 CC can detect very small differences in the nucleic acid pool. Since the
 CC method is based on comparison of nucleic acid pools, not individual
 CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
 CC capture probes used in the method of the invention.
 CC
 XX
 SQ Sequence 21 BP; 0 A; 1 C; 0 G; 20 T; 0 U; 0 Other;
 Query Match 1.1%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 4.2e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 1520 AAAAAAAAAAGTAAAA 1537
 |||||
 Db 20 AAAAAAAAAAAAAAAAAA 3
 RESULT 928
 ADK01301/c
 ID ADK01301 standard; DNA; 21 BP.
 XX
 AC ADK01301;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Rat DNA microarray capture oligonucleotide #21.
 XX
 KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
 KM blood; nerve; germ cell; food additive; food supplement.
 XX
 OS Rattus sp.
 XX
 PN DE10208794-A1.
 XX
 PD 04-SEP-2003.
 PF 28-FEB-2002; 2002DE-01008794.
 PR 28-FEB-2002; 2002DE-01008794.
 XX
 PA (DEGS) DEGUSSA BIOACTIVES GMBH.
 XX
 PI Boekenkamp D, Dieck HT, Hoppe H;
 XX

PA (DEGS) DEGUSSA BIOACTIVES GMBH.
XX Boekenkamp D, Dieck HT, Hoppe H;
XX WPI; 2003-714082/68.
DR
XX
PT Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.
XX
XX Example; Page 5; 8pp; German.
XX
XX This invention describes a novel method for sorting single-stranded
XX nucleic acids by isolation and hybridisation of nucleic acid pools, then
XX reading out, where the nucleic acids are selectively bound using capture
XX agents that are (a) immobilised on the surface of a solid matrix and (b)
XX comprise variable and non-variable regions. The capture oligonucleotides
XX have a 5'-invariable anchor region, the complement of which is present at
XX least once in each nucleic acid and a 3'-variable, discriminatory region
XX that comprises all possible combinations of up to 10 nucleotides to allow
XX binding of particular sorts of single stranded nucleic acids. The capture
XX agents are particularly locked nucleic acids (LNA) and the anchor region
XX comprises a sequence of 10-50, particularly 15-25, T residues. The
XX capture oligonucleotides are biotinylated and immobilised on a surface by
XX interaction with streptavidin. The matrix is of plastic, ceramic, glass,
XX metal, resin, gel, crystalline material and/or membrane, having semi-
XX conducting properties and especially in the form of a chip. Its surface
XX is particularly a layer of (bio)molecular filaments and binding of single
XX stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
XX physical, stimulated by an electrical field or through a molecular sieve.
XX The method is used (i) for analysis of patterns, especially in mucosal,
XX hair root, blood, nerve or germ cells and (ii) for determining the
XX activity of pharmaceuticals and/or nutritional compounds, e.g. food
XX additives or supplements, especially minerals, trace elements, organic
XX acids (amino, carboxylic or fatty acid) or their derivatives, salts and
XX mixtures. The method provides rapid, inexpensive and reproducible
XX representation of differences in pools of nucleic acids from cells. It
XX allows imaging of the complete pattern of all nucleic acid in a cell, and
XX can detect very small differences in the nucleic acid pool. Since the
XX method is based on comparison of nucleic acid pools, not individual
XX genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
XX capture probes used in the method of the invention.
XX
S0 Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAAGTAAAA 1537
DB 18 AAAAAAAAAAAAAAAAAA 1
RESULT 929
ADK01312/C
ID ADK01312 standard; DNA; 21 BP.
XX
XX ADK01312;
XX
XX 06-MAY-2004 (first entry)
XX
XX Rat DNA microarray capture oligonucleotide #32.
XX
XX ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
XX blood; nerve; germ cell; food additive; food supplement.
XX
XX Rattus sp.
XX
XX DE10208794-A1.
XX
XX 04-SEP-2003.
XX

PF 28-FEB-2002; 2002DE-01008794.
XX
XX 28-FEB-2002; 2002DE-01008794.
XX
XX (DEGS) DEGUSSA BIOACTIVES GMBH.
XX
XX Boekenkamp D, Dieck HT, Hoppe H;
XX WPI; 2003-714082/68.
DR
XX
XX
XX
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PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.
XX
XX Example; Page 5; 8pp; German.
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XX This invention describes a novel method for sorting single-stranded
XX nucleic acids by isolation and hybridisation of nucleic acid pools, then
XX reading out, where the nucleic acids are selectively bound using capture
XX agents that are (a) immobilised on the surface of a solid matrix and (b)
XX comprise variable and non-variable regions. The capture oligonucleotides
XX have a 5'-invariable anchor region, the complement of which is present at
XX least once in each nucleic acid and a 3'-variable, discriminatory region
XX that comprises all possible combinations of up to 10 nucleotides to allow
XX binding of particular sorts of single stranded nucleic acids. The capture
XX agents are particularly locked nucleic acids (LNA) and the anchor region
XX comprises a sequence of 10-50, particularly 15-25, T residues. The
XX capture oligonucleotides are biotinylated and immobilised on a surface by
XX interaction with streptavidin. The matrix is of plastic, ceramic, glass,
XX metal, resin, gel, crystalline material and/or membrane, having semi-
XX conducting properties and especially in the form of a chip. Its surface
XX is particularly a layer of (bio)molecular filaments and binding of single
XX stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
XX physical, stimulated by an electrical field or through a molecular sieve.
XX The method is used (i) for analysis of patterns, especially in mucosal,
XX hair root, blood, nerve or germ cells and (ii) for determining the
XX activity of pharmaceuticals and/or nutritional compounds, e.g. food
XX additives or supplements, especially minerals, trace elements, organic
XX acids (amino, carboxylic or fatty acid) or their derivatives, salts and
XX mixtures. The method provides rapid, inexpensive and reproducible
XX representation of differences in pools of nucleic acids from cells. It
XX allows imaging of the complete pattern of all nucleic acid in a cell, and
XX can detect very small differences in the nucleic acid pool. Since the
XX method is based on comparison of nucleic acid pools, not individual
XX genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
XX capture probes used in the method of the invention.
XX
S0 Sequence 21 BP; 0 A; 0 C; 1 G; 20 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAAGTAAAA 1537
DB 18 AAAAAAAAAAAAAAAAAA 1
RESULT 930
ADK01326/C
ID ADK01326 standard; DNA; 21 BP.
XX
XX ADK01326;
XX
XX 06-MAY-2004 (first entry)
XX
XX Rat DNA microarray capture oligonucleotide #46.
XX
XX ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
XX blood; nerve; germ cell; food additive; food supplement.
XX
XX Rattus sp.
XX
XX

XX DE10208794-A1.
PD 04-SEP-2003.
XX
PF 28-FEB-2002; 2002DE-01008794.
XX
PR 28-FEB-2002; 2002DE-01008794.
XX
PA (DEGS) DEGUSA BIOACTIVES GMBH.
PI Boekenkamp D, Dieck HT, Hoppe H;
XX
XX WPI; 2003-714082/68.
DR
PT Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.
PS
XX Example; Page 5; 8pp; German.
XX
CC This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC reading out, where the nucleic acids are selectively bound using capture
CC agents that are (a) immobilised on the surface of a solid matrix and (b)
CC comprise variable and non-variable regions. The capture oligonucleotides
CC have a 5'-invariable anchor region, the complement of which is present at
CC least once in each nucleic acid and a 3'-variable, discriminatory region
CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particularly sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
CC The method is used (i) for analysis of patterns, especially in mucosal,
CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC additives or supplements, especially minerals, trace elements, salts and
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC mixtures. The method provides rapid, inexpensive and reproducible
CC representation of differences in pools of nucleic acids from cells. It
CC allows imaging of the complete pattern of all nucleic acid in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix minimisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.
XX
SQ Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4, 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0
QY 1520 AAAAAAAAAAGTAAA 1537
Db 18 AAAAAAAAAAAAAAA 1
AC
XX RESULT 931
ID ADK01305/c
XX ADK01305 standard; DNA; 21 BP.
DT 06-MAY-2004 (first entry)
XX
XX Rat DNA microarray capture oligonucleotide #25.
XX seq; hybridization; capture oligonucleotide; pattern; mucosal; hair root;

XX	blood; nerve; germ cell; food additive; food supplement.
OS	Rattus sp.
FN	DE10208794-A1.
PD	04-SEP-2003.
XX	
PF	26-FEB-2002; 2002DE-01008794.
XX	
PR	26-FEB-2002; 2002DE-01008794.
PA	(DEGUS) DEGUSSA BIOACTIVES GMBH.
XX	
P1	Boekenkamp D, Dieck HT, Hoppe H;
XX	WPI; 2003-714082/68.
DR	
XX	
PT	Sorting single-stranded nucleic acid, useful for analyzing expression
PT	patterns and screening active agents, uses capture agent with variable
PT	and constant regions.
PS	
XX	Example; Page 5; Bpp; German.
CC	This invention describes a novel method for sorting single-stranded
CC	nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC	reading out, where the nucleic acids are selectively bound using capture
CC	agents that are (a) immobilised on the surface of a solid matrix and (b)
CC	comprise variable and non-variable regions. The capture oligonucleotides
CC	have a 5'-invariable anchor region, the complement of which is present at
CC	least once in each nucleic acid and a 3'-variable, discriminatory region
CC	that comprises all possible combinations of up to 10 nucleotides to allow
CC	binding of particular sorts of single stranded nucleic acids. The capture
CC	agents are particularly locked nucleic acids (LNA) and the anchor region
CC	comprises a sequence of 10-50, particularly 15-25, T residues. The
CC	capture oligonucleotides are biotinylated and immobilised on a surface by
CC	interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC	metal, resin, gel, crystalline material and/or membrane, having semi-
CC	conducting properties and especially in the form of a chip. Its surface
CC	is particularly a layer of (bio)molecular filaments and binding of single
CC	stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC	physical, stimulated by an electrical field or through a molecular sieve.
CC	The method is used (i) for analysis of patterns, especially in mucosal,
CC	hair root, blood, nerve or germ cells and (ii) for determining the
CC	activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC	additives or supplements, especially minerals, trace elements, organic
CC	acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC	mixtures. The method provides rapid, inexpensive and reproducible
CC	representation of differences in pools of nucleic acids from cells. It
CC	allows imaging of the complete pattern of all nucleic acid in a cell, and
CC	can detect very small differences in the nucleic acid pool. Since the
CC	method is based on comparison of nucleic acid pools, not individual
CC	genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
CC	capture probes used in the method of the invention.
XX	
SQ	Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other:
	Query Match 1.1%; Score 14.8; DB 1; Length 21;
	Best Local Similarity 89.9%; Pred. No. 4.2e+02;
	Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy	1520 AAAAAAAAAAAGTAA 1537 18 AAAAAAAAAAAAAAAAAA 1
Dd	
	RESULT 932
ID	ADK01310/c
AC	ADK01310 standard; DNA; 21 BP.
XX	ADK01310;
XX	
XX	06-MAY-2004 (first entry)

```
XX DE Rat DNA microarray capture oligonucleotide #30.
XX
XX 88; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
XX blood; nerve; germ cell; food additive; food supplement.
XX
XX Ractus sp.
XX
XX DE10208794-A1.
XX
XX 04-SEP-2003.
XX
XX 28-FEB-2002; 2002DE-01008794.
XX
XX 28-FEB-2002; 2002DE-01008794.
XX
XX (DEGS ) DEGUSSA BIOACTIVES GMBH.
XX
XX Boekenkamp D, Dieck HT, Hoppe H;
XX
XX WPI; 2003-714082/68.
XX
XX Example; Page 5; 8bp; German.
XX
XX This invention describes a novel method for sorting single-stranded
XX nucleic acids by isolation and hybridisation of nucleic acid pools, then
XX reading out, where the nucleic acids are selectively bound using capture
XX agents that are (a) immobilised on the surface of a solid matrix and (b)
XX comprise variable and non-variable regions. The capture oligonucleotides
XX have a 5'-invariable anchor region, the complement of which is present at
XX least once in each nucleic acid and a 3'-variable, discriminatory region
XX that comprises all possible combinations of up to 10 nucleotides to allow
XX binding of particular sorts of single stranded nucleic acids. The capture
XX agents are particularly locked nucleic acids (LNA) and the anchor region
XX comprises a sequence of 10-50, particularly 15-25, T residues. The
XX capture oligonucleotides are biotinylated and immobilised on a surface by
XX interaction with streptavidin. The matrix is of plastic, ceramic, glass,
XX metal, resin, gel, crystalline material and/or membrane, having semi-
XX conducting properties and especially in the form of a chip. Its surface
XX is particularly a layer of (bio)molecular filaments and binding of single
XX stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
XX physical, stimulated by an electrical field or through a molecular sieve.
XX The method is used (i) for analysis of patterns, especially in mucosal,
XX hair root, blood, nerve or germ cells and (ii) for determining the
XX activity of pharmaceuticals and/or nutritional compounds, e.g. food
XX additives or supplements, especially minerals, trace elements, organic
XX acids (amino, carboxylic or fatty acid) or their derivatives, salts and
XX mixtures. The method provides rapid, inexpensive and reproducible
XX representation of differences in pools of nucleic acids from cells. It
XX allows imaging of the complete pattern of all nucleic acid in a cell, and
XX can detect very small differences in the nucleic acid pool. Since the
XX method is based on comparison of nucleic acid pools, not individual
XX genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
XX capture probes used in the method of the invention.
XX
XX Sequence 21 BP; 0 A; 0 C; 2 G; 19 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 21;
XX Best Local Similarity 88.9%; Pred. No. 4.2e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1520 AAAAAAAAAAGTAAAA 1537
XX ||||| |||||
XX 18 AAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 933
XX ADK01336/C
XX ID ADK01336 standard; DNA; 21 BP.
```

```
XX AC ADK01336;
XX
XX 06-MAY-2004 (first entry)
XX
XX Rat DNA microarray capture oligonucleotide #56.
XX
XX 88; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
XX blood; nerve; germ cell; food additive; food supplement.
XX
XX Ractus sp.
XX
XX DE10208794-A1.
XX
XX 04-SEP-2003.
XX
XX 28-FEB-2002; 2002DE-01008794.
XX
XX 28-FEB-2002; 2002DE-01008794.
XX
XX (DEGS ) DEGUSSA BIOACTIVES GMBH.
XX
XX Boekenkamp D, Dieck HT, Hoppe H;
XX
XX WPI; 2003-714082/68.
XX
XX Example; Page 6; 8bp; German.
XX
XX This invention describes a novel method for sorting single-stranded
XX nucleic acids by isolation and hybridisation of nucleic acid pools, then
XX reading out, where the nucleic acids are selectively bound using capture
XX agents that are (a) immobilised on the surface of a solid matrix and (b)
XX comprise variable and non-variable regions. The capture oligonucleotides
XX have a 5'-invariable anchor region, the complement of which is present at
XX least once in each nucleic acid and a 3'-variable, discriminatory region
XX that comprises all possible combinations of up to 10 nucleotides to allow
XX binding of particular sorts of single stranded nucleic acids. The capture
XX agents are particularly locked nucleic acids (LNA) and the anchor region
XX comprises a sequence of 10-50, particularly 15-25, T residues. The
XX capture oligonucleotides are biotinylated and immobilised on a surface by
XX interaction with streptavidin. The matrix is of plastic, ceramic, glass,
XX metal, resin, gel, crystalline material and/or membrane, having semi-
XX conducting properties and especially in the form of a chip. Its surface
XX is particularly a layer of (bio)molecular filaments and binding of single
XX stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
XX physical, stimulated by an electrical field or through a molecular sieve.
XX The method is used (i) for analysis of patterns, especially in mucosal,
XX hair root, blood, nerve or germ cells and (ii) for determining the
XX activity of pharmaceuticals and/or nutritional compounds, e.g. food
XX additives or supplements, especially minerals, trace elements, organic
XX acids (amino, carboxylic or fatty acid) or their derivatives, salts and
XX mixtures. The method provides rapid, inexpensive and reproducible
XX representation of differences in pools of nucleic acids from cells. It
XX allows imaging of the complete pattern of all nucleic acid in a cell, and
XX can detect very small differences in the nucleic acid pool. Since the
XX method is based on comparison of nucleic acid pools, not individual
XX genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
XX capture probes used in the method of the invention.
XX
XX Sequence 21 BP; 0 A; 0 C; 1 G; 20 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 14.8; DB 1; Length 21;
XX Best Local Similarity 88.9%; Pred. No. 4.2e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1520 AAAAAAAAAAGTAAAA 1537
XX ||||| |||||
XX 19 AAAAAAAAAAAAAAAAAA 2
XX
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RESULT 934
ADK01342/c
ID ADK01342 standard; DNA; 21 BP.
XX
XX ADK01342;
AC
XX 06-MAY-2004 (first entry)
XX
XX Rat DNA microarray capture oligonucleotide #62.
DE
XX
XX seq; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KM blood; nerve; germ cell; food additive; food supplement.
XX
XX Rattus sp.
OS
XX DE10208794-A1.
PN
XX 04-SEP-2003.
PD
XX 28-FEB-2002; 2002DE-01008794.
PF
XX 28-FEB-2002; 2002DE-01008794.
PR
XX 28-FEB-2002; 2002DE-01008794.
PA (DEGS ) DEGUSSA BIOACTIVES GMBH.
XX
XX Boekenkamp D, Dieck HT, Hoppe H;
PI
XX WPI; 2003-714082/68.
DR
XX
XX Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.
XX
XX Example; Page 6; 8pp; German.
XX
XX This invention describes a novel method for sorting single-stranded
XX nucleic acids by isolation and hybridisation of nucleic acid pools, then
XX reading out, where the nucleic acids are selectively bound using capture
XX agents that are (a) immobilised on the surface of a solid matrix and (b)
XX comprise variable and non-variable regions. The capture oligonucleotides
XX have a 5'-invariable anchor region, the complement of which is present at
XX least once in each nucleic acid and a 3'-variable, discriminatory region
XX that comprises all possible combinations of up to 10 nucleotides to allow
XX binding of particular sorts of single stranded nucleic acids. The capture
XX agents are particularly locked nucleic acids (LNA) and the anchor region
XX comprises a sequence of 10-50, particularly 15-25, T residues. The
XX capture oligonucleotides are biotinylated and immobilised on a surface by
XX interaction with streptavidin. The matrix is of plastic, ceramic, glass,
XX metal, resin, gel, crystalline material and/or membrane, having semi-
XX conducting properties and especially in the form of a chip. Its surface
XX is particularly a layer of (bio)molecular filaments and binding of single
XX stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
XX physical, stimulated by an electrical field or through a molecular sieve.
XX The method is used (i) for analysis of patterns, especially in mucosal,
XX hair root, blood, nerve or germ cells and (ii) for determining the
XX activity of pharmaceuticals and/or nutritional compounds, e.g. food
XX additives or supplements, especially minerals, trace elements, organic
XX acids (amino, carboxylic or fatty acid) or their derivatives, salts and
XX mixtures. The method provides rapid, inexpensive and reproducible
XX representation of differences in pools of nucleic acids from cells. It
XX allows imaging of the complete pattern of all nucleic acid in a cell, and
XX can detect very small differences in the nucleic acid pool. Since the
XX method is based on comparison of nucleic acid pools, not individual
XX genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
XX capture probes used in the method of the invention.
XX
XX Sequence 21 BP; 0 A; 0 C; 1 G; 20 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 86.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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OY 1520 AAAAAAAAAAAGTAAA 1537
Db 20 AAAAAAAAAAAAAAAAAA 3
XX
XX RESULT 935
XX ADK01308/c
XX ID ADK01308 standard; DNA; 21 BP.
XX
XX ADK01308;
AC
XX 06-MAY-2004 (first entry)
XX
XX Rat DNA microarray capture oligonucleotide #28.
DE
XX
XX seq; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KM blood; nerve; germ cell; food additive; food supplement.
XX
XX Rattus sp.
OS
XX DE10208794-A1.
PN
XX 04-SEP-2003.
PD
XX 28-FEB-2002; 2002DE-01008794.
PF
XX 28-FEB-2002; 2002DE-01008794.
PR
XX 28-FEB-2002; 2002DE-01008794.
PA (DEGS ) DEGUSSA BIOACTIVES GMBH.
XX
XX Boekenkamp D, Dieck HT, Hoppe H;
PI
XX WPI; 2003-714082/68.
DR
XX
XX Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.
XX
XX Example; Page 5; 8pp; German.
XX
XX This invention describes a novel method for sorting single-stranded
XX nucleic acids by isolation and hybridisation of nucleic acid pools, then
XX reading out, where the nucleic acids are selectively bound using capture
XX agents that are (a) immobilised on the surface of a solid matrix and (b)
XX comprise variable and non-variable regions. The capture oligonucleotides
XX have a 5'-invariable anchor region, the complement of which is present at
XX least once in each nucleic acid and a 3'-variable, discriminatory region
XX that comprises all possible combinations of up to 10 nucleotides to allow
XX binding of particular sorts of single stranded nucleic acids. The capture
XX agents are particularly locked nucleic acids (LNA) and the anchor region
XX comprises a sequence of 10-50, particularly 15-25, T residues. The
XX capture oligonucleotides are biotinylated and immobilised on a surface by
XX interaction with streptavidin. The matrix is of plastic, ceramic, glass,
XX metal, resin, gel, crystalline material and/or membrane, having semi-
XX conducting properties and especially in the form of a chip. Its surface
XX is particularly a layer of (bio)molecular filaments and binding of single
XX stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
XX physical, stimulated by an electrical field or through a molecular sieve.
XX The method is used (i) for analysis of patterns, especially in mucosal,
XX hair root, blood, nerve or germ cells and (ii) for determining the
XX activity of pharmaceuticals and/or nutritional compounds, e.g. food
XX additives or supplements, especially minerals, trace elements, organic
XX acids (amino, carboxylic or fatty acid) or their derivatives, salts and
XX mixtures. The method provides rapid, inexpensive and reproducible
XX representation of differences in pools of nucleic acids from cells. It
XX allows imaging of the complete pattern of all nucleic acid in a cell, and
XX can detect very small differences in the nucleic acid pool. Since the
XX method is based on comparison of nucleic acid pools, not individual
XX genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
XX capture probes used in the method of the invention.
XX
XX Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;
SQ

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Query Match 1.1%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 4.2e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAGTAAA 1537
 |||||
 18 AAAAAAAAAAAAAAAAAA 1

RESULT 936
 ADK01311/c
 ID ADK01311 standard; DNA; 21 BP.
 AC ADK01311;
 XX
 XX 06-MAY-2004 (first entry)
 DE
 DE Rat DNA microarray capture oligonucleotide #31.
 XX
 XX ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
 KW blood; nerve; germ cell; food additive; food supplement.
 XX
 OS Rattus sp.
 XX
 PN DE10208794-A1.
 XX
 PD 04-SEP-2003.
 XX
 PE 28-FEB-2002; 2002DE-01008794.
 XX
 PR 28-FEB-2002; 2002DE-01008794.
 XX
 PA (DEGS) DEGUSA BIOACTIVES GMBH.
 XX
 PI Boekenkamp D, Dieck HT, Hoppe H;
 XX
 DR WPI; 2003-714082/68.
 XX
 PT Sorting single-stranded nucleic acid, useful for analyzing expression
 PT patterns and screening active agents, uses capture agent with variable
 PT and constant regions.
 XX
 PS Example; Page 5; 8pp; German.

This invention describes a novel method for sorting single-stranded nucleic acids by isolation and hybridisation of nucleic acid pools, then reading out, where the nucleic acids are selectively bound using capture agents that are (a) immobilised on the surface of a solid matrix and (b) comprise variable and non-variable regions. The capture oligonucleotides have a 5'-invariable anchor region, the complement of which is present at least once in each nucleic acid and a 3'-variable, discriminatory region that comprises all possible combinations of up to 10 nucleotides to allow binding of particular sorts of single stranded nucleic acids. The capture agents are particularly locked nucleic acids (LNA) and the anchor region comprises a sequence of 10-50, particularly 15-25, T residues. The capture oligonucleotides are biotinylated and immobilised on a surface by interaction with streptavidin. The matrix is of plastic, ceramic, glass, metal, resin, gel, crystalline material and/or membrane, having semi-conducting properties and especially in the form of a chip. Its surface is particularly a layer of (bio)molecular filaments and binding of single stranded nucleic acids to the surface is (quasi)covalent, supramolecular, physical, stimulated by an electrical field or through a molecular sieve. The method is used (i) for analysis of patterns, especially in mucosal, hair root, blood, nerve or germ cells and (ii) for determining the activity of pharmaceuticals and/or nutritional compounds, e.g. food additives or supplements, especially minerals, trace elements, organic acids (amino, carboxylic or fatty acid) or their derivatives, salts and mixtures. The method provides rapid, inexpensive and reproducible representation of differences in pools of nucleic acids from cells. It allows imaging of the complete pattern of all nucleic acid in a cell, and can detect very small differences in the nucleic acid pool. Since the method is based on comparison of nucleic acid pools, not individual genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent

CC capture probes used in the method of the invention.
 XX
 SQ Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 4.2e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAGTAAA 1537
 |||||
 18 AAAAAAAAAAAAAAAAAA 1

RESULT 937
 ADK01321/c
 ID ADK01321 standard; DNA; 21 BP.
 AC ADK01321;
 XX
 XX 06-MAY-2004 (first entry)
 DE
 DE Rat DNA microarray capture oligonucleotide #41.
 XX
 XX ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
 KW blood; nerve; germ cell; food additive; food supplement.
 XX
 OS Rattus sp.
 XX
 PN DE10208794-A1.
 XX
 PD 04-SEP-2003.
 XX
 PE 28-FEB-2002; 2002DE-01008794.
 XX
 PR 28-FEB-2002; 2002DE-01008794.
 XX
 PA (DEGS) DEGUSA BIOACTIVES GMBH.
 XX
 PI Boekenkamp D, Dieck HT, Hoppe H;
 XX
 DR WPI; 2003-714082/68.
 XX
 PT Sorting single-stranded nucleic acid, useful for analyzing expression
 PT patterns and screening active agents, uses capture agent with variable
 PT and constant regions.
 XX
 PS Example; Page 5; 8pp; German.

This invention describes a novel method for sorting single-stranded nucleic acids by isolation and hybridisation of nucleic acid pools, then reading out, where the nucleic acids are selectively bound using capture agents that are (a) immobilised on the surface of a solid matrix and (b) comprise variable and non-variable regions. The capture oligonucleotides have a 5'-invariable anchor region, the complement of which is present at least once in each nucleic acid and a 3'-variable, discriminatory region that comprises all possible combinations of up to 10 nucleotides to allow binding of particular sorts of single stranded nucleic acids. The capture agents are particularly locked nucleic acids (LNA) and the anchor region comprises a sequence of 10-50, particularly 15-25, T residues. The capture oligonucleotides are biotinylated and immobilised on a surface by interaction with streptavidin. The matrix is of plastic, ceramic, glass, metal, resin, gel, crystalline material and/or membrane, having semi-conducting properties and especially in the form of a chip. Its surface is particularly a layer of (bio)molecular filaments and binding of single stranded nucleic acids to the surface is (quasi)covalent, supramolecular, physical, stimulated by an electrical field or through a molecular sieve. The method is used (i) for analysis of patterns, especially in mucosal, hair root, blood, nerve or germ cells and (ii) for determining the activity of pharmaceuticals and/or nutritional compounds, e.g. food additives or supplements, especially minerals, trace elements, organic acids (amino, carboxylic or fatty acid) or their derivatives, salts and mixtures. The method provides rapid, inexpensive and reproducible representation of differences in pools of nucleic acids from cells. It

```
CC allows imaging of the complete pattern of all nucleic acid in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix mislaburisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.
XX
SQ Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAGTAAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1
RESULT 938
ADK01322/c
ID ADK01322 standard; DNA; 21 BP.
XX
AC ADK01322;
XX
DT 06-MAY-2004 (first entry)
XX
DE Rat DNA microarray capture oligonucleotide #42.
XX
KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KW blood; nerve; germ cell; food additive; food supplement.
XX
OS Rattus sp.
XX
DE10208794-A1.
XX
PD 04-SEP-2003.
XX
PF 28-FEB-2002; 2002DE-01008794.
XX
PR 28-FEB-2002; 2002DE-01008794.
XX
PA (DEGS ) DEGUSA BIOACTIVES GMBH.
XX
PI Boekenkamp D, Dieck HT, Hoppe H;
XX
DR WPI; 2003-714082/68.
XX
PT Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.
XX
PS Example; Page 5; 8pp; German.
XX
CC This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC reading out, where the nucleic acids are selectively bound using capture
CC agents that are (a) immobilised on the surface of a solid matrix and (b)
CC comprise variable and non-variable regions. The capture oligonucleotides
CC have a 5'-invariable anchor region, the complement of which is present at
CC least once in each nucleic acid and a 3'-variable, discriminatory region
CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
CC physical, stimulated by an electrical field or through a molecular sieve.
CC The method is used (i) for analysis of patterns, especially in mucosal,
CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
```

```
CC additives or supplements, especially minerals, trace elements, organic
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC mixtures. The method provides rapid, inexpensive and reproducible
CC representation of differences in pools of nucleic acids from cells. It
CC allows imaging of the complete pattern of all nucleic acid in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix mislaburisation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.
XX
SQ Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAGTAAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1
RESULT 939
ADK01324/c
ID ADK01324 standard; DNA; 21 BP.
XX
AC ADK01324;
XX
DT 06-MAY-2004 (first entry)
XX
DE Rat DNA microarray capture oligonucleotide #44.
XX
KW ss; hybridisation; capture oligonucleotide; pattern; mucosal; hair root;
KW blood; nerve; germ cell; food additive; food supplement.
XX
OS Rattus sp.
XX
DE10208794-A1.
XX
PD 04-SEP-2003.
XX
PF 28-FEB-2002; 2002DE-01008794.
XX
PR 28-FEB-2002; 2002DE-01008794.
XX
PA (DEGS ) DEGUSA BIOACTIVES GMBH.
XX
PI Boekenkamp D, Dieck HT, Hoppe H;
XX
DR WPI; 2003-714082/68.
XX
PT Sorting single-stranded nucleic acid, useful for analyzing expression
PT patterns and screening active agents, uses capture agent with variable
PT and constant regions.
XX
PS Example; Page 5; 8pp; German.
XX
CC This invention describes a novel method for sorting single-stranded
CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
CC reading out, where the nucleic acids are selectively bound using capture
CC agents that are (a) immobilised on the surface of a solid matrix and (b)
CC comprise variable and non-variable regions. The capture oligonucleotides
CC have a 5'-invariable anchor region, the complement of which is present at
CC least once in each nucleic acid and a 3'-variable, discriminatory region
CC that comprises all possible combinations of up to 10 nucleotides to allow
CC binding of particular sorts of single stranded nucleic acids. The capture
CC agents are particularly locked nucleic acids (LNA) and the anchor region
CC comprises a sequence of 10-50, particularly 15-25, T residues. The
CC capture oligonucleotides are biotinylated and immobilised on a surface by
CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
CC metal, resin, gel, crystalline material and/or membrane, having semi-
CC conducting properties and especially in the form of a chip. Its surface
CC is particularly a layer of (bio)molecular filaments and binding of single
CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
```


CC physical, stimulated by an electrical field or through a molecular sieve.
CC The method is used (i) for analysis of patterns, especially in mucosal,
CC hair root, blood, nerve or germ cells and (ii) for determining the
CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
CC additives or supplements, especially minerals, trace elements, organic
CC acids (amino, carboxylic or fatty acid) or their derivatives, salts and
CC mixtures. The method provides rapid, inexpensive and reproducible
CC representation of differences in pools of nucleic acids from cells. It
CC allows imaging of the complete pattern of all nucleic acid in a cell, and
CC can detect very small differences in the nucleic acid pool. Since the
CC method is based on comparison of nucleic acid pools, not individual
CC genes, matrix mislabelation is possible. ADK01281-ADK01344 represent
CC capture probes used in the method of the invention.

CC Sequence 21 BP; 0 A; 2 C; 0 G; 19 T; 0 U; 0 Other;

SO Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAA 1537
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 940
ADM96310/C
ID ADM96310 standard; DNA; 21 BP.
AC ADM96310;
DT 17-JUN-2004 (first entry)
DE Human ATP5F1 gene, RT-PCR primer #1.
XX
XX ss; human; H+ transporting; mitochondrial ATP synthase; subunit B;
KW Isoform 1; ATP5F1; reverse transcriptase; RT-PCR; primer.
XX
XX Synthetic.
OS
XX US2003211483-A1.
FN 13-NOV-2003.
PD 09-MAY-2002; 2002US-0014179.
PE 09-MAY-2002; 2002US-0014179.
PR 09-MAY-2002; 2002US-0014179.
XX
XX (SCHR/) SCHROEDER B G.
PA (CHEN/) CHEN C.
PA (SCHR/) SCHROTH G P.
XX
XX Schroeder BG, Chen C, Schroth GP;
PI
DR WPI; 2003-901581/82.
XX
XX Entriching low abundance polynucleotides in a sample, useful for gene
XX expression analysis, comprises exposing the sample to an enzymatically
XX non-extendable nucleobase oligomer to block polymerase activity on high
XX abundance species.
XX
XX Example 1; Page 20; 43pp; English.

XX The invention relates to a method of enriching a low abundance
XX polynucleotide in a sample of polynucleotides comprising a low abundance
XX and a high abundance polynucleotide. The method comprises exposing the
XX sample to an enzymatically non-extendable nucleobase oligomer having a
XX nucleobase sequence complementary to a sequence within the high abundance
XX polynucleotide under conditions so that base pairing occurs, and
XX subjecting the sample to conditions for polymerase extension. Preferably,
XX the enzymatically non-extendable nucleobase oligomer does not have a
XX ribose-containing oligomeric structure. It is a peptide nucleic acid
XX (PNA) oligomer or is a modified nucleotide oligomer or internucleotide

CC analogue oligomer. The modified nucleotide oligomer is selected from 2'-
CC modified and 3'-modified nucleotide oligomers. The 2'-modified and 3'-
CC modified nucleotide oligomers are selected from 2'-O-alkyl modified
CC nucleotide oligomers and 3'-alkyl modified nucleotide oligomers. The 2'-O-
CC alkyl modified nucleotide oligomers are 2'-O-methyl nucleotide
CC oligomers. The modified nucleotide oligomer or internucleotide analogue
CC oligomer is selected from locked nucleic acids (LNA), N³-P⁵
CC phosphoramidate (NP) oligomers, minor groove binder-linked
CC oligonucleotides (MGB-linked oligonucleotides), phosphorothioate (PS)
CC oligomers, C1-C4 alkylphosphonate oligomers, phosphoramidates, beta-
CC phosphodiester oligonucleotides, and alpha-phosphodiesters.
CC oligonucleotides. The C1-C4 alkylphosphonate oligomers are methyl
CC phosphonate (MP) oligomers. The enzymatically non-extendable nucleobase
CC oligomer is chimeric. The sample comprises more than one high abundance
CC polynucleotide. The sample comprises RNA, and polymerase extension is by
CC reverse transcription to yield a first strand cDNA. The method further
CC comprises second strand cDNA synthesis. The sample is exposed to the
CC nucleobase oligomer during the first and/or second strand cDNA synthesis.
CC The method further comprises an amplification step, which is by
CC polymerase chain reaction (PCR) or by in vitro transcription. The RNA is
CC mRNA or cDNA or total cellular RNA. Alternatively, the sample comprises
CC DNA, and polymerase extension is by DNA-dependent DNA polymerase in a
CC PCR. The method also comprises labelling the amplified polynucleotides.
CC The labelling is concomitant with or subsequent to amplification. The
CC methods are useful in selective enrichment of low abundance
CC polynucleotides in a sample. The pool of enriched polynucleotides may be
CC used in analysing gene expression and in creating cDNA libraries. The
CC present sequence represents a reverse transcriptase (RT)-PCR primer which
CC was used to amplify the human import precursor of subunit B of the H+
CC transporting, mitochondrial ATP synthase, subunit B, isoform 1 (ATP5F1)
CC gene.

SO Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAA 1537
DB 21 AAAAAAAAAAAAAAAAAA 4

RESULT 941
ABD25907
ID ABD25907 standard; DNA; 21 BP.
AC ABD25907;
DT 29-JUN-2004 (first entry)
DE A1654215-derived oligonucleotide SEQ ID 4919.
XX
XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; anti-allergic; anti-inflammatory; antiaesthetic;
KW analgesic; hypotensive; immunosuppressive; cyostatic; cystic fibrosis;
KW beta-adrenergic agonists; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX
XX Homo sapiens.
OS
XX WO200285309-A2.
FN 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013143.
PE 24-APR-2001; 2001US-0286036P.
PR (EPIG-) EPIGENESIS PHARM INC.

```

XX Myce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-093058/08.
XX
XX Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acid associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
XX Claim 15, SEQ ID NO 4919; 763pp; English.
XX
XX This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c) the composition
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, antihistaminic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
XX Sequence 21 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 1 Other;
SQ
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Cy 1520 AAAAAAAAAAGTAA 1537
Db 1 AAAAAAAAAAAAAAAAA 18

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XX 09-MAY-2003; 2003US-00435489.
XX
XX 09-MAY-2002; 2002US-00144179.
XX
XX (SCHR/) SCHROEDER B G.
PA (CHEN/) CHEN C.
PA (SCHR/) SCHROTH G P.
XX
PI Schroeder BG, Chen C, Schroth GP;
XX
XX WPI; 2004-121562/12.
XX
XX Enriching low abundance polynucleotide relative to a high abundance
PT polynucleotide in a sample, for analyzing gene expression and creating
PT cDNA libraries, comprises blocking polymerase activity on high abundance
PT polynucleotides.
XX
XX Example 1; SEQ ID NO 41; 62pp; English.
XX
XX The present invention relates to methods for the selective enrichment of
CC low abundance polynucleotides. The invention is useful for analysing gene
CC expression in a sample and creating cDNA libraries. The present sequence
CC is reverse transcriptase (RT) primer used in the synthesis of an
CC artificial gene transcript.
XX
XX Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Cy 1520 AAAAAAAAAAGTAA 1537
Db 21 AAAAAAAAAAAAAAAAA 4

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RESULT 942
ADJ88057/c
ID ADJ88057 standard; DNA; 21 BP.
XX
XX ADJ88057;
XX
XX 06-MAY-2004 (first entry)
XX
XX RT primer used in the synthesis of an artificial gene transcript.
XX
XX Selective enrichment; gene expression; RT; reverse transcriptase; primer;
XX ss.
XX
XX Unidentified.
XX
XX US2004014105-A1.
XX
XX 22-JAN-2004.
PD

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RESULT 943
ADJ07216/c
ID ADJ07216 standard; DNA; 21 BP.
XX
XX ADJ07216;
XX
XX 15-JUL-2004 (first entry)
XX
XX Control primer used in cDNA first strand synthesis.
XX
XX Double-stranded cDNA synthesis; cDNA first strand synthesis;
XX cDNA second strand synthesis; RNA template; RNA amplification;
XX differential gene expression; primer; ss.
XX
XX Synthetic.
XX
XX US2004081962-A1.
XX
XX 29-APR-2004.
XX
XX 23-OCT-2002; 2002US-00278760.
XX
XX 23-OCT-2002; 2002US-00278760.
XX
XX 23-OCT-2002; 2002US-00278760.
XX
XX (CHEN/) CHEN C.
PA (SCHR/) SCHROEDER B.
PA (BRAN/) BRANDIS J.
PA (SCHR/) SCHROTH G.
XX
PI Chen C, Schroeder B, Brandis J, Schroth G;
XX
XX WPI; 2004-340131/31.
XX
XX Synthesizing double-stranded cDNA, by synthesizing a cDNA strand from RNA
PT template, removing the template and synthesizing double-stranded cDNAs
PT using the cDNA as template in the presence of processive DNA polymerase

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```
PT and random primers.
XX
PS Example 1; SEQ ID NO 2; 19pp; English.
XX
CC The present invention relates to a method for synthesizing double-
CC stranded cDNA, by synthesizing first cDNA strands in a first reaction
CC mixture comprising reverse transcriptase, RNA template, and first strand
CC primer complementary to template, removing the template, synthesizing
CC double-stranded cDNA in a second reaction mixture comprising processive
CC DNA polymerase, DNA ligase, first cDNA strand as template and random
CC primers having a mixture of oligonucleotides having random DNA sequences.
CC Also disclosed is a method for amplifying a population of RNA molecules
CC to produce a pool of double-stranded cDNA molecules, and a kit for
CC synthesizing double-stranded cDNA. The generated cDNA products are useful
CC in determining quantitative information about the genetic profile of
CC nucleic acid in original RNA sample. The method of the invention is
CC useful in differential gene expression assays for the analysis of
CC diseased and normal tissue and for large-scale correlation studies on
CC sequences, mutations, variants or polymorphisms among samples. The method
CC is efficient in synthesizing improved cDNA molecules and effective in
CC generating useful quantities of an amplified cDNA product that comprises
CC a population of cRNA molecules in substantially the same relative molar
CC ratio as the RNA or mRNA starting material. The present sequence
CC represents a primer used for cDNA first strand synthesis.
XX
SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other:
XX
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 1520 AAAAAAAAAAGTAAA 1537
Db 21 AAAAAAAAAAAAAAAA 4
XX
RESULT 944
ADP09287/C
ID ADP09287 standard; DNA; 21 BP.
XX
AC ADP09287;
XX
DT 26-AUG-2004 (first entry)
XX
DE Extend primer 82 used to genotype human chromogranin B polymorphism.
XX
XX breast cancer; cytostatic; gene therapy; human; chromogranin B; CHGB;
XX secretogranin 1; SCG1; chromosome 20pter-p12; ss; PCR; primer; SNP;
XX single nucleotide polymorphism.
XX
OS Homo sapiens.
XX
XX
XX MO2004047767-A2.
XX
XX 10-JUN-2004.
XX
XX 25-NOV-2003; 2003WO-US037966.
XX
XX 25-NOV-2002; 2002US-0429136P.
XX
XX 24-JUL-2003; 2003US-0490234P.
XX
XX (SEQU-) SEQUENOM INC.
XX
XX
XX Roch RB, Nelson MR, Braun A, Kammerer SM, Reneland R;
XX
XX WPI; 2004-441082/41.
XX
XX Identifying a subject at risk of breast cancer by detecting the presence
XX of absence of one or more nucleotide polymorphic variations, useful for
XX diagnosing, preventing and/or treating breast cancer.
XX
XX Example 5; Page 103; 286pp; English.
XX
```

```
CC The invention relates to a novel method for identifying a subject at risk
CC of breast cancer which comprises detecting the presence or absence of one
CC or more polymorphic variations associated with breast cancer in a nucleic
CC acid sample from a subject. The method of the invention has cytostatic
CC applications and may be useful for identifying a risk of breast cancer,
CC as well as therapeutic and prophylactic treatments that specifically
CC target breast cancer, such as gene therapy. The current sequence is that
CC of an extend primer of the invention which was used to genotype single
CC nucleotide polymorphisms within human chromogranin B (CHGB;secretogranin
CC 1,SCG1) DNA which is located at chromosomal position 20pter-p12.
XX
XX
SQ Sequence 21 BP; 9 A; 5 C; 2 G; 5 T; 0 U; 0 Other:
XX
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 1311 TTTATTTTCAGACAGCA 1328
Db 21 TTTTTTGCAGACAGCA 4
XX
RESULT 945
ABL60935
ID ABL60935 standard; DNA; 24 BP.
XX
AC ABL60935;
XX
DT 23-SEP-2002 (first entry)
XX
DE Human nucleotide reducing enzyme 59.62 cDNA isolating primer 2.
XX
XX Nucleotide reducing enzyme 59.62; embryo development; teratogenesis;
XX blood system disease; human; RT-PCR; primer; ss.
XX
XX Homo sapiens.
XX
XX
XX CN1333352-A.
XX
XX 30-JAN-2002.
XX
XX 07-JUL-2000; 2000CN-00117037.
XX
XX 07-JUL-2000; 2000CN-00117037.
XX
XX 07-JUL-2000; 2000CN-00117037.
XX
XX (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.
XX
XX Mao Y, Xie Y;
XX
XX WPI; 2002-305607/35.
XX
XX Human nucleotide reducing enzyme 59.62 polypeptide and its encoding
XX polynucleotide, for treating e.g. embryo development teratogenesis.
XX
XX Example 2; Page 17 (disclosure); 34pp; Chinese.
XX
XX
XX The invention relates to a novel human nucleotide reducing enzyme 59.62
XX polypeptide and encoding polynucleotide. The polynucleotide, polypeptide
XX and its antagonist are useful for treating e.g. embryo development
XX teratogenesis, blood system disease, and growth development disturbance
XX disease. The present sequence represents the human nucleotide reducing
XX enzyme 59.62 cDNA isolating RT-PCR primer
XX
XX
SQ Sequence 24 BP; 6 A; 2 C; 2 G; 14 T; 0 U; 0 Other:
XX
Query Match 1.1%; Score 14.8; DB 1; Length 24;
Best Local Similarity 88.9%; Pred. No. 3.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 1250 TGTGTTGTTTATATCA 1267
Db 3 TTTTGTGTTTATATCA 20
```

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RESULT 946
AAT69640/c
ID AAT69640 standard; DNA; 19 BP.
XX
AC AAT69640;
XX
DT 20-FEB-1998 (first entry)
XX
DE Telomerase Oligo-dT-Primer P3.
XX
KM Telomerase; substrate; primer; detection; 5'-region; retrovirus;
KM long terminal repeat 2; LTR-2; diagnosis; tumour; screening;
KM effector compound; PCR; amplification; Oligo-dT-Primer; ss.
XX
OS Synthetic.
XX
PN DE19664302-A1.
XX
PD 05-JUN-1997.
XX
PF 24-OCT-1996; 96DE-01044302.
XX
PR 28-NOV-1995; 95DE-01044317.
XX
PA (BOEP ) BOEHRINGER MANNHEIM GMBH.
XX
PI Emrich T, Leying H, Hinzpeter M, Karl G;
DR WPI; 1997-299542/28.
XX
PT Measuring telomerase activity, useful for tumour diagnosis and compound
PT screening - by extending substrate primer, followed by amplification and
PT immobilising product for detection.
XX
PS Example; Page 11; 21pp; German.
XX
CC The present sequence is a telomerase Oligo-dT-Primer, which can be used
CC in a novel method for detecting telomerase activity. The method comprises
CC adding to a test sample a 1st primer, that serves as telomerase
CC substrate, and nucleoside triphosphate (dNTP) and incubating to allow
CC primer extension by the telomerase, amplifying the extension product,
CC immobilising the amplification product (AP) on a solid phase and
CC qualitative and/or quantitative detection of AP, where the substrate
CC primer is preferably from the 5'-region of the long terminal repeat 2
CC (LTR-2) sequence of a retrovirus. The method can be used to diagnose
CC tumours and screen compounds for effector activity. Immobilisation of AP
CC provides a signal that is reproducibly representative of telomerase
CC activity, eliminates the need for gel electrophoretic separation and
CC provides high sensitivity. Radioactive labels are not required and the
CC method can be automated for routine use. Specific detection is achieved
CC by proper choice of hybridisation conditions, without separation of the
CC telomerase extension product. A specific signal is generated by 1-10 cell
CC equivalents, but for tumour analysis 10-1000 ng of tissue is usually used
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 2 Other;
XX
Query Match 1.0%; Score 14.6; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 5.1e+02;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
XX
OY 1518 TTTAAAAAAGTAAA 1536
DB 19 DKAAAAAAGTAAA 1
XX
RESULT 947
ADM16445/c
ID ADM16445 standard; RNA; 19 BP.
XX
AC ADM16445;
XX
DT 17-JUN-2004 (first entry)

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```

XX
DE RNA intron poly-pyrimidine tract, seq id 2.
XX
KM Cytostatic; antimicrobial; virucide; gene therapy; RNA intron; cancer;
KM viral; microbial; infection; poly-pyrimidine tract; ds.
XX
OS Unidentified.
XX
FH Key
FH misc_feature
FT 2..4
FT /tag= a
FT /note= "optionally between 1-3 bases at this position"
FT misc_feature
FT 5
FT /tag= b
FT /note= "optionally absent base"
FT misc_feature
FT 6..17
FT /tag= c
FT /note= "optionally between 7-12 bases at this position"
FT misc_feature
FT 19
FT /tag= d
FT /note= "optionally absent base"
XX
PN WO2004024940-A2.
XX
PD 25-MAR-2004.
XX
PF 16-SEP-2003; 2003WO-US029274.
XX
PR 16-SEP-2002; 2002US-0411062P.
PR 12-OCT-2002; 2002US-0418405P.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Lin S, Ying S;
XX
DR WPI; 2004-270056/25.
XX
PT New isolated RNAs comprising an intron RNA that is released in a cell,
PT thus modulating the function of a target gene, useful for treating and
PT preventing diseases such as cancer and viral/microbial infections.
XX
PS Claim 2; SEQ ID NO 2; 54pp; English.
XX
CC The invention relates to isolated RNAs comprising an intron RNA that is
CC released in a cell, thus modulating the function of a target gene. Also
CC disclosed is a DNA template for the isolated RNA, an expression vector
CC comprising the DNA, and a composition comprising one or more agents that
CC induce RNA-mediated modulation of the functions of two or more target
CC genes in a cell, such as a mammalian cell. The isolated RNAs and
CC compositions are useful for modulating the function of a target gene in a
CC cell, e.g. to inhibit a cancer-related gene, potential viral gene, and
CC microbe-related gene, and thus useful for treating and preventing
CC diseases such as cancer and viral/microbial infections. The current
CC sequence represents a potential poly-pyrimidine tract of the artificial
CC RNA intron.
XX
SQ Sequence 19 BP; 0 A; 3 C; 0 G; 0 T; 13 U; 3 Other;
XX
Query Match 1.0%; Score 14.6; DB 1; Length 19;
Best Local Similarity 82.4%; Pred. No. 5.1e+02;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
XX
OY 1520 AAAAAAAGTAAA 1536
DB 17 AAAAAAAGTAAA 1
XX
RESULT 948
AAQ75722
ID AAQ75722 standard; DNA; 21 BP.
XX
AC AAQ75722;
XX
DT

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DT	04-AUG-1995	(first entry)
XX		
DE	Reverse transcription primer used in cDNA analysis technique.	
XX		
KW	Analysis; gene expression; reverse transcription; primer; CDNA;	
KW	aggregate; restriction enzyme; ss.	
XX		
OS	Synthetic.	
XX		
PN	JP0630397-A.	
XX		
PD	01-NOV-1994.	
XX		
PF	16-APR-1993; 93JP-00112515.	
XX		
PR	16-APR-1993; 93JP-00112515.	
XX		
PA	(NITE) NIPPON TELEGRAPH & TELEPHONE CORP.	
XX		
DR	WPI; 1995-018287/03.	
XX		
PT	Analysis of cDNA and gene expression - by amplification of mRNA followed	
XX	by digestion with restriction enzymes.	
XX		
PB	Disclosure; Page 8; 11pp; Japanese.	
XX		
CC	A method for the analysis of cDNA comprises (a) preparing an aggregate of	
CC	double-stranded cDNAs by using an aggregate of mRNAs and a plural type of	
CC	labelled reverse transcription primers (GENSEQ files AAQ75547-075798)	
CC	and using the aggregate of mRNAs as the template for each reverse	
CC	transcription primer; (b) digesting each of the prepared aggregates of	
CC	the double-stranded cDNAs with restriction enzyme and; (c)	
CC	electrophoresing the digested aggregate of cDNAs in separate lanes. The	
CC	method can be used to analyse gene expression rapidly and easily	
XX		
SO	Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;	
	Query Match	1.0%; Score 14.6; DB 1; Length 21;
	Best Local Similarity	81.0%; Pred. No. 4, 6e+02;
	Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0.	
OY	1246 TCCTGTTTGTTTTTAATC 1266	
DB	1 TTTTTTTTTTTTTTAAAC 21	
	RESULT 949	
ID	AAQ75726	
ID	AAQ75726 standard; DNA, 21 BP.	
XX		
AC	AAQ75726;	
XX		
DT	04-AUG-1995 (first entry)	
XX		
DE	Reverse transcription primer used in cDNA analysis technique.	
XX		
KW	Analysis; gene expression; reverse transcription; primer; CDNA;	
KW	aggregate; restriction enzyme; ss.	
XX		
OS	Synthetic.	
XX		
PN	JP0630397-A.	
XX		
PD	01-NOV-1994.	
XX		
PF	16-APR-1993; 93JP-00112515.	
XX		
PR	16-APR-1993; 93JP-00112515.	
XX		
PA	(NITE) NIPPON TELEGRAPH & TELEPHONE CORP.	
XX		
DR	WPI; 1995-018287/03.	
XX		

PT	Analysis of cDNA and gene expression - by amplification of mRNA followed
PT	by digestion with restriction enzymes.
PS	Disclosure; Page 8; 11pp; Japanese.
CC	A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC	double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC	labelled reverse transcription primers (GENBSEQ files AAQ75547-Q75798)
CC	and using the aggregate of mRNAs as the template for each reverse
CC	transcription primer; (b) digesting each of the prepared aggregates of
CC	the double-stranded cDNAs with restriction enzyme and; (c)
CC	electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC	method can be used to analyse gene expression rapidly and easily
SQ	Sequence 21 BP; 3 A; 1 C; 0 G; 17 T; 0 U; 0 Other;
OY	Query Match 1.0%; Score 14.6; DB 1; Length 21; Best Local Similarity 81.0%; Pred. No. 4.6e+02; Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
DB	1246 TCCTTGTGTTGGTTTTTAATC 1266 1 TTTTTCCTTGTGTTTAAAC 21
RESULT 950	
ID	AAQ75734
XX	AAQ75734 standard; DNA; 21 BP.
AC	
XX	AAQ75734;
DT	
XX	04-AUG-1995 (first entry)
DE	
XX	Reverse transcription primer used in cDNA analysis technique.
KW	Analysis: gene expression; reverse transcription; primer; cDNA;
XX	aggregate; restriction enzyme; ss.
OS	
XX	Synthetic.
PN	
XX	JP06303997-A.
PD	
XX	01-NOV-1994.
Pf	
XX	16-APR-1993; 93JP-00112515.
PR	
XX	16-APR-1993; 93JP-00112515.
PA	
XX	(NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
DR	
XX	WI; 1995-018287/03.
PT	
XX	Analysis of cDNA and gene expression - by amplification of mRNA followed
PT	by digestion with restriction enzymes.
PS	
XX	Disclosure; Page 8; 11pp; Japanese.
CC	
CC	A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC	double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC	labelled reverse transcription primers (GENBSEQ files AAQ75547-Q75798)
CC	and using the aggregate of mRNAs as the template for each reverse
CC	transcription primer; (b) digesting each of the prepared aggregates of
CC	the double-stranded cDNAs with restriction enzyme and; (c)
CC	electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC	method can be used to analyse gene expression rapidly and easily
SQ	
XX	Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 U; 0 Other;
OY	Query Match 1.0%; Score 14.6; DB 1; Length 21; Best Local Similarity 81.0%; Pred. No. 4.6e+02; Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY	1246 TCCTTGTGTTGGTTTTTAATC 1266

OS Rattus sp.
 XX
 PN DE10208794-A1.
 XX
 PD 04-SEP-2003.
 XX
 PF 28-FEB-2002; 2002DE-01008794.
 XX
 PR 28-FEB-2002; 2002DE-01008794.
 XX
 PA (DEGSS) DEGUSSA BIOACTIVES GMBH.
 XX
 PI Boekenkamp D, Dieck HT, Hoppe H;
 XX
 DR WPI; 2003-714082/68.
 XX
 PT Sorting single-stranded nucleic acid, useful for analyzing expression
 PT patterns and screening active agents, uses capture agent with variable
 PT and constant regions.
 XX
 PS Example; Page 5; 8pp; German.
 XX
 CC This invention describes a novel method for sorting single-stranded
 CC nucleic acids by isolation and hybridisation of nucleic acid pools, then
 CC reading out, where the nucleic acids are selectively bound using capture
 CC agents that are (a) immobilised on the surface of a solid matrix and (b)
 CC comprise variable and non-variable regions. The capture oligonucleotides
 CC have a 5'-invariable anchor region, the complement of which is present at
 CC least once in each nucleic acid and a 3'-variable, discriminatory region
 CC that comprises all possible combinations of up to 10 nucleotides to allow
 CC binding of particular sorts of single stranded nucleic acids. The capture
 CC agents are particularly locked nucleic acids (LNA) and the anchor region
 CC comprises a sequence of 10-50, particularly 15-25, T residues. The
 CC capture oligonucleotides are biotinylated and immobilised on a surface by
 CC interaction with streptavidin. The matrix is of plastic, ceramic, glass,
 CC metal, resin, gel, crystalline material and/or membrane, having semi-
 CC conducting properties and especially in the form of a chip. Its surface
 CC is particularly a layer of (bio)molecular filaments and binding of single
 CC stranded nucleic acids to the surface is (quasi)covalent, supramolecular,
 CC physical, stimulated by an electrical field or through a molecular sieve.
 CC The method is used (i) for analysis of patterns, especially in mucosal,
 CC hair root, blood, nerve or germ cells and (ii) for determining the
 CC activity of pharmaceuticals and/or nutritional compounds, e.g. food
 CC additives or supplements, especially minerals, trace elements, organic
 CC acids (amino, carboxylic or lactic acid) or their derivatives, salts and
 CC mixtures. The method provides rapid, inexpensive and reproducible
 CC representation of differences in pools of nucleic acids from cells. It
 CC allows imaging of the complete pattern of all nucleic acids in a cell, and
 CC can detect very small differences in the nucleic acid pool. Since the
 CC method is based on comparison of nucleic acid pools, not individual
 CC genes, matrix miniaturisation is possible. ADK01281-ADK01344 represent
 CC capture probes used in the method of the invention.
 XX
 SQ Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 U; 0 Other;
 XX
 Query Match 1.0%; Score 14.6; DB 1; Length 21;
 Best Local Similarity 81.0%; Pred. No. 4.6e+02;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 XX
 QY 1246 TCTTGTGTTGTTTATC 1266
 | | | | | | | | | | | | | | | | | | | | | |
 DB 1 TTTT TTTT TTTT TTTT ATC 21

XX
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 PR 16-APR-1993; 93JP-00112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX
 PS Disclosure; Page 8; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESBQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;
 XX
 Query Match 1.0%; Score 14.6; DB 1; Length 21;
 Best Local Similarity 81.0%; Pred. No. 4.6e+02;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 XX
 QY 1246 TCTTGTGTTGTTTATC 1266
 | | | | | | | | | | | | | | | | | | | | | |
 DB 1 TTTT TTTT TTTT TTTT ATC 21

RESULT 955
 AAQ75634
 ID AAQ75634 standard; DNA; 21 BP.
 XX
 AC AAQ75634;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 PR 16-APR-1993; 93JP-00112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX

```
PS Disclosure; Page 6; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily.
XX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
QY Query Match 1.0%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 4.6e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1246 TCTTGTGTTGTTTAAATC 1266
DB 1 TTTTGTGTTTGTGATC 21
RESULT 956
AAQ75682 standard; DNA; 21 BP.
XX
AC AAQ75682;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KM Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
WP1; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily.
XX
SQ Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 U; 0 Other;
QY Query Match 1.0%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 4.6e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1246 TCTTGTGTTGTTTAAATC 1266
DB 1 TTTTGTGTTTGTGATC 21
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RESULT 957
AAQ75753/c
ID AAQ75753 standard; DNA; 21 BP.
XX
AC AAQ75753;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KM Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
WP1; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily.
XX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
QY Query Match 1.0%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 4.6e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1510 ACTGTTAATTAAAAA 1530
DB 21 ACTGAAAAA 1
RESULT 958
AAQ75764 standard; DNA; 21 BP.
XX
AC AAQ75764;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KM Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
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XX 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 9; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENSEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 14.6; DB 1; Length 21;
XX Best Local Similarity 81.0%; Pred. No. 4.6e+02;
XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
OY 1302 TCTATTTTATTTTATTTTCAGA 1322
OY | | | | | | | | | | | | | | | | | | | |
OY 1 TTTT TTTT TTTT TTTT TTTT CACA 21
OY
XX
XX RESULT 959
XX AAQ75714
XX ID AAQ75714 standard; DNA; 21 BP.
XX
XX AAQ75714;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JF06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 8; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENSEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX

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SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 14.6; DB 1; Length 21;
XX Best Local Similarity 81.0%; Pred. No. 4.6e+02;
XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
OY 1246 TCTTTGTTTGT TTTTATTC 1266
OY | | | | | | | | | | | | | | | | | | | |
OY 1 TTTT TTTT TTTT TTTT TTTT TATC 21
OY
XX
XX RESULT 960
XX AAQ75760
XX ID AAQ75760 standard; DNA; 21 BP.
XX
XX AAQ75760;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JF06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 8; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENSEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX
XX Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 14.6; DB 1; Length 21;
XX Best Local Similarity 81.0%; Pred. No. 4.6e+02;
XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
OY 1302 TCTATTTTATTTTATTTTCAGA 1322
OY | | | | | | | | | | | | | | | | | | | |
OY 1 TTTT TTTT TTTT TTTT TTTT CACA 21
OY
XX
XX RESULT 961
XX AAQ75756
XX ID AAQ75756 standard; DNA; 21 BP.
XX
XX AAQ75756;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX

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KM Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX Synthetic.
OS
XX JP06303997-A.
XX
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 8; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENSEQ files AAQ75547-075798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 3 A; 1 C; 0 G; 17 T; 0 U; 0 Other;
SQ
XX
XX Query Match 1.0%; Score 14.6; DB 1; Length 21;
XX Best Local Similarity 81.0%; Pred.No. 4.6e+02;
XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0.
OY 1302 TCTATTTTATTTATTTTCAGA 1322
Db 1 TTTTTTTTTTTTTTTCAAA 21

```

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENBANK files AB075547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily

XX Sequence 21 BP, 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;

QY Query Match 1.0%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 4.6e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0.

Db 1246 TCCTTGGTTGTTTTTAATC 1266
1 TTTTTCCTTGGTTTCTACCTC 21

RESULT 963
ABAG3238/c
ID ABAG3238 standard; DNA; 22 BP.
XX
AC ABA93238;
XX
DT 18-APR-2002 (first entry)
XX
DE PolyA adaptor oligonucleotide SEQ ID NO:1.
XX
KF Detection; comparative detection; adaptor; ss.
OS Synthetic.
XX
PN JP200133800-A.
PD 04-DEC-2001.
PF 30-MAY-2000; 2000JP-00160324.
XX
PR 30-MAY-2000; 2000JP-00160324.
XX
PA (UNIT-) UNITECH CO LTD.
DR WPI; 2002-135950/18.
XX
PS Comparative detection of the amounts of RNA and DNA.
XX
XX Disclosure; Page 9; 9pp; Japanese.

XX The present invention describes a method for the comparative detection of
CC the amount of an RNA. The method comprises: (a) cDNAs obtained by
CC transcribing respectively from at least two tissue RNAs are respectively
CC fragmented by using a same restriction enzyme; (b) each different adaptor
CC and a common adaptor are added to each of the cDNA fragments derived from
CC the same or different tissues; (c) the resultant adaptor-
CC added cDNAs are mixed together; (d) an adaptor primer having the common
CC sequence to said different adaptor and a gene-specific adaptor are used
CC to amplify said adaptor-added cDNAs containing no region derived from
CC polyadenylic acid of the mRNA before the addition of the adaptor among
CC the adaptor-added cDNAs prepared by the step (b); (e) the ratios of the
CC cDNA amounts are measured between the tissues; (f) the RNA is detected
CC from the measured result; (g) each different adaptor and a common adaptor
CC are added to each of the genomic DNA fragments derived from a same or
CC different individuals; (h) the resultant adaptor-added genomic DNAs are
CC mixed together; (i) the adaptor-added genomic DNAs are amplified by using
CC an adaptor primer having the common sequence to the different adaptor and
CC a sequence-specific adaptor; and (j) the ratios of the amplified amounts
CC of the genomic DNAs are measured between the individuals. The method is
CC used for the detection of the amounts of RNA and DNA. The present
CC sequence represents an oligonucleotide which is used in the
CC exemplification of the present invention

```
XX Sequence 22 BP; 19 A; 1 C; 1 G; 1 T; 0 U; 0 Other;
SQ
Query Match 1.0%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 4.e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 1246 TCTTGGTTGTTTATC 1266
DB 21 TTTTGTGTGTGTGTATC 1

RESULT 964
ABK6361
ID AAI66361 standard; DNA; 24 BP.
XX
AC AAI66361;
XX
DT 23-JAN-2002 (first entry)
XX
DE Human phosphatidylinositol-3 kinase 35 CDNA PCR primer #2.
XX
KW Human; phosphatidylinositol-3 kinase 35; PTDINS-3 kinase 35; cancer;
KW haemopathy; development disorder; HIV infection; immunological disease;
KW inflammation; gene therapy; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200175014-A2.
XX
PD 11-OCT-2001.
XX
PF 16-MAR-2001; 2001WO-CN000328.
XX
PR 17-MAR-2000; 2000CN-00114973.
XX
PA (BIOV-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-025836/03.
XX
PT New human phosphatidylinositol-3 (PTDINS3) kinase 35 for diagnosing and
PT treating malignant tumor, hemopathy, human immunodeficiency virus
PT infection, immunological diseases and various inflammations.
XX
PS Example 2; Page 12; 34pp; Chinese.
XX
CC The present invention provides the protein and coding sequences of human
CC phosphatidylinositol-3 (PTDINS-3) kinase 35. The sequences can be used in
CC the treatment of cancer, haemopathy, HIV infection, development
CC disorders, immunological diseases and inflammation. The present sequence
CC is a PCR primer for the coding sequence of the invention
XX
SQ Sequence 24 BP; 3 A; 0 C; 1 G; 20 T; 0 U; 0 Other;
Query Match 1.0%; Score 14.6; DB 1; Length 24;
Best Local Similarity 81.0%; Pred. No. 4.e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 1302 TCTATTTTATTTTATTCAGA 1322
DB 4 TTTTGTGTGTGTGTGTATTAAGA 24

RESULT 965
ABK6169/C
ID ABR66169 standard; DNA; 24 BP.
XX
AC ABR66169;
XX
DT 24-SEP-2002 (first entry)
XX
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```
DE Oligo dT primer #2 used in method to study gene expression.
XX
KW Oligo dT primer; gene expression analysis; primer; ss.
XX
OS Synthetic.
XX
PN WO200236828-A2.
XX
PD 10-MAY-2002.
XX
PF 01-NOV-2001; 2001WO-US045401.
XX
PR 01-NOV-2000; 2000US-0244933P.
XX
PA (GENO-) GENOMIC SOLUTIONS INC.
XX
PI Kane MD, Dombkowski AA, Nagel AC;
XX
DR WPI; 2002-508123/54.
XX
PT Identifying and characterizing gene expression in samples, for
PT identifying mRNAs expressed at different levels, comprises employing an
PT identifier having a oligo-dT primer of a specific sequence and a
PT detectable marker at its 5' end.
XX
PS Disclosure; Page 11; 45pp; English.
XX
CC The invention relates to systems for identification and characterization
CC of gene expression in one or more samples, comprising an identifier having
CC a specific oligo-dT primer sequence, where the identifier comprises a
CC detectable marker at its 5' end. The system is useful for identifying any
CC or all genes expressed in a given in vivo or in vitro RNA sample, as well
CC as the relative differences in mRNA between 2 or more samples, where
CC desired, for supporting discovery of new genes, and for identifying mRNAs
CC that are expressed at different levels between 2 or more samples. The new
CC system or method addresses limitations of prior methods by comprising
CC compositions and systems that incorporate new strategies where molecular
CC or biochemical assay compositions and systems are linked to DNA or RNA
CC sequence databases for optimal resource efficiency in assaying gene
CC expression. The system has the following advantages over existing
CC methods: (a) prior sequence information or clone library construction is
CC not needed to enable the assay; (b) provides immediate sequence
CC information in addition to information concerning changes or differences
CC in mRNA level; (c) determines mRNA expression level and mRNA identification
CC in one assay; (d) generates cDNA fragments from all mRNAs present in the
CC sample for subsequent investigation by common molecular biology
CC techniques; and (e) does not require prior knowledge of the sequence of
CC the genome of the organism under investigation and can be employed in
CC organisms lacking significant genomic sequence information. The present
CC sequence represents an oligo dT primer used in the method of the
XX
SQ Sequence 24 BP; 20 A; 0 C; 1 G; 3 T; 0 U; 0 Other;
Query Match 1.0%; Score 14.6; DB 1; Length 24;
Best Local Similarity 81.0%; Pred. No. 4.e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 1246 TCTTGGTTGTTTATC 1266
DB 21 TTTTGTGTGTGTGTATC 1

RESULT 966
ABK6168
ID ABR66168 standard; DNA; 24 BP.
XX
AC ABR66168;
XX
DT 24-SEP-2002 (first entry)
XX
DE Oligo dT primer #1 used in method to study gene expression.
XX
```

KM	Oligo dT primer; gene expression analysis; primer; ss.
XX	Synthetic.
OS	
PN	WO200236828-A2.
XX	
PD	10-MAY-2002.
XX	
PP	01-NOV-2001; 2001WO-US045401.
PR	01-NOV-2000; 2000US-0244933P.
XX	
PA	(GENO-) GENOMIC SOLUTIONS INC.
XX	
P1	Kane MD, Dombkowski AA, Nagel AC;
DR	WPI; 2002-508123/54.
XX	
PT	Identifying and characterizing gene expression in samples, for
PT	identifying mRNAs expressed at different levels, comprises employing an
PT	identifier having a Oligo-dT primer of a specific sequence and a
XX	detectable marker at its 5' end.
PS	
XX	Disclosure; Page 11; 45pp; English.
XX	
CC	The invention relates to systems for identification and characterisation
CC	of gene expression in one or more samples, comprising an identifier having
CC	a specific oligo-dt primer sequence, where the identifier comprises a
CC	detectable marker at its 5' end. The system is useful for identifying any
CC	or all genes expressed in a given in vivo or in vitro RNA sample, as well
CC	as the relative differences in mRNA between 2 or more samples, where
CC	desired, for supporting discovery of new genes, and for identifying mRNAs
CC	that are expressed at different levels between 2 or more samples. The new
CC	system or method addresses limitations of prior methods by comprising
CC	compositions and systems that incorporate new strategies where molecular
CC	or biochemical assay compositions and systems are linked to DNA or RNA
CC	sequence databases for optimal resource efficiency in assaying gene
CC	expression. The system has the following advantages over existing
CC	methods: (a) prior sequence information or clone library construction is
CC	not needed to enable the assay; (b) provides immediate sequence
CC	information in addition to information concerning changes or differences
CC	in mRNA level, to determine mRNA expression level and mRNA identification
CC	in one assay; (c) generates cDNA fragments from all mRNAs present in the
CC	sample for subsequent investigation by common molecular biology
CC	techniques; and (d) does not require prior knowledge of the sequence of
CC	the genome of the organism under investigation and can be employed in
CC	organisms lacking significant genomic sequence information. The present
CC	sequence represents an oligo dt primer used in the method of the
CC	invention
XX	
XX	
SO	Sequence 24 BP; 3 A; 1 C; 0 G; 20 T; 0 U; 0 Other:
Query Match	1.0%; Score 14.6; DB 1; Length 24;
Best Local Similarity	81.0%; Pred. No. 4e+02;
Matches 17; Conservative	0; Mismatches 4; Indels 0; Gaps 0;
Gy	1246 TCTTTGTTGGTTTTATC 1266
Db	4 TTTTGTTCCTTTTAAAC 24
RESULT 967	
ID	ADB04575/c
XX	ADB04575 standard; DNA; 25 BP.
XX	
AD	ADB04575;
XX	
DT	20-NOV-2003 (first entry)
XX	
DE	Human MDZ7 scanning oligonucleotide SEQ ID 5561.
XX	
CYC	Cyclostat; immunostimulant; gene therapy; vaccine; human;
ZNF	zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
XX	

KW	chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX	developmental disorder; ss.
XX	
XX	Homo sapiens.
XX	
PN	EP1281758-A2.
XX	
PD	05-FEB-2003.
XX	
PF	30-JUL-2002; 2002EP-00016874.
XX	
PR	02-AUG-2001; 2001US-00922181.
XX	
PA	(AEOM-) AEOMICA INC.
XX	
PI	Shannon M, Gu Y, Nguyen C;
XX	
DR	WPI; 2003-423107/40.
XX	
PT	New zinc finger-containing proteins and nucleic acid, useful in
PT	manufacturing a medicament for treating or preventing a disorder
PT	associated with decreased or increased expression or activity of MD23,
PT	MD24, MD27 or MD212, e.g. cancer.
XX	
ES	Example 8; SEQ ID NO 5561; 103pp; English.
XX	
CC	The present invention relates to novel human zinc finger-containing
CC	proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC	encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC	MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC	15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC	or in manufacturing a medicament for treating or preventing a disorder
CC	associated with decreased or increased expression or activity of MD23,
CC	MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC	acids and proteins are also useful for diagnosing or monitoring a disease
CC	caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC	acids can also be used as probes to detect and characterize gross
CC	alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC	useful in constructing microarrays for measuring gene expression. The
CC	proteins are useful as therapeutic agents for gene therapy or as
CC	vaccines. The present sequence was used to illustrate the invention.
XX	
SQ	Sequence 25 BP; 4 A; 2 C; 3 G; 16 T; 0 U; 0 Other;
XX	
Query Match	1.0%; Score 14.6; DB 1; Length 25;
Best Local Similarity	81.0%; Pred. No. 3.8e+02;
Matches	17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY	1512 TGTTAATTAAAAAAAAAAG 1532
DB	21 TCTCAAAAAAAAAAAG 1
XX	
RESULT 968	
ID	AAN50186/c
XX	AAN50186 standard; DNA; 16 BP.
XX	
AC	AAN50186;
XX	
DT	25-MAR-2003 (revised)
DT	01-NOV-1991 (first entry)
XX	
DE	Sequence of human immunoglobulin gene enhancer region called unit E1.
XX	
KW	Immunoglobulin gene; enhancer; promoter; expression cassette; ss.
XX	
OS	Homo sapiens.
XX	
PN	EP146743-A.
XX	
PD	03-JUL-1985.
XX	
PF	06-NOV-1984; 84EP-00113371.
XX	

```
XX 08-NOV-1993; 83JP-00208383.
PR 06-DEC-1993; 83JP-00229037.
PR 04-JUN-1994; 84JP-00113047.
PR 05-JUN-1994; 84JP-00113854.
XX
PA (TEIJ ) TEIJIN LTD.
PI Kudo A, Nakamura S, Sumi Y, Ichikawa Y, Watanabe T;
XX
XX WPI; 1985-160489/27.
DR
XX Fragments derived from chromosomal DNA of human immunoglobulin gene -
PT useful in transcription and translation procedures.
XX
PS Claim 10; Page 34; 49pp; English.
XX
CC The inventors claim a gene fragment comprising (a) the enhancer DNA
CC segment and (b) a structural gene such as human D, V and J gene, and a
CC promoter. Using the gene fragments of the invention, transcription and
CC translation efficiency are enhanced. (Updated on 25-MAR-2003 to correct
CC PA field.)
XX
SQ Sequence 16 BP; 5 A; 0 C; 0 G; 11 T; 0 U; 0 Other;
Query Match 1.0%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 6.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1514 TTAATTAAAAAAA 1529
DB 16 TTAATTAAAAAATTA 1
RESULT 969
AAK69795/C
ID AAK69795 standard; RNA; 17 BP.
XX
AC AAK69795;
XX
XX 28-JUN-1999 (first entry)
DT
XX Human fli1 VEGF receptor hammerhead ribozyme substrate #1090.
DE
XX
XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KM KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KM tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KM fme-like tyrosine kinase 1; kinase insert domain containing receptor;
KM foetal liver kinase 1; ss.
XX
XX Homo sapiens.
OS
XX
XX W09715662-A2.
PN
XX
XX 01-MAY-1997.
PD
XX
XX 25-OCT-1996; 96WO-US017480.
PE
XX
XX 26-OCT-1995; 95US-0005974P.
PR
XX 11-JAN-1996; 96US-00584040.
PR
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX (CHIR ) CHIRON CORP.
PA
PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX
XX WPI; 1997-259017/23.
DR
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.
XX
PS Claim 4; Page 79; 218pp; English.
```

```
XX
CC The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fme-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAK67275 to AAK75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX
SQ Sequence 17 BP; 1 A; 3 C; 0 G; 0 T; 13 U; 0 Other;
Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 6.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1521 AAAAAAAAAAGTAAA 1536
DB 17 AAAAAAAAAAGTAGA 2
RESULT 970
AAA21311/C
ID AAA21311 standard; RNA; 17 BP.
XX
AC AAA21311;
XX
XX 19-JUN-2000 (first entry)
DT
XX Integrin alpha 6 subunit substrate sequence SEQ ID NO:4537.
DE
XX
XX Human; aryl hydrocarbon nuclear transport; ARNT; TIR-2; angiogenesis;
KM integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KM hammerhead ribozyme; angiogenic factor; cytosstatic; antidiabetic;
KM ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
KM dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KM age related macular degeneration; inflammation; neovascular glaucoma;
KM myopic degeneration; psoriasis; verruca vulgaris; angiodiroma;
KM tubercous sclerosis; pct-wine stain; Sturge Weber syndrome;
KM Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
XX Homo sapiens.
OS
XX
XX W09950403-A2.
PN
XX
XX 07-OCT-1999.
PD
XX
XX 24-MAR-1999; 99WO-US006507.
PE
XX
XX 27-MAR-1998; 98US-0079678P.
PR
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX
XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
PI
XX
XX WPI; 1999-591315/50.
DR
XX
XX Novel ribozymes for modulating the synthesis, expression and/or stability
PT of an mRNA encoding an angiogenic factors.
XX
XX Claim 55; Page 200; 305pp; English.
XX
XX The present invention describes enzymatic nucleic acid molecules with RNA
CC cleaving activity, which specifically cleave RNA encoded by an aryl
CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
CC AAA17167 and AAA17622 represent ribozyme sequences for ARNT,
CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
CC and AAA19155 to AAA19222 represent their corresponding target sequences;
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CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC AAA21596 to AAA21688 represent their corresponding target sequences;
CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
CC AAA23342 represent their corresponding target sequences. The ribozymes of
CC the invention are used for modulating the synthesis, expression and/or
CC stability of an mRNA encoding angiogenic factor, especially ARNT,
CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC especially used to treat cancer, diabetic retinopathy, age related
CC macular degeneration (ARMD), inflammation, and arthritis, as well as
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC angioidibroma of tuberosus sclerosis, pot-wine stains, Sturge Weber
CC syndrome, Kippel-Trenunay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3
XX
SQ Sequence 17 BP; 5 A; 2 C; 0 G; 0 T; 10 U; 0 Other;
Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 6.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1512 TGTAAATTAAAAAAA 1527
DB 17 TGTAAATTAAAAAAA 2
XX
RESULT 971
ID AAA21312 standard; RNA; 17 BP.
XX
AC AAA21312;
XX
DT 19-JUN-2000 (first entry)
XX
DE Integrin alpha 6 subunit substrate sequence SEQ ID NO:4538.
XX
XX Human; aryl hydrocarbon nuclear transport; ARNT; TIR-2; angiogenesis;
XX integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
XX hammerhead ribozyme; angiogenic factor; cytoskeletal; antidiabetic;
XX ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
XX dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
XX age related macular degeneration; inflammation; neovascular glaucoma;
XX myopic degeneration; psoriasis; verruca vulgaris; angioidibroma;
XX tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;
XX Kippel-Trenunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
OS Homo sapiens.
XX
PN WO950403-A2.
XX
PD 07-OCT-1999.
XX
PF 24-MAR-1999; 99WO-US006507.
XX
PR 27-MAR-1998; 98US-0079678P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Pavco PA, Roberts E, Jarvis T, Coeshott C, Meswigen JA;
XX WPI; 1999-591315/50.
XX
PT Novel ribozymes for modulating the synthesis, expression and/or stability
PT of an mRNA encoding an angiogenic factors.
XX
PS Claim 55; Page 200; 305pp; English.
XX
CC The present invention describes enzymatic nucleic acid molecules with RNA
CC cleaving activity, which specifically cleave RNA encoded by an aryl
CC hydrocarbon nuclear transport (ARNT) gene, an integrin subunit beta 3
CC gene, an integrin alpha 6 subunit gene, or a tie-2 gene. AAA16775 to
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CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
CC and AAA19155 to AAA19222 represent their corresponding target sequences;
CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC AAA21596 to AAA21688 represent their corresponding target sequences;
CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
CC AAA23342 represent their corresponding target sequences. The ribozymes of
CC the invention are used for modulating the synthesis, expression and/or
CC stability of an mRNA encoding angiogenic factor, especially ARNT,
CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC especially used to treat cancer, diabetic retinopathy, age related
CC macular degeneration (ARMD), inflammation, and arthritis, as well as
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC angioidibroma of tuberosus sclerosis, pot-wine stains, Sturge Weber
CC syndrome, Kippel-Trenunay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3
XX
SQ Sequence 17 BP; 4 A; 2 C; 0 G; 0 T; 11 U; 0 Other;
Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 6.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1512 TGTAAATTAAAAAAA 1527
DB 16 TGTAAATTAAAAAAA 1
XX
RESULT 972
ID AAV91364 standard; RNA; 17 BP.
XX
AC AAV91364;
XX
DT 18-FEB-1999 (first entry)
XX
DE Human C-raf target site nucleotide position 2745.
XX
XX Human; C-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
XX target; substrate; catalytic; modulation; expression; Raf gene; delivery;
XX screening; identification; synthesis; deprotection; purification; cancer;
XX inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;
XX restenosis; rheumatoid arthritis; ss.
XX
OS Homo sapiens.
XX
PN WO9850530-A2.
XX
PD 12-NOV-1998.
XX
PF 05-MAY-1998; 98WO-US009249.
XX
PR 09-MAY-1997; 97US-0046059P.
XX
PR 09-JUN-1997; 97US-0049002P.
XX
PR 03-JUL-1997; 97US-0051718P.
XX
PR 22-AUG-1997; 97US-0056808P.
XX
PR 02-OCT-1997; 97US-0061321P.
XX
PR 02-OCT-1997; 97US-0061324P.
XX
PR 05-NOV-1997; 97US-0064866P.
XX
PR 19-DEC-1997; 97US-0068212P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Jarvis T, Matulic-Adamic J, Reynolds M, Kisch K, Bellon L;
PI Perry T, Beigelman L, Meswigen JA, Karpelsky A, Burgin A;
PI Thompson J, Workman CT, Beaudry A, Sweedler D;
XX WPI; 1999-009494/01.
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XX
PT - especially new catalytic nucleic acid that modulates selected processes
PT - especially ribozymes that cleave Raf RNA for treating cancer.
PT - restenosis, and also new ribozymes and modified nucleoside triphosphates
PT used as antiviral agents and synthons.
XX
PS Claim 177, Page 153; 259pp; English.
XX
CC A method has been developed for the identification of a nucleic acid
CC capable of modulating a process in a biological system. The method
CC comprises: (a) introducing into the system a random library of nucleic
CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising
CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC
CC in systems where modulation has occurred and/or determining the sequence
CC of at least part of the SBDs in such systems. Nucleic acid molecules with
CC endonuclease activity and catalytic activity, from the present invention,
CC are used to modulate gene expression in plant and mammalian cells and to
CC cleave target nucleic acid, particularly for treating systemic diseases
CC caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic
CC mutations in diseased cells and to determine c-rat RNA. Specifically NACs
CC with RNA-cleaving activity that modulate expression of the Raf gene, are
CC used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or
CC generally any condition associated with the level of c-rat. Introduction
CC of sugar/phosphate modifications increases stability against nuclease and
CC activity. AAV90922 to AAV93877 represent NACs that can be used in the
CC method, specifically for modulating the expression of a Raf gene
CC
XX
SQ Sequence 17 BP; 2 A; 3 C; 3 G; 0 T; 9 U; 0 Other;
XX
Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 37.5%; Pred. No. 6.2e+02;
Matches 6; Conservative 9; Mismatches 1; Indels 0; Gaps 0;
QY 806 TGCTGAATTTGTGTT 821
DB 1 UGCUGAUUUUUGUCUU 16
XX
RESULT 973
AA238362/C
ID AA238362 standard; DNA; 17 BP.
XX
AC AA238362;
XX
DT 15-FEB-2000 (first entry)
XX
DE SPl consensus binding element.
XX
KW SPl; consensus; competition gel mobility shift assay; apolipoprotein AI;
KW apo AI; low density lipoprotein; LDL; cholesterol;
KW coronary artery disease; promoter; flanking region; plasmid; DRG;
KW drug responsive element; reporter gene; drug screening; candidate;
KW expression; identification; rapid; automation; enhancer; element; ds.
XX
OS Synthetic.
XX
PN US5994061-A.
XX
PD 30-NOV-1999.
XX
PF 29-SEP-1995; 95US-00536559.
XX
PR 29-SEP-1995; 95US-00536559.
XX
PA (TOOH ) UNIV QUEENS KINGSTON.
XX
PI Tam S, Zhang X;
XX
DR WPI; 2000-038251/03.
XX
PT Screening for drugs that increase expression of the apolipoprotein AI
PT gene, which may then be useful for treating coronary artery disease.
```

```
XX
PS Example 7, Col 23-24; 38pp; English.
XX
CC Sequences AA238358-238364 represent double-stranded oligonucleotide
CC probes which comprise various different enhancer elements. These were
CC used as competitor probes in competition gel mobility shift assays
CC performed to determine the specificity of drug-inducible nuclear proteins
CC to a fragment of the 5' flanking region of the human apolipoprotein AI
CC (apo AI) gene comprising the sequence between bases -79 and -44 from the
CC transcriptional start site (AA238357). This apo AI fragment contains two
CC DRs (AA238355, AA238356) in opposite orientations, and was used in the
CC construction of plasmids pGL2 (apoAI-DRS)TK/luc (AA238352), which
CC contains one copy of this fragment, and pGL2 (4xapoAI-DRS)TK/luc
CC (AA238353) which contains four copies. The promoter and luciferase
CC upstream of the HSV thymidine kinase (TK) promoter and luciferase
CC reporter gene in the pGL2 TK/luc vector. The pGL2 TK/luc vector also
CC comprises a functional polyadenylation sequence downstream of the
CC reporter gene. Plasmids pGL2 (apoAI-DRS)TK/luc and pGL2 (4xapoAI-
CC DRS)TK/luc are used in a novel method for screening for a drug that
CC increases expression of a gene for apolipoprotein (apo AI), which is
CC associated with coronary artery disease. Such plasmids may be transformed
CC into mammalian cells, which are treated with a candidate compound, lysed
CC and assayed for reporter gene activity relative to extracts from
CC untreated cells. The method is useful for screening and identifying drugs
CC that increase apo AI gene expression, the identified drugs would be
CC useful for treating coronary artery disease. The method is simple, rapid,
CC and lends itself to automation
XX
SQ Sequence 17 BP; 2 A; 4 C; 10 G; 1 T; 0 U; 0 Other;
XX
Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 6.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 345 CTGCGCCGCCCGCCGAG 360
DB 16 CTGCCCCGCCCGCCGAG 1
XX
RESULT 974
AAA25444/C
ID AAA25444 standard; DNA; 17 BP.
XX
AC AAA25444;
XX
DT 19-JUL-2000 (first entry)
XX
DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1942.
XX
KW Oestrogen receptor; c-rat; k-ras; bcl-2; ribozyme; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW gene expression modification; cancer; phosphothioate; endonuclease;
KW anticancer; breast cancer; endometrial cancer; ss.
XX
OS Homo sapiens.
XX
PN WO9954459-A2.
XX
PD 28-OCT-1999.
XX
PF 19-APR-1999; 99WO-US008547.
XX
PR 20-APR-1998; 98US-0082404P.
XX
PA 23-JUN-1998; 98US-00103636.
XX
PI (RIBO-) RIBOZYME PHARM INC.
XX
PI Thompson JD, Belgelman L, Meswigen JA, Karpelisky A, Bellon L;
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Heberli P;
PI Matulic-Adamic J;
XX
DR WPI; 2000-013248/01.
XX
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PT New nucleic acids that interact, and optionally cleave, target sequences,
PT used to treat cancer.
PS Claim 77; Page 79; 148pp; English.
XX
CC The present invention describes nucleic acids (A) that interact stably
CC with a target sequence and contain at least one phosphorodi)thioate
CC link, having endonuclease activity. (A), and more generally any catalytic
CC nucleic acid (A') that modulates expression of the oestrogen receptor
CC gene, are used to treat cancer (particularly of breast or endometrium),
CC in vivo or by transforming cells ex vivo and implanting treated cells, or
CC for other conditions associated with levels of oestrogen receptor.
CC Because of the high selectivity for targeted RNA, (A) can also be used to
CC correlate inhibition of gene expression with alterations in phenotype,
CC particularly for identification of therapeutic targets, and as research
CC reagents (for RNA, in the same way that restriction endonucleases are
CC used with DNA). The combination of modifications in (A) improves
CC resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences,
CC AAA24748 to AAA25992 represent their corresponding target sequences.
CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
CC sequences, and AAA26107 to AAA26218 represent their corresponding target
CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC antisense oligonucleotides used in the exemplification of the present
CC invention
XX
SQ Sequence 17 BP; 2 A; 0 C; 1 G; 14 T; 0 U; 0 Other;
Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 6.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1521 AAAAAAAAAAGTAA 1536
Db 17 AAAAAAAAAAACTAA 2
RESULT 975
AAA25446/C
ID AAA25446 standard; DNA; 17 BP.
AC AAA25446;
XX
DT 19-JUL-2000 (first entry)
XX
DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1944.
XX
KW Oestrogen receptor; c-ras; bcl-2; ribozyme; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW gene expression modification; cancer; phosphothioate; endonuclease;
KW anticancer; breast cancer; endometrium cancer; ss.
XX
OS Homo sapiens.
XX
PN WO954459-A2.
XX
PD 28-OCT-1999.
XX
PF 19-APR-1999; 99WO-US008547.
XX
PR 20-APR-1998; 98US-0082404P.
PR 23-JUN-1998; 98US-00103636.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Thompson JD, Beigelman L, Mcswiggen JA, Karpelsky A, Bellon L;
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haeblerl P;
PI Matulic-Adamic J;
XX
DR WPI; 2000-013248/01.
XX
PT New nucleic acids that interact, and optionally cleave, target sequences,
PT used to treat cancer.

XX
PS Claim 77; Page 79; 148pp; English.
XX
CC The present invention describes nucleic acids (A) that interact stably
CC with a target sequence and contain at least one phosphorodi)thioate
CC link, having endonuclease activity. (A), and more generally any catalytic
CC nucleic acid (A') that modulates expression of the oestrogen receptor
CC gene, are used to treat cancer (particularly of breast or endometrium),
CC in vivo or by transforming cells ex vivo and implanting treated cells, or
CC for other conditions associated with levels of oestrogen receptor.
CC Because of the high selectivity for targeted RNA, (A) can also be used to
CC correlate inhibition of gene expression with alterations in phenotype,
CC particularly for identification of therapeutic targets, and as research
CC reagents (for RNA, in the same way that restriction endonucleases are
CC used with DNA). The combination of modifications in (A) improves
CC resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences,
CC AAA24748 to AAA25992 represent their corresponding target sequences.
CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
CC sequences, and AAA26107 to AAA26218 represent their corresponding target
CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC antisense oligonucleotides used in the exemplification of the present
CC invention
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 6.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1520 AAAAAAAAAAGTAA 1535
Db 16 AAAAAAAAAAACTAA 1
RESULT 976
AAF06141
ID AAF06141 standard; DNA; 17 BP.
XX
AC AAF06141;
XX
DT 16-FEB-2001 (first entry)
XX
DE Hammerhead ribozyme substrate #2938.
XX
KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
KW interferon alpha; ss.
XX
OS Homo sapiens.
XX
PN WO200061729-A2.
XX
PD 19-OCT-2000.
XX
PF 11-APR-2000; 2000WO-US009721.
XX
PR 12-APR-1999; 99US-0129390P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Zwick M, Pavco P, Mcswiggen J;
XX
DR WPI; 2000-647423/62.
XX
PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT useful for producing e.g. granulocyte colony stimulating factor protein,
PT interferon alpha and erythropoietin.
XX
PS Claim 42; Page 123; 164pp; English.
XX
CC The present invention relates to enzymatic and antisense nucleic acid
CC molecules that act as inhibitors of the expression of repressor genes
CC encoding the Tr2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription


```
CC factor gene, IRF-2 and/or the CAAAT Displacement Protein (CDP).
CC Inhibition of the repressors removes prevents inhibition (and
CC consequently increases expression of) genes involved in the production of
CC erythropoietin, granulocyte colony stimulating factor protein and
CC interferon alpha
XX
SQ Sequence 17 BP; 0 A; 1 C; 4 G; 0 T; 12 U; 0 Other;

Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 18.8%; Pred. No. 6.2e+02;
Matches 3; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

Oy 1247 CTTGTTTGTGTTT 1262
|::|::|::|::|::|
Db 1 CUUGUUUUUGUUUU 16

RESULT 977
AAF06140
ID AAF06140 standard; DNA; 17 BP.
XX
AC AAF06140;
XX
DT 16-FEB-2001 (first entry)
XX
DE Hammerhead ribozyme substrate #2937.
XX
KM Ribozyme; erythropoietin; granulocyte colony stimulating factor;
XX interferon alpha; ss.
XX
OS Homo sapiens.
XX
PN WO200061729-A2.
XX
PD 19-OCT-2000.
XX
PF 11-APR-2000; 2000WO-US009721.
XX
PR 12-APR-1999; 99US-0129390P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blact L, Zwick M, Pavco P, Mcswiggen J;
XX
DR WPI; 2000-647423/62.
XX
PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
XX useful for producing e.g. granulocyte colony stimulating factor protein,
XX interferon alpha and erythropoietin.
XX
PS Claim 42; Page 123; 164pp; English.
XX
CC The present invention relates to enzymatic and antisense nucleic acid
CC molecules that act as inhibitors of the expression of repressor genes
CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
CC factor gene, IRF-2 and/or the CAAAT Displacement Protein (CDP).
CC Inhibition of the repressors removes prevents inhibition (and
CC consequently increases expression of) genes involved in the production of
CC erythropoietin, granulocyte colony stimulating factor protein and
CC interferon alpha
XX
SQ Sequence 17 BP; 0 A; 1 C; 4 G; 0 T; 12 U; 0 Other;

Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 18.8%; Pred. No. 6.2e+02;
Matches 3; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

Oy 1247 CTTGTTTGTGTTT 1262
|::|::|::|::|::|
Db 2 CUUGUUUUUGUUUU 17

RESULT 978
```

```
ABN01468/c
ID ABN01468 standard; DNA; 17 BP.
XX
AC ABN01468;
XX
DT 29-MAY-2002 (first entry)
XX
DE Human GDMLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:1460.
XX
KM Human; genome-derived myosin-like protein 1; GDMLP-1; heart;
XX muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
XX skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
PN WO200192524-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US016981.
XX
PR 26-MAY-2000; 2000US-0207456P.
XX
PR 21-SEP-2000; 2000US-0234687P.
XX
PR 27-SEP-2000; 2000US-0236359P.
XX
PR 04-OCT-2000; 2000GB-00024263.
XX
PR 30-JAN-2001; 2001WO-US000661.
XX
PR 30-JAN-2001; 2001WO-US000662.
XX
PR 30-JAN-2001; 2001WO-US000663.
XX
PR 30-JAN-2001; 2001WO-US000664.
XX
PR 30-JAN-2001; 2001WO-US000665.
XX
PR 30-JAN-2001; 2001WO-US000666.
XX
PR 30-JAN-2001; 2001WO-US000667.
XX
PR 30-JAN-2001; 2001WO-US000668.
XX
PR 30-JAN-2001; 2001WO-US000669.
XX
PR 30-JAN-2001; 2001WO-US000670.
XX
PR 05-FEB-2001; 2001US-0266860P.
XX
PA (ABOM-) AEOMICA INC.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX
DR WPI; 2002-179446/23.
XX
PT New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
XX or as specific biomolecule capture probes for surface-enhanced laser
XX desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX
PS Disclosure; SEQ ID NO 1460; 214pp; English.
XX
CC The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMLP-1, in particular heart
CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 17 BP; 4 A; 5 C; 6 G; 2 T; 0 U; 0 Other;
```

Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 6.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 332 TTCCCGAGAGCTCCTG 347
|||||
Db 16 TTCCCGAGAGCTGCTG 1

RESULT 979
ABN01467/c
ID ABN01467 standard; DNA; 17 BP.
XX
AC ABN01467;
XX
DT 29-MAY-2002 (first entry)
DE Human GDMLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:1459.
XX
KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
FN WO200192524-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US016981.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX
DR WPI; 2002-179446/23.
XX
PT New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX
PS Disclosure; SEQ ID NO 1459; 214pp; English.

CC The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMLP-1

CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMLP-1, in particular heart
CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX

SO Sequence 17 BP; 4 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 6.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 332 TTCCCGAGAGCTCCTG 347
|||||
Db 17 TTCCCGAGAGCTGCTG 2

RESULT 980
ABN02279/c
ID ABN02279 standard; DNA; 17 BP.
XX
AC ABN02279;
XX
DT 29-MAY-2002 (first entry)
DE Human GDMLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:2271.
XX
KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
FN WO200192524-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US016981.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX
DR WPI; 2002-179446/23.
XX
PT New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX
PS Disclosure; SEQ ID NO 2271; 214pp; English.

CC The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-

CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMLP-1, in particular heart
CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence

XX
SQ Sequence 17 BP; 0 A; 8 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 6.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 396 GCCGAGGCCCGCAGG 411
DB 16 GCCGAGGCCCGCAGG 1

RESULT 981
ID ABN02278/c standard; DNA; 17 BP.
XX ABN02278;
XX
XX ABN02278; (first entry)
XX
XX 29-MAY-2002 (first entry)
XX
DE Human GDMLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:2270.
XX
XX Human; genome-derived myosin-like protein 1; GDMLP-1; heart;
XX muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
XX skeletal muscle disorder; amplicon; screening; ss.
XX
XX Homo sapiens.
XX
XX WO200192524-A2.
XX
XX 06-DEC-2001.
XX
XX 25-MAY-2001; 2001WO-US016981.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0235359P.
XX 04-OCT-2000; 2000GB-00024263.
XX 30-JAN-2001; 2001WO-US000661.
XX 30-JAN-2001; 2001WO-US000662.
XX 30-JAN-2001; 2001WO-US000663.
XX 30-JAN-2001; 2001WO-US000664.
XX 30-JAN-2001; 2001WO-US000665.
XX 30-JAN-2001; 2001WO-US000666.
XX 30-JAN-2001; 2001WO-US000667.
XX 30-JAN-2001; 2001WO-US000668.
XX 30-JAN-2001; 2001WO-US000669.
XX 30-JAN-2001; 2001WO-US000670.
XX 05-FEB-2001; 2001US-0266860P.
XX
XX (AECOM-) AECOMICA INC.
XX
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;

XX
DR WPI; 2002-179446/23.
XX
XX New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
XX or as specific biomolecule capture probes for surface-enhanced laser
XX desorption/ionization, comprises human myosin-like protein hGDMLP-1.
XX
XX
XX
XX Disclosure; SEQ ID NO 2270; 214pp; English.

CC The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMLP-1, in particular heart
CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence

XX
SQ Sequence 17 BP; 0 A; 8 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 6.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 396 GCCGAGGCCCGCAGG 411
DB 17 GCCGAGGCCCGCAGG 2

RESULT 982
ID ACN12480 standard; RNA; 17 BP.
XX ACN12480;
XX
XX ACN12480; (first entry)
XX
XX 22-APR-2004 (first entry)
XX
XX MNV minus strand Zinzyne substrate SEQ ID NO 12483.
XX
XX
XX MNV; West Nile Virus; anti-inflammatory; cytosolic; hepatotropic;
XX viraemia; neuroprotective; antibacterial; replication; pancreatitis;
XX encephalitis; myocarditis; meningitis; infection; hepatitis;
XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
XX Amberzyme; Zinzyne; ss.
XX
XX West Nile Virus.
XX
XX WO200268637-A2.
XX
XX 06-SEP-2002.
XX
XX 19-OCT-2001; 2001WO-US048350.
XX
XX 20-OCT-2000; 2000US-0242411P.
XX
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (BLATT/) BLATT L.
XX (MCSW/) MCSWIGEN J A.
XX

PI Blact L, Mcswiggen JA;
XX
XX WPI; 2002-706994/76.
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
PT (MNV), useful for treating a condition related to MNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
XX Claim 23; SEQ ID NO 12483; 495bp; English.
XX
XX The invention relates to nucleic acid molecules that modulate replication
PS of the West Nile Virus (MNV). The nucleic acid molecules are useful for
CC treating a condition related to MNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
XX Sequence 17 BP; 5 A; 5 C; 5 G; 0 T; 2 U; 0 Other;
SQ
Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 6.2e+02;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY 1544 GCAGGATGCACCCAG 1559
DB 2 GCAGGAGUUAACCCAG 17
|||||:|:|||||
ACGN01139
ID ACGN01139 standard; RNA; 17 BP.
XX
XX ACGN01139;
AC
XX 22-APR-2004 (first entry)
DT
XX MNV Hammerhead Ribozyme substrate SEQ ID NO 1129.
DE
XX MNV; West Nile Virus; antiinflammatory; cyostatic; hepatotropic;
KW virecidae; neuroprotective; antibacterial; replication; pancreatitis;
KW encephalitis; myocarditis; meningitis; infection; hepatitis;
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
KW Amberzyme; Zinzyme; ss.
XX
XX West Nile Virus.
OS
XX WO200268637-A2.
PN
XX 06-SEP-2002.
PD
XX 19-OCT-2001; 2001WO-US048350.
PF
XX 20-OCT-2000; 2000US-0242411P.
PR
XX (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
XX
XX Blact L, Mcswiggen JA;
PI
XX WPI; 2002-706994/76.
DR
XX New nucleic acid molecule that modulates replication of West Nile Virus
PT (MNV), useful for treating a condition related to MNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

PS	Claim 23; SEQ ID NO 1129; 495bp; English.
XX	
CC	The invention relates to nucleic acid molecules that modulate replication
CC	of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC	treating a condition related to WNV infection e.g. pancreatitis,
CC	encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC	liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC	molecule is selected from the group of ribozymes consisting of
CC	Hammerhead, inozyme, G-cleaver, DNAzyme, Ambazyme and Zinzyme. The
CC	nucleic acid molecules further comprise at least five ribose residues, at
CC	least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC	least three of the 5' terminal nucleotides and a 3' end modification of a
CC	3'-3', inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC	are claimed; however, SEQ ID NO 2194-2206 and 17592-17514 are not given
CC	in the specification. The present sequence is that of a nucleic acid
CC	molecule of the invention
XX	
SO	Sequence 17 BP; 3 A; 3 C; 6 G; 0 T; 5 U; 0 Other;
QY	Query Match 1.0%; Score 14.4; DB 1; Length 17;
	Best Local Similarity 68.8%; Pred. No. 6.2e+02;
	Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY	696 CGCGTGGAAATGAGCT 711
	: :
DB	2 CGCGGUCAAUGGAGU 17
RESULT 984	
ACN01209/c	
ID	ACN01209 standard; RNA; 17 BP.
AC	
XX	ACN01209;
DT	
XX	22-APR-2004 (first entry)
DE	
XX	WNV Hammerhead Ribozyme substrate SEQ ID NO 1199.
XX	
KW	WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW	viruslike; neuroprotective; antibacterial; replication; pancreatitis;
KW	encephalitis; myocarditis; meningitis; infection; hepatitis;
KW	liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
KW	Ambazyme; Zinzyme; ss.
XX	
OS	West Nile Virus.
XX	
PN	WO20026837-A2.
XX	
PD	06-SEP-2002.
XX	
PF	19-OCT-2001; 2001WO-US048350.
XX	
BR	20-OCT-2000; 2000US-0242411P.
XX	
PA	(RIBO-) RIBOZYME PHARM INC.
PA	(BLAT) BLATT L.
PA	(MCSW/) MCSWIGEN J A.
XX	
PI	Blatt L, Mcswigen JA;
XX	
DR	WPI; 2002-706994/76.
XX	
PT	New nucleic acid molecule that modulates replication of West Nile Virus
PT	(WNV), useful for treating a condition related to WNV infection e.g.
PT	pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX	
PS	Claim 23; SEQ ID NO 1199; 495bp; English.
CC	
CC	The invention relates to nucleic acid molecules that modulate replication
CC	of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC	treating a condition related to WNV infection e.g. pancreatitis,
CC	encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC	liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC	molecule is selected from the group of ribozymes consisting of
CC	Hammerhead, inozyme, G-cleaver, DNAzyme, Ambazyme and Zinzyme. The
CC	nucleic acid molecules further comprise at least five ribose residues, at
CC	least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC	least three of the 5' terminal nucleotides and a 3' end modification of a
CC	3'-3', inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC	are claimed; however, SEQ ID NO 2194-2206 and 17592-17514 are not given
CC	in the specification. The present sequence is that of a nucleic acid
CC	molecule of the invention
XX	

CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3',3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
SQ Sequence 17 BP; 3 A; 5 C; 4 G; 0 T; 5 U; 0 Other;
Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 6.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1544 GCAGGATGTCACCCAG 1559
DB 17 GCAGGATGTCACCCAG 2
RESULT 985
ACN14420/C
ID ACN14420 standard; RNA; 17 BP.
XX
AC ACN14420;
XX
DT 22-APR-2004 (first entry)
XX
DE MNV minus strand Amberzyme substrate SEQ ID NO 14423.
XX
OS MNV, West Nile Virus; antiinflammatory; cytosstatic; hepatotropic;
KW viruslike; neuroprotective; antibacterial; replication; pancreatitis;
KW encephalitis; myocarditis; meningitis; infection; hepatitis;
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
KW Amberzyme; Zinzyme; ss.
XX
OS West Nile Virus.
XX
PN WO200268637-A2.
XX
PD 06-SEP-2002.
XX
PF 19-OCT-2001; 2001WO-US048350.
XX
PR 20-OCT-2000; 2000US-0242411P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGEN J A.
XX
PI Blact L, Mcswigen JA;
XX
DR WPI; 2002-706994/76.
XX
PT New nucleic acid molecule that modulates replication of West Nile Virus
PT (MNV), useful for treating a condition related to MNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
PS Claim 23; SEQ ID NO 14423; 495bp; English.
XX
CC The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (MNV). The nucleic acid molecules are useful for
CC treating a condition related to MNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3',3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
SQ Sequence 17 BP; 3 A; 3 C; 7 G; 0 T; 4 U; 0 Other;
Query Match 1.0%; Score 14.4; DB 1; Length 17;

CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
SQ Sequence 17 BP; 5 A; 6 C; 3 G; 0 T; 3 U; 0 Other;
Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 6.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 696 CGCTGTGATGAGCT 711
DB 16 CGCTGTGATGAGCT 1
RESULT 986
ACN03016
ID ACN03016 standard; RNA; 17 BP.
XX
AC ACN03016;
XX
DT 22-APR-2004 (first entry)
XX
DE MNV Inozyme substrate SEQ ID NO 3019.
XX
OS MNV, West Nile Virus; antiinflammatory; cytosstatic; hepatotropic;
KW viruslike; neuroprotective; antibacterial; replication; pancreatitis;
KW encephalitis; myocarditis; meningitis; infection; hepatitis;
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
KW Amberzyme; Zinzyme; ss.
XX
OS West Nile Virus.
XX
PN WO200268637-A2.
XX
PD 06-SEP-2002.
XX
PF 19-OCT-2001; 2001WO-US048350.
XX
PR 20-OCT-2000; 2000US-0242411P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGEN J A.
XX
PI Blact L, Mcswigen JA;
XX
DR WPI; 2002-706994/76.
XX
PT New nucleic acid molecule that modulates replication of West Nile Virus
PT (MNV), useful for treating a condition related to MNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
PS Claim 23; SEQ ID NO 3019; 495bp; English.
XX
CC The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (MNV). The nucleic acid molecules are useful for
CC treating a condition related to MNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3',3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
SQ Sequence 17 BP; 3 A; 3 C; 7 G; 0 T; 4 U; 0 Other;
Query Match 1.0%; Score 14.4; DB 1; Length 17;

Best Local Similarity 69.8%; Pred. No. 6.2e+02;
Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 696 CGCTGGTGAATGAGT 711
|||:||||:||||:
Db 1 CGCUGUCAUGAGU 16

RESULT 987
ACN07859/c
ID ACN07859 standard; RNA; 17 BP.

XX ACN07859;

XX 22-APR-2004 (first entry)

XX MNV minus strand Hammerhead Ribozyme substrate SEQ ID NO 7862.

XX MNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;

XX virucide; neuroprotective; antibacterial; replication; pancreatitis;

XX encephalitis; myocarditis; meningitis; infection; hepatitis;

XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;

XX Amberzyme; Zinzyme; ss.

XX West Nile Virus.

XX MO200268637-A2.

XX 19-OCT-2001; 2001WO-US048350.

XX 20-OCT-2000; 2000US-024241P.

XX (RIBO-) RIBOZYME PHARM INC.

XX (BLAT/) BLATT L.

XX (MCSW/) MCSWIGEN J A.

XX Blatt L, Mcswigen JA;

XX WPI: 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus

XX (MNV), useful for treating a condition related to MNV infection e.g. pancreatitis,

XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX Claim 23; SEQ ID NO 7862; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication

XX of the West Nile Virus (MNV). The nucleic acid molecules are useful for

XX treating a condition related to MNV infection e.g. pancreatitis,

XX encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,

XX liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid

XX molecule is selected from the group of ribozymes consisting of

XX Hammerhead, inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The

XX nucleic acid molecules further comprise at least five ribose residues, at

XX least ten 2'-O-methyl modifications, phosphorothioate linkages on at

XX least three of the 5' terminal nucleotides and a 3' end modification of a

XX 3'-3', inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080

XX are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given

RESULT 988
ABT36080/c
ID ABT36080 standard; DNA; 17 BP.

XX ABT36080;

XX 12-JUN-2003 (first entry)

XX Tumour suppression related human fukutin oligo SEQ ID NO 1717.

XX Cytoprotective; virucide; neuroprotective; nocitropic; neuroleptic; gene chip;

XX antisense; senesc; tumour; cell degeneration; cancer; Alzheimer's disease;

XX schizophrenea; protein chip; gene therapy; tumour suppression;

XX human fukutin; ds.

XX Homo sapiens.

XX MO2003025175-A2.

XX 27-MAR-2003.

XX 17-SEP-2002; 2002WO-IB04208.

XX 17-SEP-2001; 2001FR-00011978.

XX (MOLE-) MOLECULAR ENGINES LAB.

XX Telerman A, Amson R, Tuijnder M;

XX WPI: 2003-313353/30.

XX New isolated nucleic acid, useful for treating viral diseases associated

XX with tumors and cell degeneration, also related polypeptides, antibodies

XX and transfected cells.

XX Disclosure; Page 233; 720pp; French.

XX The invention relates to a novel isolated 17 mer nucleic acid sequence,

XX given in the specification, a sequence containing at least 15 consecutive

XX nucleotides from the 17 mer sequence, a sequence with, after optional

XX alignment, at least 80 % identity to the 17 mer sequence, a sequence that

XX hybridizes to them under highly stringent conditions, or the complement

XX of any of them, or the corresponding RNA. The novel isolated nucleic

XX acids of the invention are useful as probes and primers for detecting,

XX identifying, quantifying and/or amplifying a nucleic acid, e.g. as one

XX component of a gene chip, in vitro as (anti)sense reagents, and for

XX production of recombinant polypeptides. Any of the nucleic acids,

XX polypeptides, vectors containing the nucleic acids, cells containing the

XX vector or antibodies directed against the polypeptides are useful for

XX preparation of pharmaceuticals for prevention and/or treatment of viral

XX diseases that are characterised by development of tumours or cell

XX degeneration, specifically cancer but also Alzheimer's disease and

XX schizophrenea. Analysis of the expression of the 17 mer nucleic acids in

XX patient samples is useful for diagnosis and/or prognosis of these

XX diseases. The polypeptides can also be used to generate antibodies, and

XX both the polypeptide and antibodies are useful as components of protein

XX chips. The nucleic acid sequences of the invention can be used in gene

XX therapy. This polynucleotide sequence represents a tumour suppression

XX related human fukutin oligonucleotide of the invention

XX Sequence 17 BP; 6 A; 3 C; 4 G; 4 T; 0 U; 0 Other;

XX Query Match 1.0%; Score 14.4; DB 1; Length 17;

XX Best Local Similarity 93.8%; Pred. No. 6.2e+02;

XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1315 TTTTCAGAGACAGATC 1330

|||:||||:||||:
Db 16 TTTTCAGAGTCAGATC 1

RESULT 989

```
ABT35552
ID   ABT35552 standard; DNA; 17 BP.
XX
XX
AC   ABT35552;
XX
DT   12-JUN-2003 (first entry)
XX
DE   Tumour suppression related human fukutin oligo SEQ ID No 1189.
XX
XX   Cyclostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
XX   antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
XX   schizophrenia; protein chip; gene therapy; tumour suppression;
XX   human fukutin; db.
XX
XX   Homo sapiens.
XX
XX   WO2003025175-A2.
XX
XX   27-MAR-2003.
XX
XX   17-SEP-2002; 2002WO-IB004208.
XX
XX   17-SEP-2001; 2001FR-00011978.
XX
XX   (MOLE-) MOLECULAR ENGINES LAB.
XX
XX   Telerman A, Ameon R, Tuijnder M;
XX
XX   WPI; 2003-313353/30.
XX
XX   New isolated nucleic acid, useful for treating viral diseases associated
XX   with tumors and cell degeneration, also related polypeptides, antibodies
XX   and transfected cells.
XX
XX   Disclosure; Page 172; 720pp; French.
XX
XX   The invention relates to a novel isolated 17 mer nucleic acid sequence,
XX   given in the specification, a sequence containing at least 15 consecutive
XX   nucleotides from the 17 mer sequence, a sequence with, after optimal
XX   alignment, at least 80 % identity to the 17 mer sequence, a sequence that
XX   hybridizes to them under highly stringent conditions, or the complement
XX   of any of them, or the corresponding RNA. The novel isolated nucleic
XX   acids of the invention are useful as probes and primers for detecting,
XX   identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
XX   component of a gene chip, in vitro as (anti)sense reagents, and for
XX   production of recombinant polypeptides. Any of the nucleic acids,
XX   polypeptides, vectors containing the nucleic acids, cells containing the
XX   vector or antibodies directed against the polypeptides are useful for
XX   preparation of pharmaceuticals for prevention and/or treatment of viral
XX   diseases that are characterised by development of tumours or cell
XX   degeneration, specifically cancer but also Alzheimer's disease and
XX   schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
XX   patient samples is useful for diagnosis and/or prognosis of these
XX   diseases. The polypeptides can also be used to generate antibodies, and
XX   both the polypeptide and antibodies are useful as components of protein
XX   chips. The nucleic acid sequences of the invention can be used in gene
XX   therapy. This polynucleotide sequence represents a tumour suppression
XX   related human fukutin oligonucleotide of the invention
XX
SQ   Sequence 17 BP; 2 A; 4 C; 1 G; 10 T; 0 U; 0 Other;
Query Match      1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 6.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY      1348 ATTTTATTTCCCTT 1363
      |||||
      2 ATCTTATTTCCCTT 17
RESULT 990
AB264551/C
ID   AB264551 standard; RNA; 17 BP.
```

```
XX
XX   AB264551;
XX
XX   21-MAR-2003 (first entry)
XX
XX   Human HER2 DNAzyme substrate #8.
XX
XX   Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
XX   enzymatic nucleic acid; H-Ras; N-Ras; HIV; cyostatic; anti-HIV;
XX   anti-rheumatic; cancer; AIDS; ss.
XX
XX   Homo sapiens.
XX
XX   WO200297114-A2.
XX
XX   05-DEC-2002.
XX
XX   29-MAY-2002; 2002WO-US016840.
XX
XX   29-MAY-2001; 2001US-0294140P.
XX
XX   06-JUN-2001; 2001US-0296249P.
XX
XX   10-SEP-2001; 2001US-0318471P.
XX
XX   (RIBO-) RIBOZYME PHARM INC.
XX
XX   Mcawiggen J;
XX
XX   WPI; 2003-140484/13.
XX
XX   Novel short interfering RNA and enzymatic nucleic acid useful for
XX   treating cancer, modulates the expression of a nucleic acid encoding
XX   HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX
XX   Claim 4; Page 133; 185pp; English.
XX
XX   The invention relates to a novel short interfering RNA (siRNA) nucleic
XX   acid molecule or an enzymatic nucleic acid molecule, that modulates
XX   expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras,
XX   human immunodeficiency virus (HIV) or a component of HIV. The nucleic
XX   acid molecule of the invention has cyostatic, anti-HIV, and anti-
XX   rheumatic activity. The nucleic acid molecules are useful for reducing
XX   HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
XX   also useful for treating breast, ovarian, colorectal, lung, prostate,
XX   bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
XX   shown in AB259889 - AB262216, AB264544 - AB265531, AB266520 - AB266524,
XX   AB266530 - AB266585 represent substrate/target sequences for the human
XX   ribozymes of the invention
XX
SQ   Sequence 17 BP; 1 A; 9 C; 7 G; 0 T; 0 U; 0 Other;
Query Match      1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 6.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY      469 GGGGGCGCGGCTGAC 484
      |||||
      17 GGGGCGCGGCTGCC 2
RESULT 991
ACD60861/C
ID   ACD60861 standard; RNA; 17 BP.
XX
XX   ACD60861;
XX
XX   24-SEP-2003 (first entry)
XX
XX   HCV DNAzyme substrate sequence #2047.
XX
XX   Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
XX   RNA stability; RNA expression; RNA synthesis; antisense;
XX   enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinozyme;
XX   amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
```

KM HBV reverse transcriptase; Enhancer I region; viral replication;
 KM degenerative; disease state; HBV infection; HCV infection; cirrhosis;
 KM liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
 KM virucide; antiinflammatory; substrate; ss.
 XX
 OS Hepatitis C virus.
 XX
 PN WO200281494-A1.
 XX
 PD 17-OCT-2002.
 XX
 PF 26-MAR-2002; 2002WO-US009187.
 XX
 PR 26-MAR-2001; 2001US-00817879.
 PR 08-JUN-2001; 2001US-00877478.
 PR 08-JUN-2001; 2001US-0296876P.
 PR 24-OCT-2001; 2001US-0335058P.
 PR 05-DEC-2001; 2001US-0337055P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MACE/) MACEJAK D.
 PA (MCSM/) MCSWIGEN J.
 PA (MORC/) MORRISSEY D.
 PA (PAVC/) PAVCO P.
 PA (LEEP/) LEE P.
 PA (DRAP/) DRAPER K.
 PA (ROBE/) ROBERTS E.
 XX
 PI Blatt L, Macejak D, Mcswigen J, Morrissey D, Pavco P, Lee P,
 PI Draper K, Roberts E;
 DR WPI; 2003-229207/22.
 XX
 PT Novel compound useful for treating cirrhosis, liver failure,
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus
 PT infection.
 XX
 PS Claim 1; Page 270; 387pp; English.
 XX
 CC The present invention relates to nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes,
 CC inozymes, zinczymes, ambezymes, and G-cleaver ribozymes. Also disclosed
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV
 CC DNA. The nucleic acids may be used to modulate the expression of HBV
 CC genes and HBV viral replication. Also disclosed is a method for screening
 CC compounds and/or potential therapies directed against HBV, and compounds
 CC that modulate the expression and/or replication of HCV. The compounds and
 CC methods of the invention are useful for the treatment of degenerative and
 CC disease states related to HBV and HCV infection, replication and gene
 CC expression such as cirrhosis, liver failure, and hepatocellular
 CC carcinoma. The present sequence represents a substrate for one of the HCV
 CC DNAzyme or minus strand DNAzyme sequences disclosed in the present
 CC invention
 XX
 SQ Sequence 17 BP; 1 A; 7 C; 7 G; 0 T; 2 U; 0 Other;
 QY Query Match 1.0%; Score 14.4; DB 1; Length 17;
 Db Best Local Similarity 93.8%; Pred. No. 6.2e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 961 TCGCGCGCGCGCGCG 976
 Db 17 TCGCGCGCGCGCGCG 2
 RESULT 992
 ADB44694
 ID ADB44694 standard; DNA; 17 BP.

XX ADB44694;
 AC 18-DEC-2003 (first entry)
 XX
 DT
 XX
 DE Tumour suppression/reversion associated nucleotide #5017.
 KM cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
 KM primer; probe; tumour suppression; tumour reversion; apoptosis;
 KM virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
 KM diagnosis.
 XX
 OS Homo sapiens.
 XX
 PN WO2003040369-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 17-SEP-2002; 2002WO-IB004219.
 XX
 PR 17-SEP-2001; 2001FR-00011981.
 XX
 PA (MOLE-) MOLECULAR ENGINES LAB.
 PA
 PA Telerman A, Amson R, Tuijnder M;
 PI
 DR WPI; 2003-441574/41.
 XX
 PT New nucleic acid encoding human prostate membrane-specific antigen,
 PT useful e.g. for treatment of tumors and viral infection, also related
 PT polypeptide and antibodies.
 XX
 PS Disclosure; Page 618; 771pp; French.
 XX
 CC The invention relates to the isolation of 6327 nucleotide sequences,
 CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
 CC sequence having at least 80% identity, after optimal alignment, with the
 CC nucleotides, a sequence that hybridizes under stringent conditions with
 CC the nucleotides, or the complement, or corresponding RNA, of the
 CC nucleotides. The nucleotides are used as probes or primers for detecting,
 CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
 CC sense and antisense sequences, of nucleotides involved in tumour
 CC suppression or reversion, apoptosis and or viral resistance, to produce
 CC recombinant polypeptides, and to prepare transgenic animals, as
 CC experimental models. The nucleotides (also vectors containing them and
 CC cells containing the vectors), the encoded polypeptides and antibodies
 CC (Ab) against the polypeptides are useful for prevention and/or treatment
 CC of viral infections or diseases characterized by development of tumours
 CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
 CC Analyses of the expression of the nucleotides can be used for diagnosis
 CC and/or prognosis of these diseases. The nucleotides and polypeptides can
 CC also be used to screen for their specific interactive molecules,
 CC potentially useful for treating diseases associated with abnormal
 CC expression of the nucleotides.
 XX
 SQ Sequence 17 BP; 2 A; 4 C; 1 G; 10 T; 0 U; 0 Other;
 QY Query Match 1.0%; Score 14.4; DB 1; Length 17;
 Db Best Local Similarity 93.8%; Pred. No. 6.2e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1348 ATTTTATTTTCCCTT 1363
 Db 2 ATCTTATTTTCCCTT 17
 RESULT 993
 ACC54422
 ID ACC54422 standard; DNA; 17 BP.
 XX
 AC ACC54422;
 XX
 DT 27-JUN-2003 (first entry)

XX DE Human tumour suppressor sequence #3189.
XX KW ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
XX KW tumour regression; apoptosis; virus resistance; diagnosis;
XX KW cellular degeneration.
XX OS Homo sapiens.
XX FN FR2826373-A1.
XX PD 27-DEC-2002.
XX PE 20-JUN-2001; 2001FR-00008139.
XX PR 20-JUN-2001; 2001FR-00008139.
XX PA (MOLE-) MOLECULAR ENGINES LAB SA.
XX PI Tuijnder M, Telerman A, Amson R;
XX WPI; 2003-250498/25.
XX DR
XX PT New nucleic acid sequences associated with tumor suppression, regression,
XX PT apoptosis or virus resistance are useful to diagnose and treat viral
XX PT disease, development of tumor cells and cell degeneration.
XX PS Claim 1; Page 776; 798pp; French.
XX CC This sequence represents an isolated nucleic acid sequence associated
XX CC with tumour suppression or regression, apoptosis or virus resistance. The
XX CC invention relates to these sequences or sequences having at least 80%
XX CC identity to them, and polypeptides encoded by the sequences or
XX CC polypeptides having 80% identity to the polypeptide sequences. The
XX CC invention is used to diagnose or treat viral disease or disease
XX CC characterized by development of tumour cells or cellular degeneration
XX SQ Sequence 17 BP; 2 A; 4 C; 1 G; 10 T; 0 U; 0 Other;
Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 6.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1348 ATTTTATTTCCCTT 1363
DB 2 ATCTTATTTCCCTT 17
RESULT 994
AD184801/C
ID AD184801 standard; RNA; 17 BP.
XX AC AD184801;
XX DT 03-JUN-2004 (first entry)
XX DE HCV DNAzyme substrate sequence #2047.
XX KW ss; enzymatic nucleic acid; RNA cleavage; hepatitis C virus; HCV;
XX KW HCV infection; type I interferon; DNAzyme.
XX OS Hepatitis C virus.
XX FN US2003125270-A1.
XX PD 03-JUL-2003.
XX PE 18-DEC-2000; 2000US-00740332.
XX PR 18-DEC-2000; 2000US-00740332.
XX PA (BLAT/) BLATT L.
XX PA (MCSW/) MCSWIGEN J.

PA (ROBE/) ROBERTS E.
PA (PAVC/) PAVCO P A.
PA (MACE/) MACEJACK D.
XX PI Blact L, Mcswigen J, Roberts E, Pavco PA, Macejack D;
XX DR WPI; 2004-031273/03.
XX PT Enzymatic nucleic acid molecules which specifically cleave RNA derived
XX PT from hepatitis C virus (HCV), useful for the treatment of HCV infections,
XX PT especially in combination with type I interferon therapy.
XX PS Claim 1; SEQ ID NO 2047; 198pp; English.
XX CC The invention relates to an enzymatic nucleic acid molecule which
XX CC specifically cleaves RNA derived from hepatitis C virus (HCV), in which
XX CC the binding arms of the enzymatic nucleic acid molecule comprises
XX CC sequences complementary to any of the defined substrate sequences given
XX CC in the specification. The nucleic acid molecule may be administered for
XX CC the treatment of HCV infections, especially in combination with type I
XX CC interferons. The present sequence represents a HCV DNAzyme substrate
XX CC sequence.
XX SQ Sequence 17 BP; 1 A; 7 C; 7 G; 0 T; 2 U; 0 Other;
Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 6.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 961 TCGCGCGCGCCCGCG 976
DB 17 TCGCGCGCGCACCGCG 2
RESULT 995
AAA92546/C
ID AAA92546 standard; DNA; 18 BP.
XX AC AAA92546;
XX DT 04-JAN-2001 (first entry)
XX DE Antisense oligonucleotide ISIS# 30213.
XX KW Human; SRA; steroid receptor RNA activator; cytostatic; antiinflammatory;
XX KW SRA inhibitor; cancer; infection; antisense oligonucleotide; ss.
XX OS Synthetic.
XX FN US6107092-A.
XX PD 22-AUG-2000.
XX PE 29-MAR-1999; 99US-00280409.
XX PR 29-MAR-1999; 99US-00280409.
XX PA (ISIS-) ISIS PHARM INC.
XX PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX PI Cowseert LM, Bennett CF, O'malley BW;
XX DR WPI; 2000-586211/55.
XX PT Antisense compounds targeted to steroid receptor RNA activator useful for
XX PT diagnosis, prophylaxis and treatment of diseases associated with the
XX PT steroid activator, such as infection, inflammation or tumor formation.
XX PS Claim 3; Col 41; 47pp; English.
XX CC The present sequence is one of a large number of antisense
XX CC oligonucleotides which is directed against one of four human steroid
XX CC receptor RNA activator (SRA) nucleic acid sequences. Two series of

CC antisense oligonucleotides were synthesised. The first series comprised 8
CC -30 oligodeoxynucleotides with a phosphorochiolate backbone. The second
CC series comprised chimeric oligonucleotides composed of a central gap
CC region, consisting of ten 2'-deoxynucleotides, which was flanked on both
CC sides by four-nucleotide wings. The wings were composed of 2'-
CC methoxyethyl (2'-MOE) nucleotides. Both series contained the same
CC nucleotide sequences. The antisense compounds are useful for research,
CC diagnosis, treatment and prophylaxis to prevent or delay infection,
CC inflammation or tumour formation. Therapeutically the oligonucleotides
CC are highly safe and are effectively administered to humans
XX
SQ Sequence 18 BP; 4 A; 4 C; 1 G; 9 T; 0 U; 0 Other;
Query Match 1.0%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 5.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1491 ACATTAAATTCAGAAA 1506
DB 18 AGATTAAATTCAGAAA 3
RESULT 996
AAH44097
ID AAH44097 standard; DNA; 18 BP.
XX
AC AAH44097;
XX
DT 12-SEP-2001 (first entry)
XX
DE Oryza sativa peroxidase PCR primer/probe SEQ ID NO:48.
XX
KM Oryza sativa; rice; peroxidase; POX; characteristic; gene expression;
XX modification; plant; bacterial infection; Magnaporthe grisea; probe;
KM PCR primer; ss.
XX
OS Oryza sativa.
XX
PN WO200142475-A1.
XX
PD 14-JUN-2001.
XX
PF 08-DEC-2000; 2000WO-JP008728.
XX
PR 10-DEC-1999; 99JP-00352472.
XX
PA (NORO) JAPAN MIN AGRIC FORESTRY & FISHERIES.
XX
PI Ohashi Y, Mitsuhashi I, Sasaki T, Nagamura Y, Ito H, Iwai T;
PI Hiraga S;
XX
XX WPI; 2001-381695/40.
XX
PT New set of rice peroxidase genes for analysis of peroxidase expression in
PT rice under varying conditions and production of rice plants with desired
PT characteristics.
XX
PS Example 2; Page 62; 258bp; Japanese.
XX
CC The present invention describes a set of peroxidase genes found in
CC plants, especially rice, and their homologues, modified forms and
CC fragments, where the sequences of the peroxidase genes in the set are
CC given in AAH44071 to AAH44091. Also described are: (1) promoters for the
CC control of the gene set; (2) the preparation of cassette vectors using the
CC the genes and promoters; (3) analysis of plant characteristics using the
CC peroxidase set by isolating RNA from the plant, binding the RNA to a
CC membrane, mixing with a labelled peroxidase gene set, incubating, and
CC detecting the label signal to show which genes in the set are expressed
CC in the sample plant; and (4) DNA microarrays for peroxidase gene
CC expression analysis. The set of genes are used for the analysis of the
CC pattern of peroxidase gene expression in particular rice plants and their
CC component tissues and under different environmental conditions, and
CC modification of rice plants to provide desired specificities of

CC peroxidase gene expression to impart particular characteristics to the
CC plants such as response to bacterial infection by Magnaporthe grisea. The
CC present sequence represents a PCR primer/probe for a rice peroxidase
CC (POX) gene, which is used in an example from the present invention
XX
SQ Sequence 18 BP; 2 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
Query Match 1.0%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 5.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 669 TCACCTCTGACGGCC 684
DB 2 TCACCTCTGACGGCC 17
RESULT 997
ABS52682/C
ID ABS52682 standard; DNA; 18 BP.
XX
AC ABS52682;
XX
DT 15-NOV-2002 (first entry)
XX
DE mRNA display splint oligonucleotide.
XX
KM Translation; ss; splint; cell-free translation system; insulin;
XX growth hormone; erythropoietin; ribosome display; mRNA display.
XX
OS Synthetic.
XX
PN WO200259293-A2.
XX
PD 01-AUG-2002.
XX
PF 25-JAN-2002; 2002MO-US002344.
XX
PR 25-JAN-2001; 2001US-0264147P.
XX
PA (FORS/) FORSTER A C.
PA (BLAC/) BLACKLOW S C.
XX
PI Forster AC, Blacklow SC;
XX
XX WPI; 2002-608454/65.
XX
PT A new reconstituted cell-free translation system comprising translation
PT factors and tRNA species capable of translating exogenously added mRNAs,
PT useful for the synthesis of peptides or protein ligands or catalysts,
PT e.g. insulin.
XX
PS Disclosure; Page 15; 83pp; English.
XX
CC This invention relates to a novel reconstituted cell-free translation
CC system comprising translation factors and transfer ribonucleic acid
CC (tRNA) species which translate exogenously added messenger RNA (mRNA)
CC with highly selective incorporation at each codon to form a peptide or a
CC polypeptidomeric product when the system includes one or more tRNA species
CC charged with a synthetic amino acid or amino acid analogue. The
CC translation system of the invention is useful for the synthesis of
CC peptide or protein ligands or catalysts, such as insulin, growth hormone
CC or erythropoietin, and for pure ribosome display and pure mRNA display
CC selection experiments. The translation process provides a simplified,
CC highly purified system that offers potentially improved routes to all
CC peptides and proteins currently synthesised by alternative routes. This
CC overcomes the limitations of the prior art, e.g. difficulty in
CC maintaining purified components and trace contaminants or inefficient
CC peptide and protein display in a pure system, such as an expected lack of
CC post-translational modification of peptides, lack of proteases which
CC often cause protein degradation problem and a lack of competition from
CC contaminants in the selection steps. The present sequence represents a
CC splint oligonucleotide used in the mRNA display method used in the

```
CC Invention
XX Sequence 18 BP; 4 A; 2 C; 0 G; 12 T; 0 U; 0 Other;
SQ Query Match 1.0%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 5.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1514 TTAATTAATAAAAAA 1529
Db 16 TGAATTAATAAAAAA 1

RESULT 998
AD120873 ID AD120873 standard; DNA; 18 BP.
XX AC AD120873;
XX DT 06-MAY-2004 (first entry)
XX DE MS SnuPE detection oligonucleotide for DD3 #13.
XX KM DD3; CpG dinucleotide; cell proliferative disorder; ss.
XX OS Synthetic.
XX PN WO2004005543-A1.
XX PD 15-JAN-2004.
XX PF 25-JUN-2003; 2003WO-EP006690.
XX PR 08-JUL-2002; 2002DE-01030692.
XX PA (EPIC-) EPIDENOMICS AG.
XX PI Horns T;
XX PI WPI; 2004-091385/09.
XX PT Detecting methylation of 5' and promoter region of DD3 gene for
PT diagnosing proliferative disorders comprising contacting target nucleic
PT acid with a reagent that distinguishes between methylated and non-
PT methylated CpG dinucleotide.
XX PS Claim 6; SEQ ID NO 76; 56bp; English.
XX CC The present invention relates to detecting the methylation state of the
CC 5' and promoter region of the gene DD3 within a subject comprising
CC contacting a target nucleic acid having one or more sequences selected
CC from 5 3581 base pair sequences in a biological sample with at least one
CC reagent or a series of reagents. The method is useful for detecting the
CC methylation state of the 5' and promoter region of the gene DD3 within a
CC subject. The set of oligonucleotides comprising at least three of the
CC oligomers is useful for detecting the cytosine methylation state and/or
CC single nucleotide polymorphisms (SNPs) within SEQ. ID NO. 1-5 and its
CC complementary sequences. The set of oligomers is also useful for
CC detecting the methylation state of all CpG dinucleotides within SEQ ID
CC NO. 1 and its complementary sequences. The set of at least two
CC oligonucleotides can be used as primer oligonucleotides for the
CC amplification of DNA sequences selected from SEQ ID NO. 1-5 and its
CC complementary sequences. The DNA- and/or PNA-array is useful for
CC analyzing diseases associated with the methylation state of the gene DD3
CC comprising at least one nucleic acid. The methods, nucleic acids,
CC oligonucleotide or PNA-oligomer, kit, array or the set of
CC oligonucleotides is useful for the characterization, classification,
CC differentiation, grading, staging, and/or diagnosis of cell proliferative
CC disorders, or the predisposition to cell proliferative disorders. It can
CC also be used for the therapy of cell proliferative disorders. The present
CC sequence represents a detection oligonucleotide of the invention.
XX Sequence 18 BP; 2 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
```

```
Query Match 1.0%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 5.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1302 TCATATTTTTTTTATTT 1317
Db 3 TGTATTTTTTTTATTT 18

RESULT 999
ADP84381 ID ADP84381 standard; DNA; 20 BP.
XX AC ADP84381;
XX DT 23-SEP-2004 (first entry)
XX DE 5' donor site at the exon 19 splice junction of human AAA1 DNA.
XX KM ss; AAT-1; asthma; IGE mediated disease; human; GPRA;
XX KM G-protein coupled receptor for asthma susceptibility; AAA1;
XX KM asthma associated alternatively spliced gene 1;
XX KM chronic obstructive pulmonary disease; cancer; rhinitis; dermatitis;
XX KM cytosolic; antiasthmatic; transgenic; asthma locus-1.
XX OS Homo sapiens.
XX PN WO2004056866-A1.
XX PD 08-JUL-2004.
XX PF 19-DEC-2003; 2003WO-FI000973.
XX PR 20-DEC-2002; 2002US-0435846P.
XX PR 03-JAN-2003; 2003US-0437895P.
XX PR 26-MAR-2003; 2003US-0458767P.
XX PR 09-JUL-2003; 2003US-0486000P.
XX PA (GENE-) GENEOS OY.
XX PI Laitinen T, Kere J, Laitinen LA, Polvi A, Maekela S, Vendelin J;
XX PI Pulkinen V, Salmikangas P;
XX PI WPI; 2004-500286/47.
XX DR New GPRA polypeptides, useful in preparing a composition for diagnosing,
XX PT treating or preventing asthma, other IGE-mediated disease, chronic
XX PT obstructive pulmonary disease or cancer.
XX PS Example 7, Page 83; 265bp; English.
XX CC This invention relates to the identification of a novel susceptibility
XX CC locus AAT-1 for asthma and other IGE mediated diseases mapped to the
XX CC human chromosome 7p14-p15. Specifically, it refers to two overlapping
XX CC genes namely GPRA (G-protein coupled receptor for asthma susceptibility)
XX CC and AAA1 (asthma associated alternatively spliced gene 1). The present
XX CC invention describes identifying single nucleotide polymorphisms, as well
XX CC as insertion or deletion polymorphisms, occurring at different positions
XX CC in the AAT-1 locus, and furthermore providing vectors, host cells,
XX CC primers and probes in order to determine the status of an individual.
XX CC Accordingly, it provides a kit to diagnose or assess predisposition to
XX CC asthma, chronic obstructive pulmonary disease or cancer and other IGE
XX CC mediated diseases including rhinitis and dermatitis, such that derived
XX CC pharmaceutical compositions exhibit cytostatic and antiasthmatic
XX CC activities. Furthermore, it provides a transgenic animal comprising the
XX CC asthma locus-1 (AAT-1) DNA. This oligonucleotide sequence is a 5' splice
XX CC junction of the human AAA1 gene, given in Table 11 of the invention.
SQ Sequence 20 BP; 12 A; 1 C; 0 G; 7 T; 0 U; 0 Other;
Query Match 1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.3e+02;
```

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1515 TAATTAATAAAAAAAAA 1530
|||
DB 5 TAATTAATAATAATAA 20

RESULT 1000
AAQ68872/c
ID AAQ68872 standard; DNA; 20 BP.

XX AAQ68872;
AC
DT 25-MAR-2003 (revised)
DT 31-MAR-1995 (first entry)

DE Oligonucleotide (SNA2/ml) used as control in antisense therapy.

XX Oligonucleotide; antisense; self paired; nuclease resistant;
KM dermatological disorders; viral infection; cancer; atypical dermatitis;
KM psoriasis; melanoma; T cell lymphoma; herpes simplex; papilloma;
KM hepatitis; HIV; human immunodeficiency virus; oncogene; collagenase;
KM elastase; bone marrow graft; ss.

XX Synthetic.

XX FR2703053-A1.

XX 30-SEP-1994.

XX 26-MAR-1993; 93FR-00003514.

XX 26-MAR-1993; 93FR-00003514.

XX (GEST) GENSET.

PI Vasseur M, Blumenfeld M, Megueni S, Poddevin B;

DR WPI; 1994-312170/39.

XX New oligonucleotide(s) self paired at one or both ends - have improved
PT resistance to nuclease(s) and reduced toxicity, useful as antisense
PT molecules for treating dermatological disorders, virus infections,
PT cancer, etc.

XX Example 1; Fig 4a; 40pp; French.

XX New hooked or semi-hooked oligonucleotides (see AAQ68869-71, AAQ68873,
CC AAQ68875, AAQ68877, AAQ68879 and AAQ68880) are useful as therapeutic
CC antisense molecules for treating dermatological disorders (e.g. atypical
CC dermatitis, psoriasis, melanoma, T cell lymphoma etc.) viral infections
CC (e.g. herpes simplex, papilloma, hepatitis or HIV); or cancer (when
CC directed against an oncogene), due to their ability to hybridise with
CC target nucleic acid. They can be used ex vivo, e.g., to treat bone marrow
CC grafts. They can also be used for diagnosis or in cosmetics e.g. to block
CC mRNA coding proteins involved in the ageing process such as collagenase
CC or elastase. This linear antisense oligonucleotide is used as a control
CC to see whether the hooked and semi-hooked oligonucleotides exhibit a
CC greater resistance to exonucleases than linear oligonucleotides. (Updated
CC on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct
CC PA field.)

XX Sequence 20 BP; 16 A; 1 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.3e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1302 TCTATTTTTTTTTTTT 1317
|||
DB 16 TCTATTTTTTTTTTTT 1

RESULT 1001
AAZ03168/c
ID AAZ03168 standard; DNA; 20 BP.
XX
XX
AC AAZ03168;

XX 07-OCT-1999 (first entry)

DE PCR primer used to amplify an ORF of Chlamydia trachomatis.

XX Vaccine; eye disease; conventional trachoma; nongonemic trachoma;
KM paratrachoma; inclusion conjunctivitis; genital disease; peritrapetitis;
KM nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;
KM Bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.

XX Synthetic.

OS Chlamydia trachomatis.

XX W09928475-A2.

XX 10-JUN-1999.

XX 27-NOV-1998; 98WO-IB001939.

XX 28-NOV-1997; 97FR-00015041.

XX 17-DEC-1997; 97FR-00016034.

XX 04-NOV-1998; 98US-0107077P.

XX (GEST) GENSET.

PI Griffiths R;

DR WPI; 1999-371125/31.

XX Genome sequence of Chlamydia trachomatis.

XX Disclosure; Page 1584; 1755pp; English.

XX PCR primers AAZ01426-206209 were used to amplify open reading frames
CC (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs
CC encode polypeptides (see AAY6754-Y37949) which can be used as vaccines
CC against Chlamydia trachomatis. Antisense and ribozyme sequences can also
CC be used to control growth of the microorganism. Chlamydia trachomatis is
CC responsible for a large number of diseases, e.g. eye diseases such as
CC conjunctivitis; genital diseases such as nongonococcal urethritis;
CC epididymitis, cervicitis, salpingitis, peritrapetitis, Bartholinitis;
CC pneumonia; in breast feeding infants, and venereal lymphogranulomatosis.
CC The polypeptides of the invention may be of use in treating these
CC diseases

XX Sequence 20 BP; 7 A; 6 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.3e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1182 TGAGCCGATTTCGT 1197
|||
DB 19 TGATGCCGATTTCGT 4

RESULT 1002

AAZ97150
ID AAZ97150 standard; DNA; 20 BP.

XX AAZ97150;

XX 13-SEP-1999 (first entry)

DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.

XX Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;

KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
KW neutralising epitope; PCR primer; ss.
OS Synthetic.
OS Chlamydia pneumoniae.
XX
XX MO9927105-A2.
XX
XX PD 03-JUN-1999.
XX
XX PF 20-NOV-1998; 98WO-IB001890.
XX
XX PR 21-NOV-1997; 97FR-00014673.
XX PR 04-NOV-1998; 98US-0107078P.
XX
XX PA (BEST) GENSET.
XX
XX PI Griffiths R;
XX
XX DR WPI, 1999-357842/30.
XX
XX PT Genome sequence of Chlamydia pneumoniae.
XX
XX PS Page 1881; Disclosure; 1912p; English.
XX
XX CC AAY91991-X97517 represent PCR primers used to amplify open reading frames
CC and other nucleic acid sequences from the genome of Chlamydia pneumoniae
CC (see AAY91990). C. pneumoniae causes respiratory disease such as
CC pneumonia and bronchitis and is thought to be a contributing factor in
CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
CC nodosum or pharyngitis. The polypeptides encoded by the open reading
CC frames of the C. pneumoniae genome (see AAY91990- AAY91999) can be used
CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
CC nucleotide sequences can also be used as immunogenic compositions,
CC especially where the vector directs the expression of a neutralising
CC epitope of C. pneumoniae .
XX
XX SQ Sequence 20 BP; 1 A; 3 C; 7 G; 9 T; 0 U; 0 Other;

Query Match 1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 725 TTGCTGTGCTGCTGCC 740
DB 2 TTGCTGTGCTGCTGCC 17

RESULT 1003
AA55806
ID AA55806 standard; DNA; 20 BP.
XX
XX AC AA55806;
XX
XX DT 01-SEP-2000 (first entry)
XX
XX DE Human histone deacetylase HD2 antisense oligonucleotide SEQ ID NO:51.
XX
XX KW Human; DNA methyltransferase; DNA Methylase; antisense oligonucleotide;
KW modulation; inhibition; gene expression; combination therapy; p16;
KW histone deacetylase; HDAC; thymidylate synthase; tumour suppressor;
KW methylation; gene therapy; tumour; cytostatic; antiasthmatic;
KW antiinflammatory; inflammation; asthma; ss.
XX
XX OS Homo sapiens.
XX
XX PN MO20023112-A1.
XX
XX PD 27-APR-2000.
XX
XX PF 19-OCT-1999; 99WO-US024278.
XX
XX PR 19-OCT-1998; 98US-0104804P.

XX
XX PA (METH-) METHYLENE INC.
XX
XX PI Beesterman JM, Macleod AR, Siders WM;
XX
XX DR WPI; 2000-339532/29.
XX
XX PT Inhibiting gene expression e.g. DNA methyltransferase, by treating cells
XX PT with a synergistic amount of antisense oligonucleotide and protein
XX PT effectors e.g. 5-aza-cytidine of gene products, useful for gene therapy
XX PT of e.g. tumors.
XX
XX PS Disclosure; Page 29; 99p; English.
XX
XX CC The present invention describes a method for inhibiting the expression of
XX CC a gene in a cell comprising contacting the cell with an effective
XX CC synergistic amount of an antisense oligonucleotide which inhibits
XX CC expression of the gene, and an effective synergistic amount of a protein
XX CC effector of a product of the gene. Also described are: (1) a method for
XX CC treating a disease responsive to inhibition of a gene in a mammal; (2) a
XX CC method for inhibiting tumour growth in mammal; (3) an inhibitor of a gene
XX CC comprising an antisense oligonucleotide which inhibits expression of the
XX CC gene in operable association with a protein effector of a gene product;
XX CC and (4) a pharmaceutical composition comprising the inhibitor of (3). The
XX CC methods and compositions are useful as analytical tools for transgenic
XX CC studies and as therapeutic tools, e.g. as gene therapy tools for human
XX CC diseases including benign and malignant tumours, inflammation or asthma.
XX CC The methods, inhibitors and compositions of the invention that inhibit
XX CC expression or activity of a gene or gene product may be used to treat
XX CC patients having, or predisposed to developing, a disease responsive to
XX CC inhibition of the gene. These may also be used to activate silenced genes
XX CC to provide missing gene functions and improve a given condition.
XX CC Furthermore, the methods and compositions are useful as probes of the
XX CC physiological function of a gene product in an experimental cell culture
XX CC or animal system; and to evaluate the effect of inhibiting gene activity
XX CC or expression. AA55758 to AA55842 represent oligonucleotide sequences
XX CC which are used in the exemplification of the present invention
XX
XX SQ Sequence 20 BP; 0 A; 7 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 726 TGCTGTGCTGCTGCC 741
DB 4 TGCTGTGCTGCTGCC 19

RESULT 1004
AA275633
ID AA275633 standard; DNA; 20 BP.
XX
XX AC AA275633;
XX
XX DT 10-SEP-2001 (first entry)
XX
XX DE Human biallelic marker downstream amplification primer SEQ ID NO:9989.
XX
XX KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO9954500-A2.
XX
XX PD 28-OCT-1999.
XX
XX PF 21-APR-1999; 99WO-IB000822.
XX

```
PR 21-APR-1998; 98US-0082614P.
PR 23-NOV-1998; 98US-0109732P.
XX
PA (GEST ) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
DR WPI; 2000-013267/01.
XX
PT Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.
XX
PS Claim 8, Page 2360; 2745pp; English.
XX
CC AA265654 to AA269578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AA26579 to AA277440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention
XX
SQ Sequence 20 BP; 3 A; 7 C; 0 G; 10 T; 0 U; 0 Other;
Query Match 1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1348 ATTTTATTTTCCCTT 1363
Db 1 ATTTATATTTTCCCTT 16
RESULT 1005
ABLS7552
ID ABL57552 standard; DNA; 20 BP.
XX
AC ABL57552;
XX
DT 26-JUL-2002 (first entry)
XX
DE Synthetic deoxyribonucleotide poly s.
XX
KW Concentration; quantification; mutation detection; polymorphic;
KW polymerase chain reaction; PCR; ss.
XX
OS Synthetic.
XX
OS EP1046717-A2.
XX
PD 25-OCT-2000.
XX
PF 20-APR-2000; 2000EP-00108643.
XX
PR 20-APR-1999; 99JP-00111601.
XX
PA (NIBI-) JAPAN BIOINDUSTRY ASSOC.
PA (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.
PA (KANK-) KANKYO ENG CO LTD.
XX
PI Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;
PI Koyama O, Furueho K;
DR WPI; 2000-657765/64.
XX
```

```
PT Determining the concentration of a target nucleic acid, useful e.g. for
PT detecting genetic mutations, comprises using a fluorescently labeled
PT probe in which emission is reduced by binding to the target nucleic acid.
XX
PS Example 6; Page 23; 55pp; English.
XX
CC The invention relates to the determination of the concentration of a
CC nucleic acid target, using a fluorescently labeled probe which produces
CC reduced fluorescence emission when hybridised to the target nucleic acid.
CC The method comprises measuring the reduction in emission caused by
CC hybridisation. The new method is particularly used to quantify target
CC nucleic acids by a real-time polymerase chain reaction, e.g. for
CC quantifying microbial cells in co-cultures or symbiotic systems, for
CC detecting gene mutations or polymorphisms, and for analysing melting
CC curves of target nucleic acids to determine a Tm value. Methods of the
CC invention allow target nucleic acids to be quantified quickly, easily and
CC accurately. Particularly there is no need to remove unbound probe, and no
CC materials are introduced that inhibit amplification by Taq polymerase (no
CC conventional PCR conditions can be used). The specificity of PCR is kept
CC high (amplification of primer dimers is delayed), and the limit of
CC quantitation is reduced. Complex probes are not needed, and amplification
CC can be monitored in real time. The working graph for data analysis
CC (automatically generated by a computer) has a higher correlation
CC coefficient than conventional graphs so more accurate quantitation is
CC possible. The current sequence represents a synthetic
CC deoxyribonucleotide that was used for investigating the effects of
CC the number of G(s) in each target nucleic acid, and the number of G(s) in
CC its corresponding invention nucleic acid probe
XX
SQ Sequence 20 BP; 4 A; 2 C; 0 G; 14 T; 0 U; 0 Other;
Query Match 1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1345 TATATTTTATTTTCC 1360
Db 5 TATATTTTATTTTCC 20
RESULT 1006
AAH43116
ID AAH43116 standard; DNA; 20 BP.
XX
AC AAH43116;
XX
DT 19-SEP-2001 (first entry)
XX
DE Antisense oligo, target HDAC-2 121-141.
XX
KW Antisense; histone deacetylase; HDAC-1; HDAC-2; HDAC-4; inhibitor;
KW cell proliferation; cancer; restenosis; poriasis; protozoal infection;
KW fungal infections; ss.
XX
OS Synthetic.
XX
OS WO200138322-A1.
XX
PD 31-MAY-2001.
XX
PF 22-NOV-2000; 2000WO-IB001881.
XX
PR 23-NOV-1999; 99US-0167035P.
XX
PA (METH-) METHYLGENE INC.
XX
PI DeJorne D, Ruel R, Lavoie R, Thibault C, Abou-Khalil E;
XX
DR WPI; 2001-432601/46.
XX
PT New inhibitors of histone deacetylase e.g. N-hydroxy-5-(4-
PT (benzenesulfonylamino)-phenyl)-4-yn-2-pentanamide for treating cancer,
PT restenosis or fungal infections.
```

XX PS Disclosure; Page 40; 147pp; English.

XX CC The sequences given in AAH43115-21 are oligonucleotides which are

XX CC antisense to the histone deacetylase gene, HDAC-2. These oligonucleotides

XX CC may be used in combination with an inhibitor of histone deacetylase

XX CC enzyme function, to given an improved inhibitory effect, thereby reducing

XX CC the amount of inhibitor required to obtain a given inhibitory effect.

XX CC Compounds containing these oligonucleotides may be used to treat cell

XX CC proliferation conditions such as cancer, reestenosis or poriasis. They

XX CC can also be used to treat protozoal and fungal infections

XX SO Sequence 20 BP; 0 A; 7 C; 7 G; 6 T; 0 U; 0 Other;

Qy Query Match 1.0%; Score 14.4; DB 1; Length 20;

Best Local Similarity 93.8%; Pred. No. 5.3e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 726 TGCTGTTGCTGCTGCC 741

4 TGCTGCTGCTGCTGCC 19

RESULT 1007

AAH9545

ID AAC89545 standard; DNA; 20 BP.

XX AC AAC89545;

XX DT 08-MAR-2001 (first entry)

XX DE Human HDAC-2 antisense sequence SEQ ID NO: 15.

XX KM Histone deacetylase; HDAC-1; HDAC-2; HDAC-3; HDAC-4; HDAC-5; HDAC-C;

XX KM HDAC-D; cell cycle; tumorigenesis; cancer; inhibitor; antisense;

XX KM gene therapy; PCR primer; ss.

XX OS Homo sapiens.

XX PN WO200071703-A2.

XX PD 30-NOV-2000.

XX PF 03-MAY-2000; 2000WO-IB001252.

XX PR 03-MAY-1999; 99US-0132287P.

XX PA (METH-) METHYLENE INC.

XX PI Macleod AR, Li Z, Beesterman JM;

XX DR WPI; 2001-016407/02.

XX PT Antisense oligonucleotide that inhibits expression of a histone

XX PT deacetylase, useful for treating and/or alleviating the symptoms of

XX PT neoplasia, or for inhibiting neoplastic cell growth in an animal.

XX PS Example 1; Page 24; 125pp; English.

XX CC The present invention provides inhibitors of histone deacetylase enzymes

XX CC such as HDAC-1, HDAC-2, HDAC-3, HDAC-4, HDAC-5, HDAC-C and HDAC-D. These

XX CC inhibitors may be antisense strands or they may be compounds identified

XX CC by contacting the enzyme with the compound and measuring the resulting

XX CC enzyme activity. These inhibitors are useful for treating cancers and for

XX CC identifying which histone deacetylase is involved in a neoplasia

XX SO Sequence 20 BP; 0 A; 7 C; 7 G; 4 T; 2 U; 0 Other;

Qy Query Match 1.0%; Score 14.4; DB 1; Length 20;

Best Local Similarity 87.5%; Pred. No. 5.3e+02;

Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 726 TGCTGTTGCTGCTGCC 741

Db :|||||

4 UGCTGCTGCTGCTGCC 19

RESULT 1008

AAH9536

ID AAC89536 standard; DNA; 20 BP.

XX AC AAC89536;

XX DT 08-MAR-2001 (first entry)

XX DE Human HDAC-2 PCR primer SEQ ID NO: 6.

XX KM Histone deacetylase; HDAC-1; HDAC-2; HDAC-3; HDAC-4; HDAC-5; HDAC-C;

XX KM HDAC-D; cell cycle; tumorigenesis; cancer; inhibitor; antisense;

XX KM gene therapy; PCR primer; ss.

XX OS Homo sapiens.

XX PN WO200071703-A2.

XX PD 30-NOV-2000.

XX PF 03-MAY-2000; 2000WO-IB001252.

XX PR 03-MAY-1999; 99US-0132287P.

XX PA (METH-) METHYLENE INC.

XX PI Macleod AR, Li Z, Beesterman JM;

XX DR WPI; 2001-016407/02.

XX PT Antisense oligonucleotide that inhibits expression of a histone

XX PT deacetylase, useful for treating and/or alleviating the symptoms of

XX PT neoplasia, or for inhibiting neoplastic cell growth in an animal.

XX PS Disclosure; Page 12; 125pp; English.

XX CC The present invention provides inhibitors of histone deacetylase enzymes

XX CC such as HDAC-1, HDAC-2, HDAC-3, HDAC-4, HDAC-5, HDAC-C and HDAC-D. These

XX CC inhibitors may be antisense strands or they may be compounds identified

XX CC by contacting the enzyme with the compound and measuring the resulting

XX CC enzyme activity. These inhibitors are useful for treating cancers and for

XX CC identifying which histone deacetylase is involved in a neoplasia

XX SO Sequence 20 BP; 0 A; 7 C; 7 G; 6 T; 0 U; 0 Other;

Qy Query Match 1.0%; Score 14.4; DB 1; Length 20;

Best Local Similarity 93.8%; Pred. No. 5.3e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 726 TGCTGTTGCTGCTGCC 741

4 TGCTGCTGCTGCTGCC 19

RESULT 1009

AAH91976/C

ID AAH91976 standard; DNA; 20 BP.

XX AC AAH91976;

XX DT 09-OCT-2001 (first entry)

XX DE Human inflammatory bowel disease associated polymorphic site #1051.

XX KM Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;

XX KM single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;

XX KM chromosome 5q31-33; forensic test; gene therapy; ds.

XX OS Homo sapiens.

```

XX Key Location/Qualifiers
FH 11
FT misc_feature 11
FT /*tag= a
FT /note= "TA repeat at this position"
XX
XX WO200142511-A2.
XX
XX 14-JUN-2001.
XX
XX 11-DEC-2000; 2000WO-US033632.
XX
XX 10-DEC-1999; 99US-0170257P.
XX
XX 10-APR-2000; 2000US-0196046P.
XX
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX (ELIT-) ELIIPSIS BIOTHERAPEUTICS CORP.
XX
XX Daly M, Hudson TJ, Lander ES, Rioux J, Siminovitch K,
XX WPI; 2001-367874/38.
XX
XX Testing for the presence of polymorphisms associated with inflammatory
XX bowel disease, using a hybridization assay.
XX
XX Claim 1; Page 84; 463bp; English.
XX
XX The present invention describes a method for detecting the presence of
XX polymorphisms associated with inflammatory bowel diseases such as
XX ulcerative colitis and Crohn's disease. The methods can be used to detect
XX the presence of genetic polymorphisms associated with inflammatory bowel
XX disease and correlating their occurrence with disease states. They may be
XX used in this way for phenotypic correlations, forensics, paternity
XX testing, medicine and genetic analysis. The present sequence is a
XX polymorphic site described in the exemplification of the invention
XX
XX Sequence 20 BP; 10 A; 3 C; 2 G; 4 T; 0 U; 1 Other;
XX
XX Query Match 1.0%; Score 14.4; DB 1; Length 20;
XX Best Local Similarity 88.2%; Pred. No. 5.3e+02;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1311 TTTATTTTCAGACAG 1327
XX |||||
XX Db 20 TTTATTTTCAGACAG 4
XX
XX RESULT 1010
XX AAC82913/C
XX ID AAC82913 standard; DNA; 20 BP.
XX
XX AAC82913;
XX
XX 21-MAR-2001 (first entry)
XX
XX Human beta-actin derived oligonucleotide #6.
XX
XX Recognition system; screening; identification; pharmaceutical; toxin;
XX plant protection agent; toxin; venom; carcinogen; venom; teratogen;
XX herbicide; fungicide; pesticide; beta-actin; human; ss.
XX
XX Homo sapiens.
XX
XX DE19923966-A1.
XX
XX 30-NOV-2000.
XX
XX 25-MAY-1999; 99DE-01023966.
XX
XX 25-MAY-1999; 99DE-01023966.
XX
XX (AVET ) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
XX

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```

PI Boekenkamp D, Hoppe H, Burgstaller P;
XX
XX WPI; 2001-050938/07.
XX
XX Recognition system; e.g. for identifying nucleic acids, comprises at
XX least one recognition unit comprising a region with a defined structure
XX adjacent to a region with a randomized structure.
XX
XX Example; Fig 1; 8pp; German.
XX
XX This invention describes a novel recognition system comprising at least 1
XX recognition unit bound to a support, each recognition unit comprising a
XX region A with a defined structure adjacent to a region B with a
XX randomized structure. The recognition system is useful for screening,
XX identifying, or characterizing at least 1 component of a sample,
XX especially nucleic acids and/or proteins, and for screening for and/or
XX identifying cellular or synthetic binding partners, preferably proteins,
XX peptides, nucleic acids, chemical agents, preferably organic compounds,
XX pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
XX teratogens, herbicides, fungicides or pesticides
XX
XX Sequence 20 BP; 2 A; 0 C; 2 G; 16 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 14.4; DB 1; Length 20;
XX Best Local Similarity 93.8%; Pred. No. 5.3e+02;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1516 AATTAAAAA 1531
XX |||||
XX Db 17 ACTTAAAAA 2
XX
XX RESULT 1011
XX AAS05714
XX ID AAS05714 standard; DNA; 20 BP.
XX
XX AAS05714;
XX
XX 09-SEP-2004 (revised)
XX
XX 07-SEP-2001 (first entry)
XX
XX Aminopurine substituted region of an RP-TRO.
XX
XX reverse phase triplex forming oligonucleotide; RP-TRO;
XX protected nucleic acid sequence; PNAS; single nucleotide polymorphism;
XX SNP; short tandem repeat; cancer; Factor V Leiden SNP; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1
XX /*tag= a
XX /mod_base= OTHER
XX /note= "A is aminopurine substituted"
XX
XX modified_base 3
XX /*tag= b
XX /mod_base= OTHER
XX /note= "A is aminopurine substituted"
XX
XX modified_base 5
XX /*tag= c
XX /mod_base= OTHER
XX /note= "A is aminopurine substituted"
XX
XX modified_base 7
XX /*tag= d
XX /mod_base= OTHER
XX /note= "A is aminopurine substituted"
XX
XX modified_base 9
XX /*tag= e
XX /mod_base= OTHER
XX /note= "A is aminopurine substituted"
XX
XX modified_base 11
XX /*tag= f
XX /mod_base= OTHER
XX

```


Query Match	Similarity	Score	DB	Length	Indels	Gaps
Best Local	88.2%	Pred. No. 5.3e+02;		20;	0;	0;
Matches	15;	Conservative	0;	Mismatches	2;	Indels
					0;	Gaps
					0;	

```

QY 1520 AAAAAAAAAAAGTAA 1536
   |||||
Db 4 AAAAAAAAAAANAAA 20

RESULT 1012
ABA97637
ID ABA97637 standard; DNA; 20 BP.
XX
XX ABA97637;
XX
DT 11-APR-2002 (first entry)
XX
DE Poly 9 nucleotide sequence.
XX
XX 88; fluorochrome; nucleic acid probe; fluorescence.
XX
OS Unidentified.
XX
XX JP2001286300-A.
XX
XX
XX 16-OCT-2001.
XX
XX 20-APR-2000; 2000JP-00120097.
XX
XX 20-APR-1999; 99JP-00111601.
XX 24-AUG-1999; 99JP-00236666.
XX 30-AUG-1999; 99JP-00242693.
XX 01-FEB-2000; 2000JP-00028896.
XX
XX (BIOI-) BIOINDUSTRY KYOKAI SH.
XX (KANR-) KANKYO ENG KK.
XX (KEIZ-) KEIZAI SANGYOSHU SANGYO GIJUTSU SOGO KEN.
XX
XX WPI, 2002-134193/18.
XX
XX Measurement of nucleic acids, using a nucleic acid probe and analysis of
XX the obtained data.
XX
XX Example 6; Page 18; 34pp; Japanese.
XX
XX This invention relates to a method for measuring nucleic acids using a
XX nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
XX decreases the fluorescence of the fluorochrome when hybridised with a
XX target nucleic acid; the decrease in the fluorescence is measured. The
XX method can be used for measuring a target nucleic acid
XX
XX Sequence 20 BP; 4 A; 2 C; 0 G; 14 T; 0 U; 0 Other:
XX
XX Query Match 1.0%; Score 14.4; DB 1; Length 20;
XX Best Local Similarity 93.8%; Pred. No. 5.3e+02;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1345 TATATTTTATTTTCC 1360
XX |||||
XX 5 TATATTTTATTTTCC 20

RESULT 1013
ACF57337/c
ID ACF57337 standard; DNA; 20 BP.
XX
XX ACF57337;
XX
DT 16-OCT-2003 (first entry)
XX
XX Human atlastin exon 10 intronic acceptor splice site.
XX
XX Human; atlastin; chromosome 14; 14q22.1; hereditary spastic paraplegia;
XX HSP; neuroprotective; gene therapy; intronic splice site; gene; de.
XX
XX Homo sapiens.
XX Synthetic.
XX

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PN      WO2003026566-A2.
PM      XX
PD      XX
PC      03-APR-2003.
PF      13-SEP-2002; 2002WO-US029165.
PG      XX
PH      21-SEP-2001; 2001US-0323997P.
PI      12-SEP-2002; 2002US-00242008.
PJ      XX
PK      (UNMI ) UNIV MICHIGAN.
PL      XX
PM      Fink JK, Zhao X;
PN      WPI; 2003-371871/35.
PO      XX
PP      New atlastin gene, useful for preparing a composition for treating
PQ      Hereditary Spastic Paraplegia (HSP) or for identifying subjects who have,
PR      or at risk of developing, HSP.
PS      Example 6; Page 102; 111pp; English.
PT      XX
PU      The present invention describes human atlastin, which is located to
PV      Chromosome 14 (more specifically to 14q22.1). Also described: (1) an
PW      isolated atlastin polypeptide; (2) identifying subjects who have, or are
PX      at risk of developing, hereditary spastic paraplegia (HSP); (3) a kit for
PY      determining if a subject has, or at risk of developing, HSP; (4) a
PZ      computer readable medium encoding a representation of the atlastin
QA      nucleic acid sequence or polypeptide; (6) identifying subjects at risk of
QB      carrying an allele for HSP; and (7) treating a patient with HSP. Atlastin
QC      has neuroprotective activity and can be used in gene therapy. The
QD      atlastin nucleic acid is useful for preparing a composition for treating
QE      HSP or for identifying subjects who have, or at risk of developing, HSP.
QF      The present sequence represents an atlastin intronic splice site
QG      oligonucleotide, which is given in an example from the present invention
QH      XX
QI      SQ      Sequence 20 BP; 2 A; 2 C; 1 G; 15 T; 0 U; 0 Other;
QJ      Query Match      1.0%; Score 14.4; DB 1; Length 20;
QK      Best Local Similarity 93.8%; Pred. No. 5.3e+02;
QL      Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0.
QM      QY      1523 AAAAAAAAAAGTAAAG 1538
QN      Db      18 AAAAAAAAAAGAAAAG 3
QO      XX
QP      RESULT 1014
QQ      ABZ86068
QR      ID      ABZ86068 standard; DNA; 20 BP.
QS      XX
QT      ABZ86068;
QU      XX
QV      DT      17-OCT-2003 (first entry)
QW      DE      Human oligonucleotide sequence.
QX      XX
QY      Human; antisense; lung dysfunction; nasal airway dysfunction;
QZ      antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
RA      antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
RB      antisense gene therapy; respiratory; lung; adenosine sensitivity;
RC      adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
RD      lung inflammation; respiratory disease; ds.
RE      XX
RF      OS      Homo sapiens.
RG      XX
RH      WO200285308-A2.
RI      XX
RJ      31-OCT-2002.
RK      XX
RL      23-APR-2002; 2002WO-US013135.
RM      XX
RN      24-APR-2001; 2001US-0286137P.
RO      XX

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PA	(BIG-) EPIGENESIS PHARM INC.
PX	
XX	Nyce JW, Li Y, Sandrasagra A, Katz E, Pablan J, Aguilar D;
PI	Miller S, Tang L, Shahuddin S;
XX	WPI; 2003-229219/22.
DR	
XX	
PT	Pharmaceutical composition for treating ailments associated with impaired
PT	respiration, has oligo(s) antisense to specific gene(s) or its
PT	corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT	ubiquone.
PS	
XX	Claim 15; SEQ ID NO 1310; 872bp; English.
CC	
CC	The invention relates to a novel pharmaceutical composition, which has a
CC	first active agent comprising an oligonucleotide antisense to the
CC	initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC	5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC	junctions of genes encoding a polypeptide associated with lung and/or
CC	nasal airway dysfunction and a second active agent comprising an
CC	antiinflammatory steroid and ubiquinone. A composition of the invention
CC	has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC	immunosuppressive, and cytosstatic activity. The composition may have a
CC	use in antisense gene therapy. The composition is useful for treating or
CC	preventing a respiratory, lung or malignant disease or condition, also
CC	for enhancing the prophylactic or therapeutic respiratory effect of an
CC	antiinflammatory steroid in a subject, for reducing or depleting levels
CC	of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC	receptor, producing bronchodilation, increasing levels of ubiquinone or
CC	lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC	lung inflammation, lung allergies, or a respiratory disease or condition.
CC	Note: The sequence date for this patent is not represented in the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pct_sequences
SQ	
Sequence	20 BP; 0 A; 8 C; 7 G; 5 T; 0 U; 0 Other;
Query Match	1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity	93.8%; Pred. No. 5.3e+02;
Matches	15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Gy	726 TGCTGTCGTGCTGCC 741 4 TGCTGTCGTGCTGCC 19
Dd	
RESULT 1015	
ID	AB287682 standard; DNA, 20 BP.
XX	AB287682;
DB	
DT	17-OCT-2003 (first entry)
XX	
DE	Human oligonucleotide sequence.
XX	
KW	Human; antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds. Homo sapiens. WO200285308-A2. 31-OCT-2002. 23-APR-2002; 2002WO-US013135. 24-APR-2001; 2001US-0286137P.

```
XX XX (EPIC-) EPIGENESIS PHARM INC.
PA
XX
XX Myce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX MPI; 2003-229219/22.
DR
XX
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
XX PS Disclosure; SEQ ID NO 2924; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 20 BP; 2 A; 1 C; 3 G; 14 T; 0 U; 0 Other:
SQ
Query Match 1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1306 TTTTATTTCAG 1321
DB 1 TTTTTCAG 16
RESULT 1016
AB288879
ID AB288879 standard; DNA; 20 BP.
XX
XX AB288879;
AC
XX
XX 17-OCT-2003 (first entry)
DT
XX
XX Human oligonucleotide sequence.
DE
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
OS
XX
XX WO200285308-A2.
PV
XX
XX 31-OCT-2002.
PD
XX
XX 23-APR-2002; 2002WO-US013135.
PF
XX
XX 24-APR-2001; 2001US-0286137P.
PR
```

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XX XX (EPIC-) EPIGENESIS PHARM INC.
PA
XX
XX Myce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX MPI; 2003-229219/22.
DR
XX
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
XX PS Disclosure; SEQ ID NO 4121; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 20 BP; 16 A; 1 C; 1 G; 2 T; 0 U; 0 Other:
SQ
Query Match 1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1516 AATTAAAAA 1531
DB 4 ACTTAAAAA 19
RESULT 1017
AB297707/C
ID AB297707 standard; DNA; 20 BP.
XX
XX AB297707;
AC
XX
XX 17-OCT-2003 (first entry)
DT
XX
XX Human CCR3 oligonucleotide sequence.
DE
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
OS
XX
XX WO200285308-A2.
PV
XX
XX 31-OCT-2002.
PD
XX
XX 23-APR-2002; 2002WO-US013135.
PF
XX
XX 24-APR-2001; 2001US-0286137P.
PR
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XX (EPiG-) EPIGENESIS PHARM INC.
PA
XX NYce JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahbuddin S;
XX WPI; 2003-229219/22.
XX
XX Pharmacological composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiqtuone.
XX
XX PS Disclosure; SEQ ID NO 12949; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiqtuone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiqtuone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 20 BP; 2 A; 4 C; 2 G; 12 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 14.4; DB 1; Length 20;
XX Best Local Similarity 93.8%; Pred. No. 5.3e+02;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1524 AAAAAAAAAAGTAAAAG 1539
XX |||||||||
XX Db 17 AAAAAAAAAAGTACAAG 2
XX
XX RESULT 1018
XX AB291518 standard; DNA; 20 BP.
XX
XX AC AB291518;
XX
XX DT 17-OCT-2003 (first entry)
XX
XX DE Human oligonucleotide sequence.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiqtuone; antiinflammatory; antiallergic;
XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
XX
XX OS Homo sapiens.
XX
XX PN W0200285308-A2.
XX
XX PD 31-OCT-2002.
XX
XX PF 23-APR-2002; 2002WO-US013135.
XX
XX PR 24-APR-2001; 2001US-0286137P.
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XX (EPiG-) EPIGENESIS PHARM INC.
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XX NYce JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahbuddin S;
XX WPI; 2003-229219/22.
XX
XX Pharmacological composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiqtuone.
XX
XX PS Disclosure; SEQ ID NO 6760; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiqtuone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiqtuone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 20 BP; 2 A; 7 C; 5 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 14.4; DB 1; Length 20;
XX Best Local Similarity 93.8%; Pred. No. 5.3e+02;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 666 GACTCACCTCTGACGC 681
XX |||||||||
XX Db 1 GACTCACCTCTGTCGC 16
XX
XX RESULT 1019
XX AB289678 standard; DNA; 20 BP.
XX
XX AC AB289678;
XX
XX DT 17-OCT-2003 (first entry)
XX
XX DE Human oligonucleotide sequence.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiqtuone; antiinflammatory; antiallergic;
XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
XX
XX OS Homo sapiens.
XX
XX PN W0200285308-A2.
XX
XX PD 31-OCT-2002.
XX
XX PF 23-APR-2002; 2002WO-US013135.
XX
XX PR 24-APR-2001; 2001US-0286137P.
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XX (EPIC-) EPIGENESIS PHARM INC.
PA
XX
XX
XX Nye JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
XX
XX Disclosure; SEQ ID NO 4920; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 20 BP; 19 A; 0 C; 0 G; 0 T; 0 U; 1 Other;
SQ
Query Match 1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1521 AAAAAAAAAAGTAAAA 1537
DB 1 AAAAAAAAAAAAAAAAAA 17
RESULT 1020
ABZ93536
ID ABZ93536 standard; DNA; 20 BP.
XX
XX ABZ93536;
AC
XX
XX 17-OCT-2003 (first entry)
DT
XX
XX Human oligonucleotide sequence.
DE
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
OS
XX
XX WO200285308-A2.
PN
XX
XX 31-OCT-2002.
PD
XX
XX 23-APR-2002; 2002WO-US013135.
PF
XX
XX 24-APR-2001; 2001US-0286137P.
PR
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XX (EPIC-) EPIGENESIS PHARM INC.
PA
XX
XX
XX Nye JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
XX
XX Disclosure; SEQ ID NO 8778; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 20 BP; 5 A; 2 C; 2 G; 11 T; 0 U; 0 Other;
SQ
Query Match 1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1295 TGGTTAATCTATTTT 1310
DB 1 TGGTTAATCTTTT 16
RESULT 1021
ABZ88813
ID ABZ88813 standard; DNA; 20 BP.
XX
XX ABZ88813;
AC
XX
XX 17-OCT-2003 (first entry)
DT
XX
XX Human oligonucleotide sequence.
DE
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
OS
XX
XX WO200285308-A2.
PN
XX
XX 31-OCT-2002.
PD
XX
XX 23-APR-2002; 2002WO-US013135.
PF
XX
XX 24-APR-2001; 2001US-0286137P.
PR
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PA	(BIG-1) EPIGENESIS PHARM INC.
XX	
XX	Nyce JW, Li Y, Sandraeagra A, Katz E, Pabalan J, Aguilar D;
PI	Miller S, Tang L, Shahabuddin S;
XX	
XX	WPI, 2003-229219/22.
DR	
XX	
PT	Pharmaceutical composition for treating ailments associated with impaired
PT	respiration, has oligo(s) antisense to specific gene(s) or its
PT	corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT	ubiquinone.
XX	
PS	Disclosure; SEQ ID NO 4055; 872pp; English.
XX	
CC	The invention relates to a novel pharmaceutical composition, which has a
CC	first active agent comprising an oligonucleotide antisense to the
CC	initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC	5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC	junctions of genes encoding a polypeptide associated with lung and/or
CC	nasal airway dysfunction and a second active agent comprising an
CC	antiinflammatory steroid and ubiquinone. A composition of the invention
CC	has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC	immunosuppressive, and cytostatic activity. The composition may have a
CC	use in antisense gene therapy. The composition is useful for treating or
CC	preventing a respiratory, lung or malignant disease or condition, also
CC	for enhancing the prophylactic or therapeutic respiratory effect of an
CC	antiinflammatory steroid in a subject, for reducing or depleting levels
CC	of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC	receptor, producing bronchodilation, increasing levels of ubiquinone or
CC	lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC	lung inflammation, lung allergies, or a respiratory disease or condition.
CC	Note: The sequence data for this patent is not represented in the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp:wipo.int/pub/published_pct_sequences
XX	
SQ	Sequence 20 BP; 16 A; 0 C; 1 G; 3 T; 0 U; 0 Other;
	Query Match 1.0%; Score 14.4; DB 1; Length 20;
	Best Local Similarity 93.8%; Pred. No. 5.3e+02;
	Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1516 AATTTAAAAAAAATA 1531
Db	2 AATTTAAAAAAAATA 17
RESULT 1022	
ABZ86072	
ID	ABZ86072 standard; DNA; 20 BP.
XX	
AC	ABZ86072;
XX	
DT	17-OCT-2003 (first entry)
XX	
DE	Human oligonucleotide sequence.
XX	
KW	Human; antisense; lung dysfunction; nasal airway dysfunction;
KW	antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW	antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW	antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW	adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW	lung inflammation; respiratory disease; ds.
XX	
OS	Homo sapiens.
PN	WO200285308-A2.
XX	
PD	31-OCT-2002.
XX	
PF	23-APR-2002; 2002MO-US013135.
XX	
PR	24-APR-2001; 2001US-0286137P.

PA	(PIG-) EPIGENESIS PHARM INC.
XX	
PI	Nyce JW, Li Y, Sandrasagra A, Katz E, Pablan J, Aguilar D;
XX	Miller S, Tang L, Shahabuddin S;
DR	WPI; 2003-229219/22.
XX	
PT	Pharmaceutical composition for treating ailments associated with impaired
PT	respiration, has oligo(s) antisense to specific gene(s) or its
PT	corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT	ubiquinone.
PS	
XX	Claim 15; SEQ ID NO 1314; 872bp; English.
CC	
CC	The invention relates to a novel pharmaceutical composition, which has a
CC	first active agent comprising an oligonucleotide antisense to the
CC	initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC	and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC	junctions of genes encoding a polypeptide associated with lung and/or
CC	nasal airway dysfunction and a second active agent comprising an
CC	antiinflammatory steroid and ubiquinone. A composition of the invention
CC	has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC	immunosuppressive, and cyostatic activity. The composition may have a
CC	use in antisense gene therapy. The composition is useful for treating or
CC	preventing a respiratory, lung or malignant disease or condition, also
CC	for enhancing the prophylactic or therapeutic respiratory effect of an
CC	antiinflammatory steroid in a subject, for reducing or depleting levels
CC	of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC	receptor, producing bronchodilation, increasing levels of ubiquinone or
CC	lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC	lung inflammation, lung allergies, or a respiratory disease or condition.
CC	Note: The sequence data for this patent is not represented in the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pct_sequences
SQ	
Sequence	20 BP; 1 A; 8 C; 6 G; 5 T; 0 U; 0 Other;
Query Match	1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity	93.8%; Pred. No. 5.3e+02;
Matches	15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY	726 TGCGTGTGCTGCTGCC 741 Db 1 TGCGTGTGCTGCTGCC 16
RESULT 1023	
ABD22298	
ID	ABD22298 standard; DNA; 20 BP.
XX	
AC	ABD22298;
DT	29-JUL-2004 (first entry)
DE	Human stannocalcin-derived oligo SEQ ID 1310.
XX	
Human	antisense; bronchoconstriction; allergy; hyposecretion; pain;
KM	respiratory tract inflammation; adenoma sensitivity; lung; cancer;
KM	surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KM	analgesic; hypotensive; immunosuppressive; cyclostatic; cystic fibrosis;
KM	beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KM	respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KM	emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KM	pulmonary transplantation rejection; ss; primer.
OS	Homo sapiens.
XX	
WO	200285309-A2.
PB	
PD	31-OCT-2002.
XX	
PF	23-APR-2002; 2002WO-USO13143.

XX 24-APR-2001; 2001US-0286036P.
PR
XX (EPIC-) EPIGENESIS PHARM INC.
PA
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahbuddin S;
XX WPI: 2003-093058/08.
DR
XX Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
XX Claim 15; SEQ ID NO 1310; 763pp; English.
XX
XX This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hyperinflation, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
CC
XX Sequence 20 BP; 0 A; 8 C; 7 G; 5 T; 0 U; 0 Other;
SQ
Query Match 1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 726 TGCTGTGCTGCTGCC 741
DB 4 TGCTGTGCTGCTGCC 19
RESULT 1024
ABD25043
ID ABD25043 standard; DNA; 20 BP.
AC ABD25043;
XX
XX 29-JUL-2004 (fixed entry)
XX
XX All28305-derived oligonucleotide SEQ ID 4055.
XX
XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;

KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX
XX Homo sapiens.
OS
XX
XX WO200285309-A2.
PN
XX
XX 31-OCT-2002.
PD
XX
XX 23-APR-2002; 2002WO-US013143.
PF
XX
XX 24-APR-2001; 2001US-0286036P.
PR
XX
XX (EPIC-) EPIGENESIS PHARM INC.
PA
XX
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahbuddin S;
XX WPI: 2003-093058/08.
DR
XX
XX Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
XX Claim 15; SEQ ID NO 4055; 763pp; English.
XX
XX This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hyperinflation, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
CC
XX Sequence 20 BP; 16 A; 0 C; 1 G; 3 T; 0 U; 0 Other;
SQ
Query Match 1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1516 AATTAAAAA 1531
DB 2 AATTAAAAA 17
RESULT 1025
ABD29766

ID ABD29766 standard; DNA; 20 BP.
XX
AC ABD29766;
XX
DT 29-JUL-2004 (first entry)
XX
DE R37953-derived oligonucleotide SEQ ID 8778.
XX
KM Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KM respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KM surfactant depletion; antiasthmatic; antiinflammatory; antiasthmatic;
KM analgesic; hypotensive; immunosuppressive; cyclostatic; cystic fibrosis;
KM beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KM respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KM emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KM pulmonary transplantation rejection; ss; primer.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI NYCE JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahbuddin S;
XX
DR WPI; 2003-093058/08.
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PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 8778; 763bp; English.
XX
XX This invention describes a novel composition (a) a first active agent,
XX comprising oligonucleotides, effective for alleviating
XX bronchoconstriction, respiratory tract inflammation, allergies and
XX reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
XX surfactant depletion or hyposecretion, when administered to a mammal. The
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XX expression of a target polypeptide associated with lung airway or lung
XX dysfunction or cancer and can be anti-sense to the corresponding mRNA.
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XX analgesic, hypotensive, immunosuppressive and cyclostatic activity, is a
XX beta-adrenergic agonist. The composition is useful for preventing or
XX treating a respiratory, lung or malignant disease. The administered
XX composition comprises oligo and is administered to reduce the production
XX or availability, or to increase the degradation of the target mRNA or to
XX reduce the amount of target polypeptide present in the lungs. The
XX pulmonary obstruction and/or bronchoconstriction and/or lung
XX inflammation, allergies and/or surfactant hypoproduction are associated
XX with a disease or condition such as pulmonary vasoconstriction,
XX inflammation, allergies, asthma, impeded respiration, respiratory
XX distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
XX hyperextension, emphysema, chronic obstructive pulmonary disease, pulmonary
XX transplantation rejection, pulmonary infections, bronchitis or cancer.
XX The reduced adenosine content of the anti-sense oligos corresponding to
XX thymidines present in the target RNA serves to prevent the breakdown of
XX the oligonucleotides into products that free adenosine into the system
XX e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
XX prevent any unwanted effects due to it
XX
XX Sequence 20 BP; 5 A; 2 C; 2 G; 11 T; 0 U; 0 Other;

Query Match 1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
DY 1295 TGGTTAATCTTATTTT 1310
DB 1 TGGTTAATCTTATTTT 16
XX
RESULT 1026
ID ABD23912 standard; DNA; 20 BP.
XX
AC ABD23912;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human calmodulin 2-derived oligonucleotide SEQ ID 2924.
XX
KM Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KM respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KM surfactant depletion; antiasthmatic; antiinflammatory; antiasthmatic;
KM analgesic; hypotensive; immunosuppressive; cyclostatic; cystic fibrosis;
KM beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KM respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KM emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KM pulmonary transplantation rejection; ss; primer.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI NYCE JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahbuddin S;
XX
DR WPI; 2003-093058/08.
XX
PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 2924; 763bp; English.
XX
XX This invention describes a novel composition (a) a first active agent,
XX comprising oligonucleotides, effective for alleviating
XX bronchoconstriction, respiratory tract inflammation, allergies and
XX reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
XX surfactant depletion or hyposecretion, when administered to a mammal. The
XX oligonucleotides are derived from a gene encoding or regulating
XX expression of a target polypeptide associated with lung airway or lung
XX dysfunction or cancer and can be anti-sense to the corresponding mRNA.
XX The invention also describes a kit, that comprises: (a) a delivery
XX device, in separate containers, (b) the oligonucleotides, (c)
XX instructions for adding a carrier and for use of the kit. The composition
XX of the invention has antiasthmatic, antiinflammatory, antiasthmatic,
XX analgesic, hypotensive, immunosuppressive and cyclostatic activity, is a
XX beta-adrenergic agonist. The composition is useful for preventing or
XX treating a respiratory, lung or malignant disease. The administered
XX composition comprises oligo and is administered to reduce the production
XX or availability, or to increase the degradation of the target mRNA or to
XX reduce the amount of target polypeptide present in the lungs. The
XX pulmonary obstruction and/or bronchoconstriction and/or lung
XX inflammation, allergies and/or surfactant hypoproduction are associated

CC	with a disease or condition such as pulmonary vasoconstriction,
CC	inflammation, allergies, asthma, impeded respiration, respiratory
CC	diseases syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC	hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC	transplantation rejection, pulmonary infections, bronchitis or cancer.
CC	The reduced adenosine content of the anti-sense oligos corresponding to
CC	thymidines present in the target RNA serves to prevent the breakdown of
CC	the oligonucleotides into products that free adenosine into the system
CC	e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC	prevent any unwanted effects due to it
XX	
SQ	Sequence 20 BP; 2 A; 1 C; 3 G; 14 T; 0 U; 0 Other;
	Query Match 1.0%; Score 14.4; DB 1; Length 20;
	Best Local Similarity 93.8%; Pred. No. 5.3e+02;
	Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0
OY	1306 TTTTATTTTCAG 1321 1 TTTTTTTTTTCAG 16
D8	
	RESULT 1027
ID	ABD30738/C
XX	ABD30738 standard; DNA; 20 BP.
AC	
XX	ABD30738;
DT	
XX	29-JUL-2004 (first entry)
DE	
XX	Human CCR3-derived oligonucleotide SEQ ID 12949.
KW	Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW	respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW	nusaractant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW	analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW	beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW	respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW	emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW	pulmonary transplantation rejection; ss; primer.
XX	
OS	Homo sapiens.
XX	
PN	WO200285309-A2.
PD	
XX	31-OCT-2002.
PF	
XX	23-APR-2002; 2002MO-US013143.
PR	
XX	24-APR-2001; 2001US-0286036P.
PA	(EPIC-) EPIGENESIS PHARM INC.
XX	
XI	Nyca JM, Li Y, Sandraseagra A, Katz E, Pabalan J, Aguilar D;
P1	Miller S, Tang L, Shahabuddin S;
XX	
DR	WPI; 2003-093058/08.
XX	
PT	Pharmaceutical composition for treating asthma, has antisense
FT	oligonucleotide containing less percentage of adenosine, targeted to
PT	nucleic acids associated with lung airway or lung dysfunction, and
PT	bronchodilating agent.
PS	
XX	Claim 15; SEQ ID NO 12949; 763bp; English.
XX	
CC	This invention describes a novel composition (a) a first active agent,
CC	comprising oligonucleotides, effective for alleviating
CC	bronchoconstriction, respiratory tract inflammation, allergies and
CC	reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC	nusaractant depletion or hyposecretion, when administered to a mammal. The
CC	oligonucleotides are derived from a gene encoding or regulating
CC	expression of a target polypeptide associated with lung airway or lung
CC	dysfunction or cancer and can be anti-sense to the corresponding mRNA.

CC	The invention also describes a kit, that comprises:	(a) a delivery device, in separate containers; (b) the oligonucleotides;	(c)	instructions for adding a carrier and for use of the kit.
CC	The composition of the invention has anti-allergic, anti-inflammatory, antiasthmatic,	analgesic, hypotensive, immunosuppressive and cytostatic activity, is a beta-adrenergic agonist.	The composition is useful for preventing or treating a respiratory, lung or malignant disease.	The administered composition comprises oligo and is administered to reduce the production or availability, or to increase the degradation of the target mRNA or to reduce the amount of target polypeptide present in the lungs.
CC	pulmonary obstruction, and/or bronchoconstriction and/or lung inflammation, allergies and/or surfactant hypoproduction are associated with a disease or condition such as pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease, cancer.	transplantation rejection, pulmonary infections, bronchitis or cancer.	The reduced adenosine content of the anti-sense oligos corresponding to thymidines present in the target RNA serves to prevent the breakdown of the oligonucleotides into products that free adenosine into the system e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to prevent any unwanted effects due to it	
XX	Sequence 20 BP; 2 A; 4 C; 2 G; 12 T; 0 U; 0 Other;			
OY	Query Match	1.0%; Score 14.4; DB 1; Length 20;		
D6	Best Local Similarity	93.8%; Pred. No. 5.3e+02;		
	Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0			
	1524 AAAAAGTAAAGG 1539			
	17 AAAAAGTACAAGG 2			
RESULT 1028				
ABD25109				
ID ABD25109 standard; DNA; 20 BP.				
XX	ABD25109;			
DT	29-JUL-2004 (first entry)			
XX	A1125228-derived oligonucleotide SEQ ID 4121.			
DE	Human; antisense; bronchoconstriction; allergy; hyposecretion; pain; respiratory tract inflammation; adenosine sensitivity; lung; cancer; surfactant depletion; anti-allergic; antiinflammatory; antiaesthetic; analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis; beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction; respiratory distress syndrome; allergic rhinitis; pulmonary hypertension; emphysema; chronic obstructive pulmonary disease; cancer; bronchitis; pulmonary transplantation rejection; ss; primer.			
KW	Homo sapiens.			
OS	WO200285309-A2.			
PN				
XX				
PD	31-OCT-2002.			
XX				
PF	23-APR-2002; 2002WO-US013113.			
XX				
PR	24-APR-2001; 2001US-0286036P.			
PA	(EPIC-) EPIGENESIS PHARM INC.			
PI	Nyze JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;			
XX	Miller S, Tang L, Shahabuddin S;			
DR	WPI; 2003-093058/08.			
PT	Pharmaceutical composition for treating asthma, has antisense oligonucleotide containing less percentage of adenosine, targeted to nucleic acids associated with lung airway or lung dysfunction, and			

KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US031313.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIC-) EPIGENESIS PHARM INC.
XX
PI Nye JW, Li Y, Sandrasegura A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-093058/08.
XX
PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
BS Claim 15; SEQ ID NO 6760; 763bp; English.
XX
CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity. Levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, anti-asthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hyperextension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc. tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
SQ Sequence 20 BP; 2 A; 7 C; 5 G; 6 T; 0 U; 0 Other;
Query Match 1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 666 GACTCAGCTGTAGCG 681
|||
DB 1 GACTCAGCTGTCTCCG 16

XX
AC ADJ59564;
XX
DT 06-MAY-2004 (first entry)
XX
DE Oligonucleotide associated to CCR3 #65.
XX
KW interleukin; IL-4 receptor; IL-5 receptor; lung disease;
KW airway inflammation; allergy; asthma; impeded respiration;
KW cystic fibrosis; acute respiratory distress syndrome;
KW pulmonary hypertension; lung inflammation; bronchitis; oligonucleotide;
KW ss.
XX
OS Homo sapiens.
XX
PN WO2004011613-A2.
XX
PD 05-FEB-2004.
XX
PF 25-JUL-2003; 2003WO-US023509.
XX
PR 29-JUL-2002; 2002US-0399076P.
XX
PA (EPIC-) EPIGENESIS PHARM INC.
XX
PI Nye JW, Tang L, Sandrasegura A, Aguilar D, Miller S;
PI Shahabuddin S, Lu H, Cong H;
XX
DR WPI; 2004-203534/19.
XX
PT Novel single or multiple target oligonucleotide anti-sense to e.g.
PT initiation codons and introns of respiratory disease-relevant genes e.g.,
PT CCR3, RANTES, MCP4, useful for prophylaxis or treating respiratory
PT disease e.g., asthma.
XX
PS Claim 2; SEQ ID NO 420; 85bp; English.
XX
CC The present invention relates to an oligonucleotide anti-sense to e.g.,
CC initiation codon, coding region with 2-10 nucleotides of 5'-end and 3'-
CC end of nucleic acid target comprising gene(s) chosen from e.g.
CC interleukin (IL)-4 receptor, IL-5 receptor or salts of the
CC oligonucleotide and optionally surfactant operatively linked to the
CC oligonucleotide. The method is useful for preventing or treating a
CC respiratory or lung disease, which involves administering to the airways
CC of a subject an effective amount of an inhibitor. The oligonucleotide is
CC useful for production of a medicament for the prevention and/or treatment
CC of a respiratory or lung disease. The respiratory or lung disease is
CC chosen from airway inflammation, allergy(ies), asthma, impeded
CC respiration, cystic fibrosis (CF), chronic obstructive pulmonary diseases
CC (COPD), allergic rhinitis (AR), acute respiratory distress syndrome
CC (ARDS), pulmonary hypertension, lung inflammation, bronchitis, airway
CC obstruction. The present sequence represents an oligonucleotide of the
CC invention.
XX
SQ Sequence 20 BP; 2 A; 4 C; 2 G; 12 T; 0 U; 0 Other;
Query Match 1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1524 AAAAAAAGTAAAGG 1539
|||
DB 17 AAAAAAAGTCAAGG 2

RESULT 1032
ADJ59564/C
ID ADJ59564 standard; DNA; 20 BP.
XX
AC ADJ59564;
XX
DT 20-MAY-2004 (first entry)
XX

DE Chimeric phosphorothioate oligonucleotide to target Nav1.3 #8214.
XX Nav1.3; Analgesic; Noctropic; Neuroprotective; post-herpetic neuralgia;
KM diabetic neuropathy; arthritic pain; migraine headache;
KM infantile epilepsy; ataxia; ss.
XX Synthetic.
OS
XX WO2004016754-A2.
XX
XX 26-FEB-2004.
XX
XX 14-AUG-2003; 2003WO-US025465.
XX
XX 14-AUG-2002; 2002US-0403416P.
XX
XX (PHAA) PHARMACIA CORP.
XX
XX Roberds SL;
XX
XX WPI; 2004-203785/19.
XX
PT New antisense compound targeted to a nucleic acid molecule encoding
PT Nav1.3, useful for treating a disease or condition associated
PT with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
PT disorder, or ataxia.
XX
XX
XX Claim 4; SEQ ID NO 8214; 417pp; English.
XX
CC The present invention relates to an antisense compound targeted to a
CC nucleic acid molecule encoding Nav1.3, where the antisense compound
CC specifically hybridizes with and inhibits the expression of Nav1.3. The
CC compound and composition are useful for treating a disease or condition
CC associated with Nav1.3, e.g. pain including but not limited to
CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
CC pain from burns, migraine headache, cluster headache, mild-to-moderate
CC headache; seizure disorder such as childhood seizure disorder, including
CC but not limited to neonatal or infantile epilepsy; or ataxia. The present
CC sequence represents a chimeric phosphorothioate oligonucleotide with
CC 2'MOE wings and a decoy gap. Used during the antisense inhibition of
CC human Nav1.3 expression, the oligonucleotides are designed to target
CC different regions of the human Nav1.3 RNA.
XX
SQ Sequence 20 BP; 11 A; 2 C; 3 G; 4 T; 0 U; 0 Other;
Query Match 1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1252 TTTTGTTTTAAATCA 1267
Db 17 TTTTGATTTTAAATCA 2
RESULT 1033
ADO45054/C
ID ADO45054 standard; DNA; 20 BP.
AC ADO45054;
XX
XX 15-JUL-2004 (first entry)
XX
DE Human oligonucleotide #420.
XX
KM Human; ss; interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5;
KM CCR1; CCR3; Botaxin-1; RANTES; MCP4; CD23; ICAM; VCAM; tryptase a;
KM tryptase b; PDE4 A; PDE4 B; PDE4 C; PDE4 D; respiratory disease;
KM lung disease; hyper-responsiveness; adenosine; adenosine A receptor;
KM asthma; lung allergy; inflammation; inflammatory disease;
KM airway inflammation; allergy; impeded respiration; cystic fibrosis; CF;
KM chronic obstructive pulmonary disease; COPD; allergic rhinitis;
KM acute respiratory distress syndrome; pulmonary hypertension;

KM lung inflammation; bronchitis; airway obstruction; bronchoconstriction.
XX
XX Homo sapiens.
XX
XX US2004049022-A1.
XX
XX 11-MAR-2004.
XX
XX 25-JUL-2003; 2003US-00627930.
XX
XX 23-APR-2002; 2002WO-US013135.
XX 23-APR-2002; 2002WO-US013143.
XX
XX (NYCE/) NYCE J W.
XX (SAND/) SANDRASAGRA A.
XX (TANG/) TANG L.
XX (AGUI/) AGUIAR D.
XX (MILL/) MILLER S.
XX (SHAH/) SHAHABUDDIN S.
XX (LUH/) LU H.
XX (CONG/) CONG H.
XX
XX NYCE JW, Sandrasagra A, Tang L, Aguilar D, Miller S;
PI Shahabuddin S, Lu H, Cong H;
PI WPI; 2004-293804/27.
XX
XX
XX Novel single or multiple target oligonucleotide anti-sense to e.g.
PT initiation codon, intron of respiratory disease-relevant gene e.g. CCR1,
PT RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g.
PT asthma.
XX
XX
XX Claim 2; SEQ ID NO 420; 174pp; English.
XX
CC The invention relates to oligonucleotides anti-sense to an initiation
CC codon, coding region, 5' or 3' intron-exon junction, intron or region
CC with 2-10 nucleotides of the 5'-end or 3'-end of a nucleic acid target
CC chosen from a gene encoding interleukin (IL)-4 receptor, interleukin (IL)
CC -5 receptor, CCR1, CCR3, Botaxin-1, RANTES, MCP4, CD23, ICAM, VCAM,
CC tryptase a, tryptase b, PDE4 A, PDE4 B, PDE4 C or PDE4 D. The invention
CC also relates to a method of screening a candidate compound that binds to
CC one or more nucleic acid target(s) or expressed product(s), for the
CC prevention and/or treatment of a respiratory or lung disease. The
CC oligonucleotides are useful for reducing or inhibiting expression of a
CC gene or mRNA encoding interleukin-4 receptor, interleukin-5 receptor,
CC CCR1, CCR3, Botaxin-1, RANTES, MCP4, CD23, ICAM, VCAM, tryptase a,
CC tryptase b, PDE4 A, PDE4 B, PDE4 C, or PDE4 D. The oligonucleotides are
CC useful for preventing or treating a respiratory or lung disease. The
CC respiratory or lung disease is associated with hyper-responsiveness to
CC and/or increased levels of, adenosine and/or levels of adenosine A
CC receptor(s), and/or asthma and/or lung allergies associated with
CC inflammation or an inflammatory disease. The respiratory or lung disease
CC is chosen from airway inflammation, allergy, asthma, impeded respiration,
CC cystic fibrosis (CF), chronic obstructive pulmonary disease (COPD),
CC allergic rhinitis, acute respiratory distress syndrome, pulmonary
CC hypertension, lung inflammation, bronchitis, airway obstruction or
CC bronchoconstriction. This sequence represents an oligonucleotide of the
CC invention.
XX
SQ Sequence 20 BP; 2 A; 4 C; 2 G; 12 T; 0 U; 0 Other;
Query Match 1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1524 AAAAAAAAAAAGTAAAGC 1539
Db 17 AAAAAAAAAAGTAAAGC 2
RESULT 1034
ADO55869/C
ID ADO55869 standard; DNA; 20 BP.

```
XX ADOS5869;
AC
XX 12-AUG-2004 (first entry)
DT
XX Human NIMA-related kinase 6 DNA target sequence #23.
DE
XX Antisense therapy; human; NIMA-related kinase 6;
XX never in mitosis gene a-related kinase 6; hyperproliferative disorder;
XX cancer; cytosstatic; ds.
XX
XX Homo sapiens.
OS
XX US2004097441-A1.
XX
XX 20-MAY-2004.
PD
XX 16-NOV-2002; 2002US-00295471.
XX
XX 16-NOV-2002; 2002US-00295471.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Dobie KM;
XX
XX WPI; 2004-389184/36.
XX
XX New antisense oligonucleotides for modulating never in mitosis, gene a
XX (NIMA)-related kinase 6 expression, useful for diagnosing, preventing or
XX treating diseases associated with the kinase, e.g. hyperproliferative
XX disorders.
XX
XX Example 15; SEQ ID NO 115; 51bp; English.
XX
XX The present invention relates to antisense compounds targeted to a
XX nucleic acid encoding human never in mitosis gene a-related kinase 6
XX (NIMA-related kinase 6). The antisense compound comprises an antisense
XX oligonucleotide that specifically hybridizes with the nucleic acid and
XX inhibits the expression of NIMA-related kinase 6. The antisense
XX oligonucleotide is a chimeric oligonucleotide. The antisense
XX oligonucleotide comprises at least one modified internucleoside linkage,
XX preferably a phosphorothioate linkage. It also comprises at least one
XX modified sugar moiety, preferably a 2'-O-methoxyethyl (2'-MOE) sugar
XX moiety. The antisense oligonucleotide further comprises at least one
XX modified nucleobase, preferably a 5-methylcytosine. The antisense
XX oligonucleotides are useful for the treatment of diseases such as
XX hyperproliferative disorders, e.g. cancer. The present sequence
XX represents a human NIMA-related kinase 6 DNA target sequence for an
XX antisense oligonucleotide.
XX
XX Sequence 20 BP; 5 A; 9 C; 4 G; 2 T; 0 U; 0 Other;
SQ
XX
XX Query Match 1.0%; Score 14.4; DB 1; Length 20;
XX Best Local Similarity 93.8%; Pred. No. 5.3e+02;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1036 AGTGGCGCGCGGTGCT 1051
DB 20 AGTGGCGCTGCGGTGCT 5
RESULT 1035
ADOS5807
ID ADOS5807 standard; DNA; 20 BP.
AC
XX ADOS5807;
XX
XX 12-AUG-2004 (first entry)
DT
XX Human NIMA-related kinase 6 DNA, antisense oligonucleotide #30.
XX
XX Antisense therapy; human; NIMA-related kinase 6;
XX never in mitosis gene a-related kinase 6; hyperproliferative disorder;
XX
```

```
KW cancer; cytosstatic; phosphorothioate; ss.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX /tag= a
XX /mod_base= OTHER
XX /note= "This oligonucleotide has a phosphorothioate
XX backbone and 2'-methoxyethyl (2'-MOE) wings at the 5'
XX and 3' ends, which are 5 nucleotides in length at each
XX end. All cytidine residues are 5-methylcytidines"
XX
XX US2004097441-A1.
XX
XX 20-MAY-2004.
PD
XX 16-NOV-2002; 2002US-00295471.
XX
XX 16-NOV-2002; 2002US-00295471.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Dobie KM;
XX
XX WPI; 2004-389184/36.
XX
XX New antisense oligonucleotides for modulating never in mitosis, gene a
XX (NIMA)-related kinase 6 expression, useful for diagnosing, preventing or
XX treating diseases associated with the kinase, e.g. hyperproliferative
XX disorders.
XX
XX Example 15; SEQ ID NO 44; 51bp; English.
XX
XX The present invention relates to antisense compounds targeted to a
XX nucleic acid encoding human never in mitosis gene a-related kinase 6
XX (NIMA-related kinase 6). The antisense compound comprises an antisense
XX oligonucleotide that specifically hybridizes with the nucleic acid and
XX inhibits the expression of NIMA-related kinase 6. The antisense
XX oligonucleotide is a chimeric oligonucleotide. The antisense
XX oligonucleotide comprises at least one modified internucleoside linkage,
XX preferably a phosphorothioate linkage. It also comprises at least one
XX modified sugar moiety, preferably a 2'-O-methoxyethyl (2'-MOE) sugar
XX moiety. The antisense oligonucleotide further comprises at least one
XX modified nucleobase, preferably a 5-methylcytosine. The antisense
XX oligonucleotides are useful for the treatment of diseases such as
XX hyperproliferative disorders, e.g. cancer. The present sequence
XX represents an antisense oligonucleotide used in the examples of the
XX present invention.
XX
XX Sequence 20 BP; 2 A; 4 C; 9 G; 5 T; 0 U; 0 Other;
SQ
XX
XX Query Match 1.0%; Score 14.4; DB 1; Length 20;
XX Best Local Similarity 93.8%; Pred. No. 5.3e+02;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1036 AGTGGCGCGCGGTGCT 1051
DB 1 AGTGGCGCTGCGGTGCT 16
RESULT 1036
ADP20520/C
ID ADP20520 standard; DNA; 20 BP.
AC
XX ADP20520;
XX
XX 26-AUG-2004 (first entry)
DT
XX Transcription factor AP-2 antisense oligonucleotide seqid 67.
XX
XX cytosstatic; AP-2-inhibitor-Alpha; AP-2 alpha; AP-2 alpha modulator;
XX AP-2 alpha associated disorder; hyperproliferative disorder; human;
XX
```

KM transcription factor; antisense oligonucleotide; antisense technology;
KM ss.
XX Homo sapiens.
OS
XX US2004109848-A1.
PN
XX 10-JUN-2004.
PD
XX 09-DEC-2002; 2002US-00315962.
PF
XX 09-DEC-2002; 2002US-00315962.
PR
XX (ISIS-) ISIS PHARM INC.
PA
PI Bennett CF, Dean NM, Freier SM, Dobie KM;
XX WPI; 2004-440306/41.
DR
XX
XX
PT New compounds targeted to nucleic acid molecules encoding AP-2 alpha and
PT inhibits the expression of AP-2 alpha, useful for treating AP-2 alpha-
PT associated disease or condition, particularly a hyperproliferative
PT disorder.
PS
XX Example 15; SEQ ID NO 67; 58bp; English.
XX
XX The invention describes a compound (I) 8-80 nucleobases in length
CC targeted to a nucleic acid molecule encoding AP-2 alpha. The compound
CC specifically hybridises with a nucleic acid molecule encoding AP-2 alpha
CC (19868 bp, SEQ ID NO: 4), and inhibits the expression of AP-2 alpha. Also
CC described are: inhibiting the expression of AP-2 alpha in cells or tissues
CC comprising contacting the cells or tissues with (I); screening for a
CC modulator of AP-2 alpha by contacting a preferred target segment of a
CC nucleic acid molecule encoding AP-2 alpha with one or more candidate
CC modulators of AP-2 alpha, and identifying one or more modulators of AP-2
CC alpha expression, which modulate the expression of AP-2 alpha; a
CC diagnostic method for identifying a disease state; and a kit or assay
CC device comprising (I). The compound is useful for treating an animal
CC having a disease or condition associated with AP-2 alpha, particularly a
CC hyperproliferative disorder. The compounds may be used for diagnosis,
CC therapeutic prophylaxis and as research reagents; or as tools in
CC differential and/or combinatorial analyses to elucidate expression
CC patterns of a portion or the entire complement of genes expressed within
CC cells and tissues. This sequence represents a human transcription factor
CC AP-2 antisense oligonucleotide.
XX
SQ Sequence 20 BP; 5 A; 6 C; 8 G; 1 T; 0 U; 0 Other;
Query Match 1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 726 TGGTGTGCTGCTGCTGCC 741
DB 18 TGCTGCTGCTGCTGCTGCC 3
RESULT 1037
ADP21858/C
ID ADP21858 standard; DNA; 20 BP.
XX
XX ADP21858;
AC
XX
DT 26-AUG-2004 (first entry)
DE Human ornithine decarboxylase 1 primer seqid 6.
XX
XX cytosolic; gene therapy; ornithine decarboxylase 1;
KM ornithine decarboxylase 1 associated disorder;
KM hyperproliferative disorder; cancer; human; PCR; primer; ss.
XX
XX Homo sapiens.
OS
PT

PN US2004110148-A1.
XX
PD 10-JUN-2004.
PF 10-DEC-2002; 2002US-00316244.
XX
PR 10-DEC-2002; 2002US-00316244.
XX
XX (ISIS-) ISIS PHARM INC.
PA
PI Bennett CF, Dobie KM;
XX WPI; 2004-440337/41.
DR
XX
XX
PT New oligonucleotide compound that inhibits expression of ornithine
PT decarboxylase 1, useful for preparing a composition for treating
PT hyperproliferative disorder, e.g. cancer.
XX
PS Claim 21; SEQ ID NO 6; 69bp; English.
XX
XX The invention describes a new compound, having a sequence comprising 8-80
CC bp targeted to a nucleic acid encoding ornithine decarboxylase 1,
CC specifically hybridises with the nucleic acid encoding ornithine
CC decarboxylase 1 comprising 2035-bp sequence and inhibits expression of
CC ornithine decarboxylase 1. Also described are: inhibiting the expression
CC of ornithine decarboxylase 1 in cells or tissues; screening for a
CC modulator of ornithine decarboxylase 1; identifying a disease state; a
CC kit or assay device comprising the compound; and treating an animal
CC having a disease or condition associated with ornithine decarboxylase 1.
CC The oligonucleotide compound is useful for preparing a composition for
CC treating hyperproliferative disorder, e.g. cancer. This sequence
CC represents a primer used to isolate DNA encoding human ornithine
CC decarboxylase 1.
XX
SQ Sequence 20 BP; 8 A; 5 C; 6 G; 1 T; 0 U; 0 Other;
Query Match 1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 729 TGGTGTGCTGCTGCTTT 744
DB 20 TGTTGCTGCTGCTCT 5
RESULT 1038
AAQ75552
ID AAQ75552 standard; DNA; 19 BP.
XX
XX AAQ75552;
AC
XX
DT 04-AUG-1995 (first entry)
DE Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
XX Synthetic.
OS
XX JP06303997-A.
PN
XX
PD 01-NOV-1994.
DE 16-APR-1993; 93JP-00112515.
PF
XX 16-APR-1993; 93JP-00112515.
PR
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX WPI; 1995-018287/03.
DR
XX
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed

PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESSEQ files AAQ75547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c) the
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 19 BP; 2 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
Query Match 1.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 6.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1246 TCTTGTGTTGTTTAA 1264
Db 1 TTTTGTGTTTGTAA 19
RESULT 1039
ADL79331
ID ADL79331 standard; RNA; 19 BP.
AC ADL79331;
XX
XX 20-MAY-2004 (first entry)
XX
DE Human HER2 (EGFR2) siNA lower strand, SEQ ID NO:496.
XX
XX RNA interference; short interfering nucleic acid; siNA;
KW short interfering RNA; siRNA; double-stranded RNA; micro-RNA; miRNA;
KW short hairpin RNA; shRNA; expression modulation; gene therapy;
KW drug screening; diagnosis; therapeutic target identification;
KW pharmacogenomics; gene function analysis; gene mapping; cancer;
KW cytostatic; human; oncogene; epidermal growth factor receptor; EGFR;
KW HER2; EGFR2; neu; erbB2; C-erb-B-2; ss.
XX
XX Homo sapiens.
XX
XX WO2003070912-A2.
XX
XX 28-AUG-2003.
XX
XX 20-FEB-2003; 2003WO-US005045.
XX
XX 20-FEB-2002; 2002US-0358580P.
XX 11-MAR-2002; 2002US-0363124P.
XX 29-MAY-2002; 2002WO-US016840.
XX 06-JUN-2002; 2002US-00163552.
XX 06-JUN-2002; 2002US-0386782P.
XX 03-JUL-2002; 2002US-0393924P.
XX 29-AUG-2002; 2002US-0406784P.
XX 05-SEP-2002; 2002US-0408378P.
XX 09-SEP-2002; 2002US-0409293P.
XX 19-SEP-2002; 2002US-00251117.
XX 21-OCT-2002; 2002US-00277494.
XX 15-JAN-2003; 2003US-0440129P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Mcswiggen J, Pavco P, Beigelman L, Fossnaugh K, Jamison S;
XX WPI, 2003-697612/66.
XX
XX New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of cancer, downregulates expression of the epidermal growth
PT factor receptor gene.
XX

PS Example 3; SEQ ID NO 496; 171pp; English.
XX
XX The invention relates to short interfering nucleic acids (siNA) which
CC downregulate expression of one or more human epidermal growth factor
CC receptor (EGFR) genes (including HER1, HER2 HER3 and HER4) by RNA
CC interference. The siNAs may or may not comprise ribonucleotides and may
CC be double or single stranded. They further comprise sense and antisense
CC regions, or alternatively are assembled from a sense oligonucleotide and
CC an antisense oligonucleotide. Specifically, the siNAs include short
CC interfering RNA (siRNA), double-stranded RNA, micro-RNA (miRNA) and short
CC hairpin RNA (shRNA). The siNAs can be unmodified or chemically modified,
CC can contain deoxyribonucleotides, and can be chemically synthesised,
CC expressed from a vector or enzymatically synthesised. The invention also
CC relates to kits for the in vitro or in vivo delivery of siNA; conjugates
CC and/or complexes of siNA; and vectors that express siNA. The siNAs are
CC used to modulate expression of EGFR genes in cells, tissue explants or
CC organisms (e.g., by ex vivo gene therapy), or in grafts and transplants
CC for the treatment of a variety of conditions. They may be used for
CC treating a wide range of cancers such as breast and ovarian cancer. The
CC siNAs are also useful for drug screening, diagnosis, therapeutic target
CC identification and validation, genetic engineering, pharmacogenomics,
CC studying gene function, and gene mapping (e.g., of single nucleotide
CC polymorphisms). The present sequence represents the lower strand of a
CC HER2 (EGFR2)-targeted double-stranded siNA.
XX
SQ Sequence 19 BP; 16 A; 2 C; 0 G; 0 T; 1 U; 0 Other;
Query Match 1.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 6.1e+02;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 1519 TAAAAAAGTAAAA 1537
Db 1 UAAAAACAAAAA 19
RESULT 1040
ADL79082/C
ID ADL79082 standard; RNA; 19 BP.
XX
XX ADL79082;
XX
XX 20-MAY-2004 (first entry)
XX
XX
XX Human HER2 (EGFR2) transcript target sequence/siNA upper strand, SEQ:247.
XX
XX RNA interference; short interfering nucleic acid; siNA;
KW short interfering RNA; siRNA; double-stranded RNA; micro-RNA; miRNA;
KW short hairpin RNA; shRNA; expression modulation; gene therapy;
KW drug screening; diagnosis; therapeutic target identification;
KW pharmacogenomics; gene function analysis; gene mapping; cancer;
KW cytostatic; human; oncogene; epidermal growth factor receptor; EGFR;
KW HER2; EGFR2; neu; erbB2; C-erb-B-2; target sequence; ss.
XX
XX Homo sapiens.
XX
XX WO2003070912-A2.
XX
XX 28-AUG-2003.
XX
XX 20-FEB-2003; 2003WO-US005045.
XX
XX 20-FEB-2002; 2002US-0358580P.
XX 11-MAR-2002; 2002US-0363124P.
XX 29-MAY-2002; 2002WO-US016840.
XX 06-JUN-2002; 2002US-00163552.
XX 06-JUN-2002; 2002US-0386782P.
XX 03-JUL-2002; 2002US-0393924P.
XX 29-AUG-2002; 2002US-0406784P.
XX 05-SEP-2002; 2002US-0408378P.
XX 09-SEP-2002; 2002US-0409293P.
XX 19-SEP-2002; 2002US-00251117.
XX 21-OCT-2002; 2002US-00277494.
XX

PR 15-JAN-2003; 2003US-0440129P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
PI McSwiggen J, Pavco P, Belgelman L, Fossnaugh K, Jamison S;
XX WPI; 2003-697612/66.
XX
XX New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of cancer, downregulates expression of the epidermal growth
PT factor receptor gene.
XX
PS Example 3; SEQ ID NO 247; 171pp; English.
XX
XX The invention relates to short interfering nucleic acids (siNA) which
CC downregulate expression of one or more human epidermal growth factor
CC receptor (EGFR) genes (including HER1, HER2 HER3 and HER4) by RNA
CC interference. The siNAs may or may not comprise ribonucleotides and may
CC be double or single stranded. They further comprise sense and antisense
CC regions, or alternatively are assembled from a sense oligonucleotide and
CC an antisense oligonucleotide. Specifically, the siNAs include short
CC interfering RNA (siRNA), double-stranded RNA, micro-RNA (miRNA) and short
CC hairpin RNA (shRNA). The siNAs can be unmodified or chemically modified,
CC can contain deoxyribonucleotides, and can be chemically synthesised,
CC expressed from a vector or enzymatically synthesised. The invention also
CC relates to kits for the in vitro or in vivo delivery of siNA; conjugates
CC and/or complexes of siNA; and vectors that express siNA. The siNAs are
CC used to modulate expression of EGFR genes in cells, tissue explants or
CC organisms (e.g., by ex vivo gene therapy), or in grafts and transplants
CC for the treatment of a variety of conditions. They may be used for
CC treating a wide range of cancers such as breast and ovarian cancer. The
CC siNAs are also useful for drug screening, diagnosis, therapeutic target
CC identification and validation, genetic engineering, pharmacogenomics,
CC studying gene function, and gene mapping (e.g., of single nucleotide
CC polymorphisms). The present sequence represents the upper strand of a
CC human HER2 (EGFR2)-targeted double-stranded siNA, which is identical to
CC the HER2 transcript target sequence.
XX
SQ Sequence 19 BP; 1 A; 0 C; 2 G; 0 T; 16 U; 0 Other;
XX
Query Match 1.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 6.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 1519 TAAAAAAGTAAAA 1537
Dy |||||
Db 19 TAAAAACAAACAAA 1
XX
RESULT 1041
ABZ89546/C
ID ABZ89546 standard; DNA; 20 BP.
XX
AC ABZ89546;
XX
XX 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cyclostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
XX OS
XX PN WO200285308-A2.
XX PD 31-OCT-2002.
XX PF 23-APR-2002; 2002WO-US013135.

XX
XX 24-APR-2001; 2001US-0286137P.
XX
XX (EPIC-) EPIGENESIS PHARM INC.
XX
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahbuddin S;
XX WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4788; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cyclostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 18 A; 0 C; 0 G; 2 T; 0 U; 0 Other;
XX
Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 5.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 1246 TCTTGTGTTTTTTTAA 1264
Dy |||||
Db 19 TTTTTTTTTTTTTTTAA 1
XX
RESULT 1042
ABD25776/C
ID ABD25776 standard; DNA; 20 BP.
XX
AC ABD25776;
XX
XX 29-JUL-2004 (first entry)
XX
DE A108559 DNA fragment.
XX
XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cyclostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ds.
XX
XX Homo sapiens.
XX OS
XX PN WO200285309-A2.
XX PD 31-OCT-2002.

XX	23-APR-2002; 2002MO-US03143.
PF	
XX	24-APR-2001; 2001US-0286036P.
XX	
XX	(EPIC-) EPICGENESIS PHARM INC.
XX	
PI	Nyge JM, Li Y, Sandrasagra A, Katz E, Pebalan J, Aguilar D;
PI	Miller S, Tang L, Shahabuddin S;
XX	
DR	WPI; 2003-093058/08.
XX	
PT	Pharmaceutical composition for treating asthma, has antisense
PT	oligonucleotide containing less percentage of adenosine, targeted to
PT	nucleic acids associated with lung airway or lung dysfunction, and
PT	bronchodilating agent.
XX	
XX	Claim 15; SEQ ID NO 4788; 763bp; English.
XX	
CC	This invention describes a novel composition (a) a first active agent,
CC	comprising oligonucleotides, effective for alleviating
CC	bronchoconstriction, respiratory tract inflammation, allergies and
CC	reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors, or
CC	surfactant depletion or hyposcretion, when administered to a mammal. The
CC	oligonucleotides are derived from a gene encoding or regulating
CC	expression of a target polypeptide associated with lung airway or lung
CC	dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC	The invention also describes a kit, that comprises: (a) a delivery
CC	device, in separate containers, (b) the oligonucleotides, (c)
CC	instructions for adding a carrier and for use of the kit. The composition
CC	of the invention has antiallergic, antiinflammatory, antasthmatic,
CC	analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC	beta-adrenergic agonist. The composition is useful for preventing or
CC	treating a respiratory, lung or malignant disease. The administered
CC	composition comprises oligo and is administered to reduce the production
CC	or availability or to increase the degradation of the target mRNA or to
CC	reduce the amount of target polypeptide present in the lungs. The
CC	pulmonary obstruction, and/or bronchoconstriction and/or lung
CC	inflammation, allergies and/or surfactant hypoproduction are associated
CC	with a disease or condition such as pulmonary vasoconstriction,
CC	inflammation, allergies, asthma, impeded respiration, respiratory
CC	diseases syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC	hyperextension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC	transplantation rejection, pulmonary infections, bronchitis or cancer.
CC	The reduced adenosine content of the anti-sense oligos corresponding to
CC	thymidines present in the target RNA serves to prevent the breakdown of
CC	the oligonucleotides into products that free adenosine into the system
CC	e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC	prevent any unwanted effects due to it
XX	
SQ	Sequence 20 BP; 18 A; 0 C; 0 G; 2 T; 0 U; 0 Other;
	Query March 1.0%; Score 14.2; DB 1; Length 20;
	Beet Local Similarity 84.2%; Pred. No. 5.8e-02;
	Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0
OY	1246 TCTTGTGTTGTTTAA 1264
Db	19 TTTTGTGTTTGTAA 1
RESULT 1043	
AA075579	
ID	AA075579 standard; DNA; 20 BP.
XX	
XX	AA075579;
XX	
DT	04-AUG-1995 (first entry)
DE	Reverse transcription primer used in cDNA analysis technique.
XX	
XX	Analysis; gene expression; reverse transcription; primer; cDNA;
XX	aggregate; restriction enzyme; ss
XX	

```

XX OS Synthetic.
XX XX JP06303997-A.
XX PN 01-NOV-1994.
XX PD 16-APR-1993; 93JP-00112515.
XX PE 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX PS Disclosure; Page 5; 11pp; Japanese.
CC CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENBSEQ files AAQ75547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c) the
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
SQ Sequence 20 BP; 2 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 5.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0.

Cy 1246 TCCTTGTTGTTGTTTTAA 1264
Db 1 TTTTTCATTTTTCATTTTA 19

RESULT 1044
AAQ75582
ID AAQ75582 standard; DNA; 20 BP.
AC AAQ75582;
XX AAQ75582;
DT 04-AUG-1995 (first entry)
DE Reverse transcription primer used in cDNA analysis technique.
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX Synthetic.
OS Synthetic.
XX JP06303997-A.
XX PN 01-NOV-1994.
XX PD 16-APR-1993; 93JP-00112515.
XX PE 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX PS Disclosure; Page 5; 11pp; Japanese.
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of

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ID AAQ75596 standard; DNA; 20 BP.
XX
XX AAQ75596;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 20 BP; 2 A; 1 C; 0 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 14.2; DB 1; Length 20;
XX Best Local Similarity 84.2%; Pred. No. 5.8e+02;
XX Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1302 TCTATTTTATTTTCA 1320
XX | | | | | | | | | |
XX 1 TTTT TTTT TTTT TTTTCA 19
XX
XX RESULT 1048
XX AAQ75597
XX ID AAQ75597 standard; DNA; 20 BP.
XX
XX AC AAQ75597;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX

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PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 14.2; DB 1; Length 20;
XX Best Local Similarity 84.2%; Pred. No. 5.8e+02;
XX Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1302 TCTATTTTATTTTCA 1320
XX | | | | | | | | | |
XX 1 TTTT TTTT TTTT TTTTCA 19
XX
XX RESULT 1049
XX AAQ75595/c
XX ID AAQ75595 standard; DNA; 20 BP.
XX
XX AC AAQ75595;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 14.2; DB 1; Length 20;
XX

```

Best Local Similarity	84.2%	Pred. No. 5.8e+02:			
Matches	16;	Conservative	0;	Mismatches	3;
				Indels	0;
				Gaps	0;
Qy	1518	TTAATAAAAAAAAAAGTATA	1536		
Db	19	TGAAAAAAAAAAAAAAAAAAAA	1		

XX	RESULT 1050
XX	ID AB285312
XX	AB285312 standard; DNA; 20 BP.
XX	AB285312;
XX	17-OCT-2003 (first entry)
XX	Human oligonucleotide sequence.
XX	Human; antisense; lung dysfunction; nasal airway dysfunction;
XX	antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
XX	antisthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX	antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX	adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX	lung inflammation; respiratory disease; ds.
XX	Homo sapiens.
XX	MO200285308-A2.
XX	31-OCT-2002.
XX	23-APR-2002; 2002WC-US011135.
XX	24-APR-2001; 2001US-0286137P.
XX	(EPIG-) EPIGENESIS PHARM INC.
XX	NYCE JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX	Miller S, Tang L, Shahabuddin S;
XX	WPI; 2003-229219/22.
XX	Pharmaceutical composition for treating ailments associated with impaired
XX	respiration, has oligo(s) antisense to specific gene(s) or its
XX	corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX	ubiquinone.
XX	Claim 15, SEQ ID NO 554; 872pp; English.
XX	The invention relates to a novel pharmaceutical composition, which has a
XX	first active agent comprising an oligonucleotide antisense to the
XX	initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX	5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX	junctions of genes encoding a polypeptide associated with lung and/or
XX	nasal airway dysfunction and a second active agent comprising an
XX	antiinflammatory steroid and ubiquinone. A composition of the invention
XX	has antiinflammatory, antiallergic, antisthmatic, hypotensive,
XX	immunosuppressive, and cytostatic activity. The composition may have a
XX	use in antisense gene therapy. The composition is useful for treating or
XX	preventing a respiratory, lung or malignant disease or condition, also
XX	for enhancing the prophylactic or therapeutic respiratory effect of an
XX	antiinflammatory steroid in a subject, for reducing or depleting levels
XX	of, or reducing sensitivity to adenosine, for reducing levels of adenosine
XX	receptor, producing bronchodilation, increasing levels of ubiquinone or
XX	lung surfactant in a subject's tissue, or treating bronchoconstriction,
XX	lung inflammation, lung allergies, or a respiratory disease or condition.
XX	Note: The sequence data for this patent is not represented in the printed
XX	specification, but was obtained in electronic format directly from WIPO
XX	at http://www.wipo.int/pub/publicated_sequences
XX	Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 U; 0 Other;
XX	Query Match 1.0%; Score 14.2; DB 1; Length 20;

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Best Local Similarity 84.2%; Pred. No. 5.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0.

QY      1302 TCTATTTTTTTTATTTTCA 1320
      | | | | | | | | | | | | | | | |
Db      2 TTTTTTTTTTTTTTTTCA 20

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RESULT 1051
 ID ABD21542
 ID ABD21542 standard; DNA; 20 BP.
 AC ABD21542;
 DT 29-JUL-2004 (first entry)
 XX
 DE S100 calcium binding protein A2-derived oligo SEQ ID 554.
 XX
 KW Human; antiense; bronchoconstriction; allergy; hyposecretion; pain;
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
 KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
 KW analgesic; hypotensive; immunosuppressive; cystostatic; cystic fibrosis;
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
 KW pulmonary transplantation rejection; ss; primer.
 XX
 OS Homo sapiens.
 XX
 XX
 XX WO200285309-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 23-APR-2002; 2002WO-US013143.
 XX
 PR 24-APR-2001; 2001US-0286036P.
 XX
 XX (EPIG-) EPIGENESIS PHARM INC.
 XX
 PI NYCE JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahbuddin S;
 DR WPI; 2003-093058/08.
 XX
 XX
 PT Pharmaceutical composition for treating asthma, has antisense
 PT oligonucleotide containing less percentage of adenosine, targeted to
 PT nucleic acids associated with lung airway or lung dysfunction, and
 PT bronchodilating agent.
 XX
 XX
 XX Claim 15; SEQ ID NO 554; 763pp; English.
 XX
 CC This invention describes a novel composition (a) a first active agent,
 CC comprising oligonucleotides, effective for alleviating
 CC bronchoconstriction, respiratory tract inflammation, allergies and
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
 CC surfactant depletion or hyposecretion, when administered to a mammal. The
 CC oligonucleotides are derived from a gene encoding or regulating
 CC expression of a target polypeptide associated with lung airway or lung
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
 CC The invention also describes a kit, that comprises: (a) a delivery
 CC device, in separate containers, (b) the oligonucleotides, (c)
 CC instructions for adding a carrier and for use of the kit. The composition
 CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
 CC analgesic, hypotensive, immunosuppressive and cystostatic activity, is a
 CC beta-adrenergic agonist. The composition is useful for preventing or
 CC treating a respiratory, lung or malignant disease. The administered
 CC composition comprises oligo and is administered to reduce the production
 CC or availability, or to increase the degradation of the target mRNA or to
 CC reduce the amount of target polypeptide present in the lungs. The
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung
 CC inflammation, allergies and/or surfactant hypoproduction are associated
 CC with a disease or condition such as pulmonary vasoconstriction,
 CC inflammation, allergies, asthma, impeded respiration, respiratory

CC diarrhoea syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hyperplasia, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX

SO Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 14.2; DB 1; Length 20;

Best Local Similarity 84.2%; Pred. No. 5.8e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1302 TCTATTTTATTTTCA 1320

DB 2 TTTTATTTTATTTTCA 20

RESULT 1052

AAQ75586

ID AAQ75586 standard; DNA; 20 BP.

XX AAQ75586;

XX 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

KW Analysis: gene expression; reverse transcription; primer; cDNA;

KW aggregate; restriction enzyme; ss.

OS Synthetic.

PN JP06303997-A.

PD 01-NOV-1994.

PF 16-APR-1993; 93JP-00112515.

PR 16-APR-1993; 93JP-00112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

DR WPI; 1995-018287/03.

PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.

XX Disclosure; Page 5; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENBSEQ files AAQ75547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily

SO Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 14.2; DB 1; Length 20;

Best Local Similarity 84.2%; Pred. No. 5.8e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1248 TTTGTTTGTATTTATC 1266

DB 2 TTTTATTTTATTTATC 20

RESULT 1053

AAQ75576

ID AAQ75576 standard; DNA; 20 BP.

XX AAQ75576;

XX 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

KW Analysis: gene expression; reverse transcription; primer; cDNA;

KW aggregate; restriction enzyme; ss.

OS Synthetic.

PN JP06303997-A.

PD 01-NOV-1994.

PF 16-APR-1993; 93JP-00112515.

PR 16-APR-1993; 93JP-00112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

DR WPI; 1995-018287/03.

PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.

XX Disclosure; Page 5; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENBSEQ files AAQ75547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily

SO Sequence 20 BP; 2 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 14.2; DB 1; Length 20;

Best Local Similarity 84.2%; Pred. No. 5.8e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1304 TATTTTATTTTATTTTCA 1322

DB 2 TTTTATTTTATTTTATTTTCA 20

RESULT 1054

AAQ68872

ID AAQ68872 standard; DNA; 20 BP.

XX AAQ68872;

XX 25-MAR-2003 (revised)

DT 31-MAY-1995 (first entry)

DE Oligonucleotide (SA12/ml) used as control in antisense therapy.

XX Oligonucleotide; antisense; self paired; nuclease resistant;
KW dermatological disorders; viral infection; cancer; atypical dermatitis;
KW psoriasis; melanoma; T cell lymphoma; herpes simplex; papilloma;
KW hepatitis; HIV; human immunodeficiency virus; oncogene; collagenase;
KW elastase; bone marrow graft; ss.

OS Synthetic.

PN FR2703053-A1.

PD 30-SEP-1994.

```

XX 26-MAR-1993; 93FR-00003514.
XX
XX 26-MAR-1993; 93FR-00003514.
XX
XX (GEST ) GENSET.
XX
XX Vasseur M, Blumenfeld M, Meguenni S, Poddevyn B;
XX WPI; 1994-312170/39.
XX
XX New oligo:nucleotide(s) self paired at one or both ends - have improved
XX resistance to nuclease(s) and reduced toxicity, useful as anti-sense
XX molecules for treating dermatological disorders, virus infections,
XX cancer, etc.
XX
XX Example 1; Fig 4a; 40bp; French.
XX
XX New hooked or semi-hooked oligonucleotides (see AA068869-71, AA068873,
XX AA068875, AA068877, AA068879 and AA068880) are useful as therapeutic
XX antisense molecules for treating dermatological disorders (e.g. atypical
XX dermatitis, psoriasis, melanoma, T cell lymphoma etc.) viral infections
XX (e.g. herpes simplex, papilloma, hepatitis or HIV); or cancer (when
XX directed against an oncogene), due to their ability to hybridise with
XX target nucleic acid. They can be used ex vivo, e.g., to treat bone marrow
XX grafts. They can also be used for diagnosis or in cosmetics e.g. to block
XX mRNA coding proteins involved in the ageing process such as collagenase
XX or elastase. This linear antisense oligonucleotide is used as a control
XX to see whether the hooked and semi-hooked oligonucleotides exhibit a
XX greater resistance to exonucleases than linear oligonucleotides. (Updated
XX on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct
XX PA field.)
XX
XX Sequence 20 BP; 16 A; 1 C; 2 G; 1 T; 0 U; 0 Other:
SQ

```

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Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 5.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1520 AAAAAAAAAAAGTAAAG 1538
Db 1 AAAAAAAAAAATGAAAG 19

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RESULT 1055
ACF57337
ID ACF57337 standard; DNA; 20 BP.
XX
XX ACF57337;
XX
XX 16-OCT-2003 (first entry)
XX
XX Human atlastin exon 10 intronic acceptor splice site.
XX
XX Human; atlastin; chromosome 14; 14q22.1; hereditary spastic paraplegia;
XX HSP; neuroprotective; gene therapy; intronic splice site; gene; ds.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX WO2003026566-A2.
XX
XX 03-APR-2003.
XX
XX 13-SEP-2002; 2002WO-US029165.
XX
XX 21-SEP-2001; 2001US-032397P.
XX
XX 12-SEP-2002; 2002US-00242008.
XX
XX (UNMI ) UNIV MICHIGAN.
XX
XX Fink JK, Zhao X;
XX
XX

```

```

DR WPI; 2003-371871/35.
XX
XX New atlastin gene, useful for preparing a composition for treating
XX Hereditary Spastic Paraplegia (HSP) or for identifying subjects who have,
XX or at risk of developing, HSP.
XX
XX Example 6; Page 102; 11pp; English.
XX
XX
XX The present invention describes human atlastin, which is located to
XX chromosome 14 (more specifically to 14q22.1). Also described: (1) an
XX isolated atlastin polypeptide; (2) identifying subjects who have, or are
XX at risk of developing, hereditary spastic paraplegia (HSP); (3) a kit for
XX determining if a subject has, or at risk of developing, HSP; (4) a
XX computer readable medium encoding a representation of the atlastin
XX nucleic acid sequence or polypeptide; (6) identifying subjects at risk of
XX carrying an allele for HSP; and (7) treating a patient with HSP. Atlastin
XX has neuroprotective activity and can be used in gene therapy. The
XX atlastin nucleic acid is useful for preparing a composition for treating
XX HSP or for identifying subjects who have, or at risk of developing, HSP.
XX The present sequence represents an atlastin intronic splice site
XX oligonucleotide, which is given in an example from the present invention
XX
XX
XX Sequence 20 BP; 2 A; 2 C; 1 G; 15 T; 0 U; 0 Other:
SQ

```

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Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 5.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1245 ATCTTGTCTTCTTTT 1263
Db 1 ATCTTGTCTTCTTTT 19

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Search completed: November 2, 2004, 12:44:19
Job time : 22 secs

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15.6	1.1	22	1	TA380A07P	ACCESSION:AL497713																	
15.6	1.1	22	1	AG194579	ACCESSION:AG194579																	
15.4	1.1	19	1	CF334610	ACCESSION:CF334610																	
15.4	1.1	20	1	CL680297	ACCESSION:CL680297																	
15.4	1.1	21	1	CF319122	ACCESSION:CF319122																	
15.4	1.1	25	1	TA9097	ACCESSION:TA9097																	
15.2	1.1	20	1	AL038460	ACCESSION:AL038460																	
15.2	1.1	20	1	CF398018	ACCESSION:CF398018																	
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15.2	1.1	21	1	CN763587	ACCESSION:CN763587																	
15.2	1.1	21	1	AC393269	ACCESSION:AC393269																	
15.2	1.1	21	1	AC625662	ACCESSION:AC625662																	
15.2	1.1	23	1	CF300172	ACCESSION:CF300172																	
15.2	1.1	15	1	AM245585	ACCESSION:AM245585																	
15	1.1	19	1	AE774536	ACCESSION:AE774536																	

ALIGNMENTS

RESULT 1
 A2827502/c 27 bp DNA linear GSS 20-FEB-2001
 LOCUS 2M0103020R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 DEFINITION clone UGCG2M0103020 R, genomic survey sequence.
 ACCESSION A2827502
 VERSION A2827502.1 GI:12997410
 KEYWORDS GSS.
 ORGANISM Mus musculus (house mouse)
 SOURCE Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 27)
 Authors Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weis,R.
 Title Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Journal Unpublished (2000)
 Comment Contact: Robert B. Weis
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0103 row: O column: 20
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 27.

FEATURES
 source

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 /sex="Male"
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 /clone_lib="Mouse 10kb plasmid UGCGIM library"
 /note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource"

Query Match 1.4%; Score 19.6; DB 1; Length 27;
 Best local similarity 84.6%; Pred. No. 4.7;
 Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 537 GTGNGTGTGGGTGGGTGGGTG 562
 26 GTGTGTATGTGTGTGTGTGTGTG 1

RESULT 2
 A2486788/c 24 bp DNA linear GSS 05-OCT-2000
 LOCUS 1M0315122F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 DEFINITION clone UGCG1M0315122 F, genomic survey sequence.
 ACCESSION A2486788
 VERSION A2486788.1 GI:10653906
 KEYWORDS GSS.
 ORGANISM Mus musculus (house mouse)
 SOURCE Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 24)
 Authors Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weis,R.
 Title Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Journal Unpublished (2000)
 Comment Contact: Robert B. Weis
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0315 row: I column: 22
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 Class: plasmid ends
 High quality sequence stop: 24.

FEATURES
 source

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 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCGIM library"
 /note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.3%; Score 18.2; DB 1; Length 24;
Best Local Similarity 87.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1515 TAAATTAATAAAAAAAAAAGTAAAA 1537
Db 23 TAAATTAATAAAAAAAAAAAAAAAAA 1

RESULT 3
LOCUS A2607198 24 bp DNA linear GSS 13-DEC-2000
DEFINITION IM0429G03R Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC1M0429G03 R, genomic survey sequence.
ACCESSION A2607198
VERSION A2607198.1 GI:11729388
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 24)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weis
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0429 row: G column: 03
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers

FEATURES
Source 1. .24
Location/Qualifiers

/organism="Mus musculus"
/mol_type="genomic DNA"
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/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.3%; Score 18.2; DB 1; Length 24;
Best Local Similarity 87.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1515 TAAATTAATAAAAAAAAAAGTAAAA 1537
Db 1 TAAATTAATAAAAAAAAAAAAAAAAA 23

RESULT 4
LOCUS A2330737 25 bp DNA linear GSS 29-SEP-2000
DEFINITION IM0056F09F Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC1M0056F09 F, genomic survey sequence.
ACCESSION A2330737
VERSION A2330737.1 GI:10392737
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 25)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weis
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0056 row: F column: 09
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers

FEATURES
Source 1. .25
Location/Qualifiers

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/clone="UUC1M0056F09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (g1473114[g1473114]Af129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.3%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1515 TAATTAATAAAAAAAAAAGTAA 1537
Db 1 TATTTAAAAAAAAAAAAAAAAA 23

RESULT 5
TA231E08Q 22 bp DNA linear GSS 13-DEC-2000
LOCUS T. brucei sheared genomic DNA clone 231e08, reverse sequence,
DEFINITION genomic survey sequence.
ACCESSION AL480935 GI:11846704
VERSION AL480935.1 GI:11846704
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE
AUTHORS 1 (bases 1 to 22)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk

COMMENT
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + 1 method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaubin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
SOURCE location/Qualifiers

1. 22
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="231e08"

Query Match 1.3%; Score 17.8; DB 1; Length 22;
Best Local Similarity 90.5%; Pred. No. 13;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAAGTAAAGG 1540
Db 1 AAAAAAAAAAAGG 21

RESULT 6
AJ663467 25 bp mRNA linear EST 28-JUN-2004
LOCUS AJ663467 CSEORAN09 Sus scrofa cDNA clone C0000027_007, mRNA
DEFINITION sequence.
ACCESSION AJ663467 GI:49347590
VERSION AJ663467.1 GI:49347590
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
1 (bases 1 to 25)
Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
TITLE Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
JOURNAL Unpublished (2004)

COMMENT
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM

Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -m1nscore 20
and -mismatch 12 options. Vector: pluescriptII (KS+) R. Site 1:
EcoRI R. Site 2: NotI Description: Normalised library constructed
from pooled tissue from day 30 placentas. Clones available from UK
Centre for Functional Genomics in Farm Animals, Roslin Institute,
Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.

FEATURES
SOURCE location/Qualifiers

1. 25
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0000027_007"
/tissue_type="placenta"
/clone_lib="CSEORAN09"
/note="Vector: pluescriptII (KS+); Site_1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pooled tissue from day 30 placentas."

Query Match 1.3%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAAGTAAAGG 1540
Db 3 AAAAAAAAAAAGG 23

RESULT 7
CF291636 24 bp mRNA linear EST 14-AUG-2003
LOCUS CF291636 14ROOT--02-C09.g1 Rice root plasmid cDNA library (14ROOT) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone 14ROOT--02-C09, mRNA
sequence.
ACCESSION CF291636 GI:33660669
VERSION CF291636.1 GI:33660669
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriocaridaceae; Oryzaceae; Oryza.

REFERENCE
AUTHORS 1 (bases 1 to 24)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193

Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES

Source

1. 24
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ROOT--02-C09"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: PCR4-TOPO, Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.3%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 16;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 424 GTGGCGCTGGCGCGCGCGCGCG 447
|||
1 GCGCGCGCGCGCGCGCGCGCGCG 24

RESULT 8
A2309553 24 bp DNA linear GSS 29-SEP-2000
LOCUS 1M0016B10F Mouse 10kb plasmid UUCG1M library Mus musculus genomic
DEFINITION clone UUCG1M0016B10 F, genomic survey sequence.
ACCESSION A2309553
VERSION A2309553.1 GI:10350837
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS 1 (bases 1 to 24)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu

Insert Length: 1000 Std Error: 0.00
Plate: 0016 row: B column: 10
Seq primer: CTTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers

FEATURES

Source

1. 24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0016B10"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PWD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD2 (g1473214[gb]AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.3%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 16;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1514 TTAATTAAAAAAGTAAA 1537
|||
1 TTTTAAAAAAGTAAAAA 24

RESULT 9
CF317007 25 bp mRNA linear EST 15-AUG-2003
LOCUS HD--06-114.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
DEFINITION library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--06-114, mRNA sequence.
ACCESSION CF317007
VERSION CF317007.1 GI:33688768
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretidae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 25)
Kim, J.S., Yun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nam, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
Contact: Nam B.H.

COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Yonsei University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

Source

1. 25
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--06-114"
/tissue_type="callus"
/dev_stage="proliferated callus on 2M6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: PCR4-TOPO, Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 1.3%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Cy 1514 TTAATTAATAAAAAAAAAAGTAAAA 1537
 ||||| ||||| ||||| ||||| |||||
 Db 25 TTAATAAAAAAAAAAAAAAAAAAAAA 2

RESULT 10
 LOCUS T49097/c
 DEFINITION yb08h08.g1 Stratagene placenta (#937225) Homo sapiens cDNA clone IMAGE70623.3, similar to gb:U62744 CLASS II HISTOCOMPATIBILITY ANTIGEN, M ALPHA CHAIN (HUMAN), mRNA sequence.

ACCESSION T49097
 VERSION T49097.1
 KEYWORDS GI:650957
 SOURCE EST.
 ORGANISM Homo sapiens (human)
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiappelli, B., Chisone, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierley-Weg, J., Trevaaskis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.
 Generation and analysis of 280,000 human expressed sequence tags
 Genome Res. 6 (9), 807-828 (1996)
 97044478
 8889549
 Other ESTs: yb08h08.x1
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu
 High quality sequence strops: 1
 High gality sequence strops: 1
 Source: IMAGE Consortium, LBNL
 This clone is available royalty-free through LBNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 Trace considered overall poor quality
 Seq primer: -21m13
 High quality sequence stop: 1.
 Location/Qualifiers
 1..25
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:491520"
 /db_xref="taxon:9606"
 /clone="IMAGE:70623"
 /sex="male"
 /lab_host="SOLR cells (kanamycin resistant)"
 /clone_1lb="Stratagene placenta (#937225)"
 /note="Organ: placenta; Vector: plasmid SK-; Site: 1; EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Caucasian. Average insert size: 1.2 kb; Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAAATCGGACGAG 3' ~3' adaptor sequence: 5' CTCGAGCTTTTCTTTTCTTTT 3'."

Query Match 1.3%; Score 17.6; DB 1; Length 25;
 Best Local Similarity 83.3%; Pred. No. 17;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Cy 1514 TTAATTAATAAAAAAAAAAGTAAAA 1537
 ||||| ||||| ||||| ||||| |||||
 Db 24 TTCTTTAAAAAAAAAAAAAAAAAAAAA 1

RESULT 11
 LOCUS AZ307896/c
 DEFINITION ABF--01-l15.g1 ABF3-overexpressing transgenic rice plasmid cDNA

DEFINITION IM0010N18F Mouse 10kb plasmid UGCM library Mus musculus genomic clone UGCM0010N18 F, genomic survey sequence.
 ACCESSION AZ307896
 VERSION AZ307896.1
 KEYWORDS GI:10347346
 SOURCE GSS.
 ORGANISM Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weis, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weis
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0010 row: N column: 18
 Seq primer: CGTTGTAACGACGCGCCACT
 Class: plasmid ends
 High quality sequence stop: 22.
 Location/Qualifiers
 1..22
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCM0010N18"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid UGCM library"
 /note="Vector: PMD42ny. Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1473211[gb|AF12972.1]) a copy-number inducible derivative of plasmid R1. The vector was ligated with adpators complementary to the insert adpators and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.2%; Score 17.2; DB 1; Length 22;
 Best Local Similarity 86.4%; Pred. No. 19;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy 1520 AAAAAAAAAAAGTAAAGCGA 1541
 ||||| ||||| ||||| ||||| |||||
 Db 22 AAAAAAAAAAACAAGCGA 1

RESULT 12
 LOCUS CF308058/c
 DEFINITION ABF--01-l15.g1 ABF3-overexpressing transgenic rice plasmid cDNA

library (ABF) *Oryza sativa* (japonica cultivar-group) cDNA clone
ABF-01-115, mRNA sequence.

ACCESSION
CF308058
VERSION
CF308058.1 GI:33679819
KEYWORDS
EST.
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretidae; Oryzaceae; Oryza.

REFERENCE
1 (bases 1 to 23)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc., Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..23
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultiVar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF-01-115"
/issue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: PCR4-TOPO, Site_1: EcoRI, leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 1.2%; Score 17.2; DB 1; Length 23;
Best Local Similarity 86.4%; Pred. No. 20;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1510 ACTGTTATTAAAAA 1531
Db 23 AGTGTAGTAAAAA 2

RESULT 13
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
MUS musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 24)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT

84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0474 row: N column: 20
Seq primer: CGGTGTAACGACGCCACAGT
Class: plasmid ends
High quality sequence stop: 24.

FEATURES
source
1..24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0474N20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g14732114[g14732114]p129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.2%; Score 17.2; DB 1; Length 24;
Best Local Similarity 86.4%; Pred. No. 21;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1521 AAAAAAAGTAAAGGAA 1542
Db 1 AAAAAAATTAAGAA 22

RESULT 14
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretidae; Oryzaceae; Oryza.

REFERENCE
1 (bases 1 to 23)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc., Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355


```

RESULT 18
LOCUS      AL038845
DEFINITION DKEF2566P1746.r1.566 (synonym: hfkcd2) Homo sapiens cDNA clone
ACCESSION  AL038845
VERSION    AL038845.1 GI:49682220
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
Wiemann, S.
TITLE      EST (Ottenwaelder, et al.)
JOURNAL    Unpublished (1999)
COMMENT    Contact: MIPS
MIPS      Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES
source
1..20
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKEF2566P1746"
/issue_type="Kidney"
/dev_stage="fetal"
/lab_host="X1-2b1ue"
/clone_lib="566 (synonym: hfkcd2)"
/note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match      1.2%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1518 TTTAAAAAAAGTAAAGG 1537
      |||||
      1 TTTAAAAAAAGTAAAGG 20

JOURNAL
COMMENT
TITLE
AUTHORS
REFERENCE
1 (bases 1 to 20)
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Niedermaier, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0150 row: P column: 21
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
location/Qualifiers
1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC2M0150P21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to

```

```

/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--01-H23"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E. coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.2%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1521 AAAAAAAAGTAAAGG 1540
      |||||
      1 AAAAAAAAGTAAAGG 20

JOURNAL
COMMENT
TITLE
AUTHORS
REFERENCE
1 (bases 1 to 20)
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niedermaier, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0150 row: P column: 21
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC2M0150P21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to

```

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.2%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1518 TTTAAAAAAGTAAAA 1537
|||||
Db 1 TTTAAAAAAGTAAAA 20

RESULT 21
AZ943299 21 bp DNA linear GSS 26-APR-2001
LOCUS 2M0203K21R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
DEFINITION clone UUGC2M0203K21 R, genomic survey sequence.
ACCESSION AZ943299
VERSION AZ943299.1 GI:13807290
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Rajam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Niedermaier, A. and Wright, D., Weis, R., Tingey, A., von
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dduan@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0203 row: K column: 21
Seq primer: CACACGAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.

FEATURES
Source
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0203K21"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PMD42v; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.2%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 24;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1521 AAAAAAAGTAAAAAGG 1540
|||||
Db 21 AAAAAAAGTAAAAAGG 2

RESULT 22
AL038477 22 bp mRNA linear EST 06-JUL-2004
LOCUS DKFZ566C1646 r1.566 (synonym: hfk42) Homo sapiens cDNA clone
DEFINITION DKFZ566C1646, mRNA sequence.
ACCESSION AL038477
VERSION AL038477.1 GI:49682139
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 22)
Ostenmaier, B., Ostermaier, B., Mewes, H.W., Gassenhuber, J. and
Wiemann, S.
EST (Ostenmaier, et al.)
Unpublished (1999)
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES
Source
1..22
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZ566C1646"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2b1ue"
/clone_lib="566 (synonym: hfk42)"
/note="Vector: PAMPI, Site_1: Noci, Site_2: Sali"

Query Match 1.2%; Score 16.8; DB 1; Length 22;
Best Local Similarity 90.0%; Pred. No. 25;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1518 TTTAAAAAAGTAAAA 1537
|||||
Db 1 TTTAAAAAAGTAAAA 20

RESULT 23
CF310486 22 bp mRNA linear EST 15-AUG-2003
LOCUS ABF--05-c16.g1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--05-c16, mRNA sequence.
ACCESSION CF310486
VERSION CF310486.1 GI:33682247
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretioideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 22)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 TITLE Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 JOURNAL Large-scale Sequencing Analysis of Rice ESTs
 COMMENT Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
 source
 1..22
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="ABF--05-C16"
 /issue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="ABF3-overexpressing transgenic rice plasmid
 cDNA library (ABP)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
 for 2hrs. Oligo-capped mRNA was reverse transcribed and
 then used for PCR. mRNA was prepared from ABA-responsive
 element binding transcription factor 3 overexpression
 line."

Query Match 1.2%; Score 16.8; DB 1; Length 22;
 Best Local Similarity 90.0%; Pred. No. 25;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1518 TTTAAAAAAAGTAAAA 1537
 Db 2 TTTAAAAAAAGTAAAA 21

RESULT 24 CF339694 23 bp mRNA linear EST 18-AUG-2003
 LOCUS NACL--05-B19.D1 Rice callus plasmid cDNA library (NACL) Oryza
 DEFINITION sativa (japonica cultivar-group) cDNA clone NACL--05-B19, mRNA
 sequence.

ACCESSION CF339694 GI:33807601
 VERSION CF339694
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 BUKARYOTA: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 23)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 TITLE Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 JOURNAL Large-scale Sequencing Analysis of Rice ESTs
 COMMENT Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
 source
 1..23
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="NACL--05-B19"
 /issue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice callus plasmid cDNA library (NACL)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 1.2%; Score 16.8; DB 1; Length 23;
 Best Local Similarity 90.0%; Pred. No. 26;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1518 TTTAAAAAAAGTAAAA 1537
 Db 23 TTTAAAAAAAGTAAAA 4

RESULT 25 CF333801 23 bp mRNA linear EST 18-AUG-2003
 LOCUS JMT--02-N11.G1 AtJMT-overexpressing transgenic rice plasmid cDNA
 DEFINITION library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
 JMT--02-N11, mRNA sequence.

ACCESSION CF333801 GI:33815910
 VERSION CF333801
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 BUKARYOTA: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 23)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 TITLE Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 JOURNAL Large-scale Sequencing Analysis of Rice ESTs
 COMMENT Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
 source
 1..23
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="JMT--02-N11"
 /issue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="AtJMT-overexpressing transgenic rice plasmid
 cDNA library (JMT)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
 was reverse transcribed and then used for PCR. mRNA was
 prepared from Arabidopsis jasmonate Carboxyl
 methyltransferase overexpression line."

Query Match 1.2%; Score 16.8; DB 1; Length 23;
 Best Local Similarity 90.0%; Pred. No. 26;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1518 TTTAAAAAAAGTAAAA 1537
 Db 23 TTTAAAAAAAGTAAAA 4

RESULT 26 AJ668301 24 bp mRNA linear EST 28-JUN-2004
 LOCUS AJ668301 CSEGRAN09 Sus scrofa cDNA clone C000045_P10, mRNA
 DEFINITION sequence.

ACCESSION AJ668301 GI:49352752
 VERSION AJ668301.1
 KEYWORDS EST.
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.

REFERENCE 1 (bases 1 to 24)
 Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
 Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle
 Unpublished (2004)
 CONTACT: Anderson SI
 Genomics and Bioinformatics
 Roslin Institute
 Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
 Single pass sequencing. Bases called and trimmed with phred v0.020423.c. Vector identified by cross_match with the -minscore 20 and -mismatch 12 options. Vector: pBluescriptII(ks+). R. Site 1: EcORI R. Site 2: NotI Description: Normalised library constructed from pooled tissue from day 30 placentas. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK. EH25 9PS, www.atkgenomics.org.

FEATURES
 source
 1..24
 /organism="Sus scrofa"
 /mol_type="mRNA"
 /db_xref="taxon:9823"
 /clone="C0000045_P10"
 /tissue_type="placenta"
 /clone_lib="CSEQRN09"
 /note="Vector: pBluescriptII(ks+); Site 1: EcORI; Site 2: NotI; Single pass sequencing. Normalised library constructed from pooled tissue from day 30 placentas."

Query Match 1.2%; Score 16.8; DB 1; Length 24;
 Best Local Similarity 90.0%; Pred. No. 28;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1518 TTTAAAAAAAGTAAA 1537
 DB 21 TTTAAAAAAAGTAAA 2

RESULT 27
 BX550903/c 23 bp mRNA linear EST 10-OCT-2003
 LOCUS BX550903 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse115e01_gtc, mRNA sequence.
 ACCESSION BX550903
 VERSION BX550903.1 GI:33374645
 KEYWORDS EST.
 SOURCE Glossina morsitans morsitans
 ORGANISM Glossina morsitans morsitans
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.
 1 (bases 1 to 23)
 Lehane, M.J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
 Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes

REFERENCE 1 (bases 1 to 23)
 Lehane, M.J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
 Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes

TITLE
 AUTHORS
 JOURNAL
 MEDLINE
 PUBMED
 COMMENT
 Contact: Hall N
 Pathogen Sequencing Unit
 The Sanger Institute The Wellcome Trust Genome Campus
 Hinxton, Cambridge, CB10 1SA, UK
 Request for clones, please contact: Mike Lehane
 Prof. M.J. Lehane
 School of Biological Sciences,

University of Wales,
 Bangor LL57 2UW
 All clones with suffix gtc are reverse primer reads starting at 5' end of the cDNA all pic reads are from the 3' end.

FEATURES
 source
 1..23
 /organism="Glossina morsitans morsitans"
 /mol_type="mRNA"
 /sub_species="morsitans"
 /db_xref="taxon:37546"
 /clone="Tse115e01_gtc"
 /tissue_type="adult infected gut"
 /clone_lib="Glossina morsitans morsitans adult infected gut"
 /note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 1.2%; Score 16.6; DB 1; Length 23;
 Best Local Similarity 82.6%; Pred. No. 30;
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1514 TTTATTTAAAAAAAGTAAA 1536
 DB 23 TTTATTTAAAAAAAGTAAA 1

RESULT 28
 BX568055/c 23 bp mRNA linear EST 14-OCT-2003
 LOCUS BX568055 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse91f03_gtc, mRNA sequence.
 ACCESSION BX568055
 VERSION BX568055.1 GI:33434952
 KEYWORDS EST.
 SOURCE Glossina morsitans morsitans
 ORGANISM Glossina morsitans morsitans
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.
 1 (bases 1 to 23)
 Lehane, M.J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
 Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes

REFERENCE 1 (bases 1 to 23)
 Lehane, M.J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
 Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes

TITLE
 AUTHORS
 JOURNAL
 MEDLINE
 PUBMED
 COMMENT
 Contact: Hall N
 Pathogen Sequencing Unit
 The Sanger Institute The Wellcome Trust Genome Campus
 Hinxton, Cambridge, CB10 1SA, UK
 Request for clones, please contact: Mike Lehane
 Prof. M.J. Lehane
 School of Biological Sciences,
 University of Wales,
 Bangor LL57 2UW
 All clones with suffix gtc are reverse primer reads starting at 5' end of the cDNA all pic reads are from the 3' end.

FEATURES
 source
 1..23
 /organism="Glossina morsitans morsitans"
 /mol_type="mRNA"
 /sub_species="morsitans"
 /db_xref="taxon:37546"
 /clone="Tse91f03_gtc"
 /tissue_type="adult infected gut"
 /clone_lib="Glossina morsitans morsitans adult infected gut"
 /note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Best Local Similarity 82.6%; Pred. No. 30;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1520 AAAAAAAAAAGTAAAGGAA 1542
Db 23 AAAAAAAAAAGAAAAAAAAA 1

RESULT 31
AZ654747/c 19 bp DNA linear GSS 14-DEC-2000
LOCUS 1M052F08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0529F08 F, genomic survey sequence.
ACCESSION AZ654747
VERSION AZ654747.1 GI:11791893
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Relliy,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
TITLE Unpublished (2000)
JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0529 row: F column: 08
Seq primer: CGTTGTAAAACGACGGCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0529F08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv. Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.2%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 27;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAATAAAA 2

RESULT 32
AZ343730 20 bp DNA linear GSS 29-SEP-2000
LOCUS 1M0077E20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0077E20 F, genomic survey sequence.
ACCESSION AZ343730
VERSION AZ343730.1 GI:10422288
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Relliy,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
TITLE Unpublished (2000)
JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0077 row: B column: 20
Seq primer: CGTTGTAAAACGACGGCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0077E20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv. Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.2%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 29;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAGTAAA 1537
 DB 18 AAAAAAAAAAGAAAA 1

RESULT 33
 LOCUS BX548564/c
 DEFINITION BX548564 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse101g03_plc, mRNA sequence.
 ACCESSION BX548564
 VERSION BX548564.1 GI:33298798
 KEYWORDS EST.
 ORGANISM Glossina morsitans morsitans
 Glossina morsitans morsitans
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.
 1 (bases 1 to 21)
 Lehane,M.J., Aksoy,S., Gibson,W., Keshornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
 Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes
 Genome Biol. 4 (10), R63 (2003)
 MEDLINE 22881942
 PUBMED 14519198
 COMMENT
 Contact: Hall N
 Pathogen Sequencing Unit
 The Sanger Institute The Wellcome Trust Genome Campus
 Hinxton, Cambridge, CB10 1SA, UK
 Request for clones, please contact: Mike Lehane
 Prof. M.J.Lehane
 School of Biological Sciences,
 University of Wales,
 Bangor LL57 2UW
 All clones with suffix g1c are reverse primer reads starting at 5' end of the cDNA all plc reads are from the 3' end.

FEATURES
 source
 1. .21
 Location/Qualifiers
 /organism="Glossina morsitans morsitans"
 /mol_type="mRNA"
 /sub_species="morsitans"
 /db_xref="taxon:37546"
 /clone="Tse101g03_plc"
 /tissue_type="adult infected gut"
 /clone_lib="Glossina morsitans morsitans adult infected gut"
 /note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 1.2%; Score 16.4; DB 1; Length 21;
 Best Local Similarity 94.4%; Pred. No. 31;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAGTAAA 1537
 DB 18 AAAAAAAAAAGAAAA 1

RESULT 34
 LOCUS TA303G05P
 DEFINITION T. brucei sheared genomic DNA clone 303g05, forward sequence, genomic survey sequence.
 ACCESSION AL497383
 VERSION AL497383.1 GI:11865504
 KEYWORDS GSS.
 ORGANISM Trypanosoma brucei
 Trypanosoma brucei
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE
 AUTHORS Hall N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
 TITLE Direct Submission
 JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk
 Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
 Email: neilsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
 source
 1. .22
 Location/Qualifiers
 /organism="Trypanosoma brucei"
 /mol_type="Genomic DNA"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="303g05"

Query Match 1.2%; Score 16.4; DB 1; Length 22;
 Best Local Similarity 94.4%; Pred. No. 33;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAGTAAA 1537
 DB 1 AAAAAAAAAAGAAAA 18

RESULT 35
 LOCUS BX564412/c
 DEFINITION BX564412 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse71e10_plc, mRNA sequence.
 ACCESSION BX564412
 VERSION BX564412.1 GI:33431592
 KEYWORDS EST.
 SOURCE Glossina morsitans morsitans
 ORGANISM Glossina morsitans morsitans
 Glossina morsitans morsitans
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.
 1 (bases 1 to 21)
 Lehane,M.J., Aksoy,S., Gibson,W., Keshornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
 Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes
 Genome Biol. 4 (10), R63 (2003)
 MEDLINE 22881942
 PUBMED 14519198
 COMMENT
 Contact: Hall N
 Pathogen Sequencing Unit
 The Sanger Institute The Wellcome Trust Genome Campus
 Hinxton, Cambridge, CB10 1SA, UK
 Request for clones, please contact: Mike Lehane
 Prof. M.J.Lehane
 School of Biological Sciences,
 University of Wales,
 Bangor LL57 2UW
 All clones with suffix g1c are reverse primer reads starting at 5' end of the cDNA all plc reads are from the 3' end.

```

FEATURES
  source
    Location/Qualifiers
      1. .21
        /organism="Glossina morsitans morsitans"
        /mol_type="mRNA"
        /sub_species="morsitans"
        /db_xref="taxon:37546"
        /clone="7se71e10_p1c"
        /issue_type="adult infected gut"
        /clone_lib="Glossina morsitans morsitans adult infected
          gut"
        /note="country: Zimbabwe; EST from adult gut infected with
          T.brucei"

Query Match      1.2%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 35;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1517 ATTAAAAAAAAAGTAAAG 1537
Db      21 ATTCAAAAAAAAAAAAAA 1

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```

RESULT 36
AZ308846/c      21 bp  DNA  linear  GSS 29-SEP-2000
LOCUS           1M0012H15F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
DEFINITION      Clone UUGCIM0012H15 F, genomic survey sequence.
ACCESSION       AZ308846
VERSION         AZ308846.1 GI:10349246
KEYWORDS        GSS.
SOURCE          Mus musculus (house mouse)
ORGANISM        Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 21)
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D., Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0012 row: H column: 15
  Seq primer: CGTGTAAACGACGCGCAGT
  Class: plasmid ends
  High quality sequence stop: 21.
  Location/Qualifiers
    1. .21
      /organism="Mus musculus"
      /mol_type="genomic DNA"
      /strain="C57BL/6J"
      /db_xref="taxon:10090"
      /clone="UUGCIM0012H15"
      /sex="Male"
      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
      /clone_lib="Mouse 10kb plasmid UUGCIM library"
      /note="Vector: PWD42nv; Purified genomic DNA from M.
        musculus C57BL/6J (male) was obtained from the Jackson
        Laboratory Mouse DNA Resource
        (http://www.jax.org/resources/documents/dnares/). The DNA
        was hydrodynamically sheared by repeated passage through a
        0.005 inch orifice at constant velocity. The sheared DNA
        was blunt end-repaired with T4 DNA polymerase and T4
        polynucleotide kinase. Adaptor oligonucleotides were

```

```

Query Match      1.2%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 35;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1520 AAAAAAAAAAGTAAAGCG 1540
Db      21 AAAAAAAAAACAAAAAG 1

```

```

RESULT 37
AZ493766
LOCUS           1M0328C1R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
DEFINITION      Clone UUGCIM0328C1 R, genomic survey sequence.
ACCESSION       AZ493766
VERSION         AZ493766.1 GI:10667750
KEYWORDS        GSS.
SOURCE          Mus musculus (house mouse)
ORGANISM        Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 21)
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D., Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0328 row: C column: 11
  Seq primer: CACACAGAAACAGCTATGACC
  Class: plasmid ends
  High quality sequence stop: 21.
  Location/Qualifiers
    1. .21
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      /mol_type="genomic DNA"
      /strain="C57BL/6J"
      /db_xref="taxon:10090"
      /clone="UUGCIM0328C1"
      /sex="Male"
      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
      /clone_lib="Mouse 10kb plasmid UUGCIM library"
      /note="Vector: PWD42nv; Purified genomic DNA from M.
        musculus C57BL/6J (male) was obtained from the Jackson
        Laboratory Mouse DNA Resource
        (http://www.jax.org/resources/documents/dnares/). The DNA
        was hydrodynamically sheared by repeated passage through a
        0.005 inch orifice at constant velocity. The sheared DNA
        was blunt end-repaired with T4 DNA polymerase and T4
        polynucleotide kinase. Adaptor oligonucleotides were
        ligated to the blunt ends in high molar excess. The

```

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (g14732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.2%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 35;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Gy 1517 ATTAATAAAAAAAAAAGTAAA 1517
Db 1 ATTAATAAAAAAAAAAAAAA 21

RESULT 38
LOCUS AZ513902 21 bp DNA linear GSS 05-OCT-2000
DEFINITION IM0360A13F Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC1M0360A13 F, genomic survey sequence.
ACCESSION AZ513902
VERSION AZ513902.1 GI:10695218
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0360 row: A column: 13
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers

FEATURES
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0360A13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: pMD2nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (g14732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.2%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 35;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Gy 545 TGTGTGTGTGTGTGTGTGCGT 565
Db 21 TGTGTGTGTGTGTGTGCGT 1

RESULT 39
LOCUS AZ626965 21 bp DNA linear GSS 13-DEC-2000
DEFINITION IM0467E1SR Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC1M0467E1S R, genomic survey sequence.
ACCESSION AZ626965
VERSION AZ626965.1 GI:11749155
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0467 row: B column: 15
Seq primer: CACACAGAAACACTATGACC
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers

FEATURES
source 1. 21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0467E1S"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: pMD2nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.2%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 35;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 542 TGTGTGGGTCGTCGTGCGTG 562
Db 1 TGTGTGTGTGTGTGTGTGCTG 21

RESULT 40
AA911173/c 22 bp mRNA linear EST 09-JUN-1998
LOCUS OK61a10.41 NCI CGAP Kid3 Homo sapiens CDNA clone IMAGE:1520346.3
DEFINITION similar to TR:Q34192 Q34192 NADH DEHYDROGENASE SUBUNIT 5.;; mRNA
sequence.
ACCESSION AA911173 GI:3050463
VERSION AA911173.1
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 22)
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaapb-rc@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNI, at:
www-bio.illn.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 520 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amerham
High quality sequence stop: 1.
Location/Qualifiers

1..22
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1520346"
/lab_host="MDH10B"
/clone_lib="NCI CGAP_Kid3"
/note="Organ: Kidney; Vector: pT773D-Pac (Pharmacia) with
a modified polylinker; Site: 1: Not 1; Site: 2: Eco RI; 1st
strand CDNA was primed with a Not I - oligo(dT) primer,
double-stranded CDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT773 vector. mRNA
source: 2 pooled kidney. Library went through one round
of normalization. Library constructed by Bento Soares and
M. Fatima Bonaldo."

Query Match 1.2%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 37;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1240 TCCTCATCTTGTGTTGTTT 1260
Db 22 TCCTTCCTTGTGTTGTTGT 2

RESULT 41
A2662734 23 bp DNA GSS 14-DEC-2000
LOCUS IM0542D04F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
DEFINITION clone UGCGIM0542D04 F, genomic survey sequence.
ACCESSION A2662734
VERSION A2662734.1 GI:11799880
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
MUS musculus
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Nederhausen,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0542 row: D column: 04
Seq primer: CATTGTTAAACGACGGCCACT
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers

FEATURES
source

1..23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGIM0542D04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGIM library"
/note="Vector: FMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g1473214|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent *E. coli* XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.2%; Score 16.2; DB 1; Length 23;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1511 CTGTTAATTAAAAA 1531

Db 2 CTACTAATAATAAAAAAAAAA 22

RESULT 42
A2801003 23 bp DNA linear GSS 16-FEB-2001
LOCUS 2M0059J16F Mouse 10kb plasmid UUCG1M library Mus musculus genomic
DEFINITION clone UUCG2M0059J16 F, genomic survey sequence.

ACCESSION A2801003
VERSION A2801003.1 GI:12953326
KEYWORDS GSS.

ORGANISM Mus musculus (house mouse)

REFERENCE
AUTHORS Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA

FEATURES
source
1..23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG2M0059J16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g14732114[gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.2%; Score 16.2; DB 1; Length 23;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1517 ATTAAAAAAAAAAGTAAA 1537
|||||

Db 1 ATAAAAAAAAAAAAAAAAA 21

RESULT 43
A2956341/c 21 bp DNA linear GSS 27-APR-2001
LOCUS 2M0222H16R Mouse 10kb plasmid UUCG2M library Mus musculus genomic
DEFINITION clone UUCG2M0222H16 R, genomic survey sequence.

ACCESSION A2956341
VERSION A2956341.1 GI:13827568
KEYWORDS GSS.

ORGANISM Mus musculus (house mouse)

REFERENCE
AUTHORS Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA

FEATURES
source
1..21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG2M0222H16"
/sex="Female"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG2M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g14732114[gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.1%; Score 16; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1069 TATTTTCAGTATATCA 1084
|||||
19 TATTTTCAGTATATCA 4

RESULT 44
AZ345795
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

19 bp DNA linear GSS 29-SEP-2000
1M0080H09R Mouse 10kb plasmid UGCG1M library Mus musculus genomic
clone UGCG1M0080H09 R, genomic survey sequence.
AZ345795
GSS.
GI:10425032
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: H column: 09
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG1M0080H09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCG1M library"
/note="Vector: PMD42nv. Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g14732114[gb|AF129072.1]), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.1%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 41;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Gy 1518 TTAATAAAAAAAAAAGTAA 1536
Db 1 TTAATAAAAAAAAAAAAAA 19

RESULT 45
AZ650575
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

19 bp DNA linear GSS 14-DEC-2000
1M0520P13R Mouse 10kb plasmid UGCG1M library Mus musculus genomic
clone UGCG1M0520P13 R, genomic survey sequence.
AZ650575
GSS.
GI:11785200
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0520 row: P column: 13
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG1M0520P13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCG1M library"
/note="Vector: PMD42nv. Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g14732114[gb|AF129072.1]), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.1%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 41;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Gy 1518 TTAATAAAAAAAAAAGTAA 1536
Db 1 TTAATAAAAAAAAAAAAAA 19

```

RESULT 46
LOCUS AL038427
DEFINITION DKFZp566a1746.r1.566 (synonym: hfkcd2) Homo sapiens cDNA clone
ACCESSION AL038427
VERSION DKFZp566a1746, mRNA sequence.
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 20)
AUTHORS Otenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
Wiemann, S.
TITLE EST (Otenwaelder, et al.)
JOURNAL Unpublished (1999)
COMMENT CONTACT: MIPS
FEATURES
SOURCE location/Qualifiers
1..20
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp566a1746"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone.lib="566 (synonym: hfkcd2)"
/note="Vector: pAMP1, Site_1: NotI, Site_2: SalI"

Query Match 1.1%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1519 TAAAAAAAAAAGTAAA 1537
Db 1 TAAAAAAAAAAAAAAAAA 19

RESULT 47
LOCUS AL038429
DEFINITION DKFZp566a1946.r1.566 (synonym: hfkcd2) Homo sapiens cDNA clone
ACCESSION AL038429
VERSION DKFZp566a1946, mRNA sequence.
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 20)
AUTHORS Otenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
Wiemann, S.
TITLE EST (Otenwaelder, et al.)
JOURNAL Unpublished (1999)
COMMENT CONTACT: MIPS
FEATURES
SOURCE location/Qualifiers
1..20
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp566a1946"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone.lib="566 (synonym: hfkcd2)"
/note="Vector: pAMP1, Site_1: NotI, Site_2: SalI"

Query Match 1.1%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1519 TAAAAAAAAAAGTAAA 1537
Db 1 TAAAAAAAAAAAAAAAAA 19

```

```

Query Match 1.1%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1519 TAAAAAAAAAAGTAAA 1537
Db 1 TAAAAAAAAAAAAAAAAA 19

RESULT 48
LOCUS AL038570
DEFINITION DKFZp566f1746.r1.566 (synonym: hfkcd2) Homo sapiens cDNA clone
ACCESSION AL038570
VERSION DKFZp566f1746, mRNA sequence.
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 20)
AUTHORS Otenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
Wiemann, S.
TITLE EST (Otenwaelder, et al.)
JOURNAL Unpublished (1999)
COMMENT CONTACT: MIPS
FEATURES
SOURCE location/Qualifiers
1..20
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp566f1746"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone.lib="566 (synonym: hfkcd2)"
/note="Vector: pAMP1, Site_1: NotI, Site_2: SalI"

Query Match 1.1%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1519 TAAAAAAAAAAGTAAA 1537
Db 1 TAAAAAAAAAAAAAAAAA 19

RESULT 49
LOCUS AL587759/c
DEFINITION AL587759 BP Chicken Brain Library Gallus gallus cDNA clone
ACCESSION AL587759
VERSION ROS061G06, mRNA sequence.
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Murray, F.
TITLE BP Chicken Brain Library
JOURNAL Unpublished (2001)
COMMENT CONTACT: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434

```

Email: frazer.murray@bsrc.ac.uk
GCGGCCGCTTTT TTTT TTTT TTTT 3' Poly A RNA purchased from Clontech
(*6854-

FEATURES

Seq primer: M13F.
Location/Qualifiers
1..20

/organism="Gallus gallus"
/mol_type="mRNA"
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/dev_stage="Unknown"
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/note="Vector: pSPB01; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. 5' adaptor sequence: 5' TCGACCTGAG 3' , 3' adaptor sequence: 5' GCGGCCGCTTTT TTTT TTTT TTTT 3' Poly A RNA purchased from Clontech (*6854-1)"

Query Match 1.1%; Score 15.8; DB 1; Length 20;

Best Local Similarity 89.5%; Pred. No. 43;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1519 TAAAAAAAAAAGTAAAA 1537

Db 20 TAAAAAAAAAAAAAAAAAAAA 2

RESULT 50

AZ45856/c

LOCUS 20 bp DNA linear GSS 29-SEP-2000

DEFINITION 1M0080G1R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0080G17 R, genomic survey sequence.

ACCESSION AZ45856

VERSION AZ45856.1 GI:10425093

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)

1 (bases 1 to 20)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausen,A. and Wright,D., Weiser,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert length: 10000 Std Error: 0.00

Plate: 0080 row: G column: 17

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1..20

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0080G17"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PMD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (g1473214|gb|AF12972.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 1.1%; Score 15.8; DB 1; Length 20;

Best Local Similarity 89.5%; Pred. No. 43;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAAGTAAAG 1538

Db 20 AAAAAAAAAAAAAAAAAAAAG 2

RESULT 51

AZ486784/c

LOCUS 20 bp DNA linear GSS 05-OCT-2000

DEFINITION 1M0315C20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0315C20 F, genomic survey sequence.

ACCESSION AZ486784

VERSION AZ486784.1 GI:10653898

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)

1 (bases 1 to 20)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausen,A. and Wright,D., Weiser,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert length: 10000 Std Error: 0.00

Plate: 0315 row: C column: 20

Seq primer: CGTTGTTAAACGACGCGCACT

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1..20

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0315C20"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PMD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1519 TAAAAAAGTAAAA 1537
|||||
Db 20 TAAAAAAGTAAAA 2

RESULT 52
LOCUS A2858419 20 bp DNA linear GSS 21-FEB-2001
DEFINITION 2M0163003R Mouse 10kb plasmid UUC2M1 library Mus musculus genomic
ACCESSION A2858419
VERSION A2858419.1 GI:13051545
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Relliy, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weise, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0163 row: 0 column: 03
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence atp: 20.

FEATURES
Source
1..20
Location/Qualifiers

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC2M0163003"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC2M1 library"
/note="Vector: pMD2nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1519 TAAAAAAGTAAAA 1537
|||||
Db 1 TAAAAAAGTAAAA 19

RESULT 53
LOCUS AL048772 21 bp mRNA linear EST 04-SEP-2003
DEFINITION DKFZP566N143.r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
ACCESSION AL048772
VERSION AL048772.1 GI:4727843
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 21)
AUTHORS Koehler, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
EST (Koehler, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS

TITLE Ingolstaedter Lander 1, D-85764 Neuherberg, Germany.
MIPS

FEATURES
Source
1..21
Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP566N143"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="XL1-Blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1; Site_1: Not; Site_2: SalI"

Query Match 1.1%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 46;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1513 GTTAATTAATAAAAAA 1531
|||||
Db 2 GTTAATAAAAAAAAAA 20

RESULT 54
LOCUS CF318152/c 21 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--08-C11.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--08-C11, mRNA sequence.
ACCESSION CF318152

```

VERSION      CF318152.1  GI:33689913
KEYWORDS     EST.
SOURCE       Oryza sativa (japonica cultivar-group)
ORGANISM     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE    1 (bases 1 to 21)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, Greengene Biotech Inc., Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
              Location/Qualifiers
              1..21
              /organism="Oryza sativa (japonica cultivar-group)"
              /mol_type="mRNA"
              /cultivar="Nackdong"
              /db_xref="taxon:39947"
              /clone="HD--08-C11"
              /issue_type="callus"
              /dev_stage="proliferated callus on 2N6 media for 2 weeks"
              /lab_host="E.Coli DH10B"
              /clone_lib="OSHDA1-overexpressing transgenic rice plasmid
              cDNA library (HD)"
              /note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
              treated with ABA(20um) for 1hr. Oligo-capped mRNA was
              reverse transcribed and then used for PCR. mRNA was
              derived from rice Histone Deacetylase overexpression
              line."

Query Match      1.1%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 46;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1520 AAAAAAAAAAAGTAAAG 1538
Db      19 AAAAAAAAAAAGTAAAG 1

RESULT 55
CN546489/c      21 bp      mRNA      linear      EST 30-APR-2004
LOCUS           EST 18633 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera
DEFINITION      CDNA clone B3CS57RB007E11 3', mRNA sequence.
ACCESSION       CN546489
VERSION         CN546489.1  GI:46911114
KEYWORDS        EST.
SOURCE          Vitis vinifera
ORGANISM        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              rosids; Vitaceae; Vitis.
REFERENCE    1 (bases 1 to 21)
AUTHORS      Abadl,P., Agasee,A., Ageorges,A., Atanassova,R., Barrieu,F.,
              Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
              Hamdi,S., Romieu,C. and Terrier,N.
TITLE        Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
              or seeds) at Various Developmental Stages
JOURNAL      Unpublished (2002)
COMMENT      Contact: Hamdi S.
              UMR 619 - Equipe Biologie de la Vigne
              Universite de Bordeaux I, Institut National de la Recherche
              Agronomique
              71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
              France
              Tel: 00-33-(0)5-57-12-25-50

```

```

FEATURES
source
1..21
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS57RB007E11"
/dev_stage="ripe stage"
/clone_lib="Ripe Grape Berry Lambda Triplex2 library"
/note="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfiI; Site_2: SfiI; Oriented library"

Query Match      1.1%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 46;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1519 TAAAAAAAAAAGTAAA 1537
Db      21 TAAAAAAAAAAGTAAA 3

RESULT 56
AZ610868/c      21 bp      DNA      linear      GSS 13-DEC-2000
LOCUS           IN0436G12F Mouse 10kb plasmid UNGC1M library Mus musculus genomic
DEFINITION      clone UNGC1M0436G12 F, genomic survey sequence.
ACCESSION       AZ610868
VERSION         AZ610868.1  GI:11733058
KEYWORDS        GSS.
SOURCE          Mus musculus (house mouse)
ORGANISM        Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE    1 (bases 1 to 21)
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
              Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
              Niederhausern,A. and Wright,D. Weis,R.
TITLE        Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weis
              University of Utah Genome Center
              Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert length: 10000      Std error: 0.00
              Plate: 0436      row: G      column: 12
              Seq primer: CGTTGTAAACGACGCGCCAGT
              Class: plasmid ends
              High quality sequence stop: 21.
              Location/Qualifiers
              1..21
              /organism="Mus musculus"
              /mol_type="genomic DNA"
              /strain="C57BL/6J"
              /db_xref="taxon:10090"
              /clone="UNG1M0436G12"
              /sex="Male"
              /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
              /clone_lib="Mouse 10kb plasmid UNGC1M library"
              /note="Vector: PWD42nv; Purified genomic DNA from M.
              musculus C57BL/6J (male) was obtained from the Jackson
              Laboratory Mouse DNA Resource
              (http://www.jax.org/resources/documents/dnares/). The DNA
              was hydrodynamically sheared by repeated passage through a
              0.005 inch orifice at constant velocity. The sheared DNA

```

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 46;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1518 TTAATAAAAAAAAAAGTAAA 1536
Db 19 TTAATAAAAAAAAAAAAAA 1

RESULT 57
A2764492 21 bp DNA linear GSS 16-FEB-2001
LOCUS JMO56DD04R Mouse 10kb plasmid UUCGM library Mus musculus genomic
DEFINITION clone UUCGM056DD04 R, genomic survey sequence.
ACCESSION A2764492
VERSION A2764492.1 GI:12879511
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Irlam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0560 row: D column: 04
Seq primer: CACACAGCAACACGTACGACC
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers

FEATURES
Source 1. .21
Location/Qualifiers

/organism="Mus musculus"
/mol_type="Genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCGM056DD04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCGM library"
/note="Vector: pMD42uv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 46;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1518 TTAATAAAAAAAAAAGTAAA 1536
Db 3 TTAATAAAAAAAAAAAAAA 21

RESULT 58
BX556059/c 22 bp mRNA linear EST 10-OCT-2003
LOCUS BX556059 Glossina morsitans morsitans adult infected gut Glossina
DEFINITION morsitans morsitans cDNA clone Tse24f09_p1c, mRNA sequence.
ACCESSION BX556059
VERSION BX556059.1 GI:33380008
KEYWORDS EST.
SOURCE Glossina morsitans morsitans
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hypoboscoidae; Glossinidae; Glossina.
1 (bases 1 to 22)
Lehane, M.J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the tsetse fly *Glossina*
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
22881942
14519198
MEDLINE
PUBMED

JOURNAL
COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all pic reads are from
the 3' end.
Location/Qualifiers

FEATURES
Source 1. .22
Location/Qualifiers

/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse24f09_p1c"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="Country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match 1.1%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. No. 48;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1519 TAAAAAAAAAAGTAAAA 1537
 Db 20 TAAAAAAAAAAAAAAAAAAAA 2

RESULT 59
 CF310806/c 22 bp mRNA linear EST 15-AUG-2003

LOCUS
 DEFINITION ABF-05-K20-g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone ABF-05-K20, mRNA sequence.

ACCESSION
 VERSION CF310806.1 GI:33682567
 SOURCE
 ORGANISM EST.
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
 AUTHORS 1 (bases 1 to 22)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 TITLE Contact: Nahm B.H.
 JOURNAL Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 COMMENT Yongin, Kyonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source Location/Qualifiers
 1..22

/organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="ABF-05-K20"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABF-responsive element binding transcription factor 3 overexpression line."

Query Match 1.1%; Score 15.8; DB 1; Length 22;
 Best Local Similarity 89.5%; Pred. No. 48;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1522 TAAAAAAAAAAGTAAAAAGG 1540
 Db 22 TAAAAAAAAAAAAAAAAAGG 4

RESULT 60
 LOCUS
 DEFINITION CO778290 22 bp mRNA linear EST 05-AUG-2004
 BL003B H01 6-Day Axolotl Tail Blastema (6DAXBL) Ambystoma mexicanum cDNA 5' similar to hypothetical protein, mRNA sequence.
 ACCESSION
 VERSION CO778290.1 GI:50994270
 KEYWORDS
 SOURCE EST.
 ORGANISM Ambystoma mexicanum (axolotl)
 Ambystoma mexicanum
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Caudata; Salamandroidae; Ambystomatidae; Ambystoma.

REFERENCE
 1 (bases 1 to 22)
 Habermann,B., Bebin,A.G., Herklotz,S., Volkmer,M., Eckelt,K.,

TITLE
 JOURNAL Pehlike,K., Eperleijn,H.H., Schacker,H.K., Wiebe,G. and Tanaka,E.M.
 COMMENT An Ambystoma mexicanum EST sequencing project: Analysis of 17,352 expressed sequence tags from embryonic and regenerating blastema cDNA libraries
 Genome Biol. (2004) In press
 Contact: Ely M. Tanaka
 Tanaka Lab
 Max Planck Institute of Molecular Cell Biology and Genetics,
 Dresden
 Proteinhaustrasse 108, 01307 Dresden, Germany
 Tel: 0049 351 210 2620
 Fax: 0049 351 210 1489
 Email: tanaka@mpi-cbg.de
 Plate: BL003B row: 01 column: H
 Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC A.
 Location/Qualifiers

FEATURES
 source

1..22
 /organism="Ambystoma mexicanum"
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 /tissue_type="Tail Blastema"
 /clone_lib="6-Day Axolotl Tail Blastema (6DAXBL)"
 /note="Vector: PCMVSPORT6; Site 1: NotI; Site 2: SalI; Unormalized cDNA plasmid library prepared by Invitrogen. Site fractionated mRNA was polydt primed and cloned into NotI-SalI site of PCMVSPORT6. Bacterial host is EMDH10B-TONA. Average insert size is 1.67 kb.
 TAG_Lib=6DAXBL"

Query Match 1.1%; Score 15.8; DB 1; Length 22;
 Best Local Similarity 89.5%; Pred. No. 48;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 TAAAAAAAAAAGTAAAAAG 1538
 Db 4 TAAAAAAAAAAAAAAAAAG 22

RESULT 61
 LOCUS
 DEFINITION A2823875 22 bp DNA linear GSS 20-FEB-2001
 2M0098K07F Mouse 10kb plasmid UDGCM library Mus musculus genomic clone UDGCM0098K07 F, genomic survey sequence.
 ACCESSION
 VERSION A2823875.1 GI:12993795
 KEYWORDS
 SOURCE GSS.
 ORGANISM Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 1 (bases 1 to 22)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weis,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL
 COMMENT Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0098 row: K column: 07
 Seq primer: CGTTGTAAACGACGCGCAGT
 Class: plasmid ends

High quality sequence stop: 22.
 Location/Qualifiers

source

1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG2M0098K07"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. No. 48;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAAGTAAAG 1538
Db 4 AAAAAAAAAAAG 22

RESULT 62

LOCUS BH000233 22 bp DNA linear GSS 27-APR-2001
DEFINITION 2M028712R Mouse 10kb plasmid UUCG2M library Mus musculus genomic clone UUCG2M0287121 R, genomic survey sequence.

ACCESSION BH000233
VERSION BH000233.1 GI:13871459

KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus. 1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah
Genome Center

Rm 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00

Plate: 0287 row: 1 column: 21
Seq primer: CACACAGCAACGCTATGACC

Class: plasmid ends
High quality sequence stop: 22.

Location/Qualifiers
1. .22

FEATURES

source

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG2M0287121"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG2M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. No. 48;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAAGTAAAG 1538
Db 3 AAAAAAAAAAAG 21

RESULT 63

LOCUS A1708831 22 bp mRNA linear EST 04-JUN-1999
DEFINITION aa27d12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318423 3' similar to TR:Q33563 Q33563 BATRO 164 KINETOPLAST ;, mRNA sequence.

ACCESSION A1708831
VERSION A1708831.1 GI:4996607

KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 22)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Scheinberg, K., Stepcoe, M., Tan, F., Thaising, B., White, Y., Wyllie, T., Waterston, R. and Wilson, R.

Washington NCI human EST Project

JOURNAL Unpublished (1997)
COMMENT Contact: Wilson RK
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LINT; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand

Seq primer: -40UP from Gibco
High quality sequence stop: 1.

Location/Qualifiers
1. .22

FEATURES
source
/organism="Homo sapiens"
/mol_type="mRNA"

/clone_1lb="AGS-1"
/note="Vector: Lambda ZAP II; Site 1: EcoRI; Site 2: XhoI;
P. carlini organisms (3x10e9) from a single rat (99-1-6,
sacrificed on 9/17/99) at Cincinnati VA facilities.
Tritol extracted RNA. Oligo dt priming, standard
conditions described by vendor, Stratagene. Further
details see www.uky.edu/Project/Pneumocystis/"

Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1516 AATTAAAAAGTAAAA 1537
DB 22 AAAAAAAAAAAAAAAAAA 1

RESULT 67
CF299342/c
LOCUS 7LEAF--03-F06.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION 7LEAF--03-F06.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sequence.
ACCESSION CF299342
VERSION CF299342.1 GI:33671103
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 22)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source
1..22
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--03-F06"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_1lb="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1516 AATTAAAAAGTAAAA 1537
DB 22 AAAAAAAAAAAAAAAAAA 1

RESULT 68
CF300133/c
LOCUS 7LEAF--04-G19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION 7LEAF--04-G19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sequence.
ACCESSION CF300133
VERSION CF300133.1 GI:33671894
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 22)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source
1..22
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--04-G19"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_1lb="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

ACCESSION CF300133
VERSION CF300133.1 GI:33671894
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 22)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
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Genomics and Genetics Institute, Greengene Biotech Inc.; Division
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Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source
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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--04-G19"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_1lb="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1516 AATTAAAAAGTAAAA 1537
DB 22 AAAAAAAAAAAAAAAAAA 1

RESULT 69
CF310366/c
LOCUS ABF--04-P14.g1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION ABF--04-P14.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--04-P14, mRNA sequence.
ACCESSION CF310366
VERSION CF310366.1 GI:33682127
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 22)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source
1..22
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--04-G19"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_1lb="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Query Match      1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. NO. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1516 AATTTAAAAAAGTAAA 1537
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    |||||
    |||||
    |||||
    |||||
    22 AAAAAAAAAAAAAAAAAAA 1

RESULT 70
CF311269/c
LOCUS CF311269                22 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--06-G21.g1 ABF3-overexpressing transgenic rice plasmid CDNA library (ABF) Oryza sativa [japonica cultivar-group] cDNA clone ABF--06-G21, mRNA sequence.
ACCESSION   CF311269
VERSION     CF311269.1 GI:33683030
KEYWORDS
SOURCE      EST.
ORGANISM    Oryza sativa [japonica cultivar-group]
AUTHORS      Oryza sativa [japonica cultivar-group]) Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoidae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 22)
            Kim,J.-S., Jun,K.M., Cheong,P.-J., Kim,M.-J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
TITLE       Contact: Nahm B.H. Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myoungji University Yongin, Kyoeongi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
JOURNAL     Location/Qualifiers
COMMENT
FEATURES             source
                     1..22
                        /organism="Oryza sativa [japonica cultivar-group]"
                        /mol_type="RNA"
                        /cultivar="Nackdong"
                        /db_xref="taxon:39947"
                        /clone="ABF--06-G21"
                        /tissue_type="leaf"
                        /dev stage="14 days after germination"
                        /lab_host="E.coli DH10B"
                        /clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
                        /note="vector: pCR4-TOPo, Site_1: EcoRI; leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

```

[illegible]

TITLE Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
JOURNAL Large-scale Sequencing Analysis of Rice ESTs
COMMENT Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc., Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
 1. .22
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="ABF--08-B15"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="ABF3-overexpressing transgenic rice plasmid
 cDNA library (ABF)"
 /note="Vector: pCR4-TOPO; Site_1: EcoRI; leaf was dried
 for 2hrs. Oligo-capped mRNA was reverse transcribed and
 then used for PCR. mRNA was prepared from ABA-responsive
 element binding transcription factor 3 overexpression
 line."

Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1516 AATTTAAAAAAGTAAAA 1537
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 1 AAAAAAAAAAAAAAAAAA 22

RESULT 73
LOCUS CF330679 22 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--06-H22.b1 Rice callus plasmid cDNA library (NACL) Oryza
 sativa (japonica cultivar-group) cDNA clone NACL--06-H22, mRNA
 sequence.
ACCESSION CF330679 GI:33809583
VERSION CF330679.1
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Euphorbiaceae; Oryzae; Oryza.
 1 (bases 1 to 22)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc., Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
 Location/Qualifiers

FEATURES
source
 1. .22
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="NACL--06-H22"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli DH10B"

/clone_lib="Rice callus plasmid cDNA library (NACL)"
 /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1516 AATTTAAAAAAGTAAAA 1537
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 22 AAAAAAAAAAAAAAAAAA 1

RESULT 74
LOCUS CF333430 22 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT--02-F04.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
 library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
 JMT--02-F04, mRNA sequence.
ACCESSION CF333430 GI:33815154
VERSION CF333430.1
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Euphorbiaceae; Oryzae; Oryza.
 1 (bases 1 to 22)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc., Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
 Location/Qualifiers

FEATURES
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 1. .22
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
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 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="AtJMT-overexpressing transgenic rice plasmid
 cDNA library (JMT)"
 /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
 was reverse transcribed and then used for PCR. mRNA was
 prepared from Arabidopsis Jasmonate Carboxyl
 methyltransferase overexpression line."

Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1516 AATTTAAAAAAGTAAAA 1537
 |||
 22 AAAAAAAAAAAAAAAAAA 1

RESULT 75
LOCUS CF334781 22 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT--04-D05.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
 library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
 JMT--04-D05, mRNA sequence.
ACCESSION CF334781

VERSION CF334781.1 GI:33817904
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretioideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 22)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
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1..22
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/issue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AcJMT-overexpressing transgenic rice plasmid
CDNA library (JMT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1516 AATTAAAAAAAGTAAAA 1537
Db 22 AAAAAAAAAAAAAAAAAA 1

RESULT 76
LOCUS CF336250 22 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT--06-D20.b1 AcJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa (japonica cultivar-group) CDNA clone
JMT--06-D20, mRNA sequence.
ACCESSION CF336250
VERSION CF336250.1 GI:33820891
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretioideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 22)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source
1..22
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/issue_type="leaf"
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/lab_host="E.coli DH10B"
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CDNA library (JMT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1516 AATTAAAAAAAGTAAAA 1537
Db 22 AAAAAAAAAAAAAAAAAA 1

RESULT 77
LOCUS CF337580 22 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT--08-B11.g1 AcJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa (japonica cultivar-group) CDNA clone
JMT--08-B11, mRNA sequence.
ACCESSION CF337580
VERSION CF337580.1 GI:33823547
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretioideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 22)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
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1..22
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/issue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AcJMT-overexpressing transgenic rice plasmid
CDNA library (JMT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 78
LOCUS CF338524/c 22 bp mRNA linear EST 18-AUG-2003
DEFINITION RC11--01-P07.g1 Regenerated callus lambda phage cDNA library (RC11)
Oryza sativa (japonica cultivar-group) cDNA clone RC11--01-P07,
mRNA sequence.
ACCESSION CF338524
VERSION CF338524.1 GI:33825436
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 22)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of BioScience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..22
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="RC11--01-P07"
/cissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library
(RC11)"
/note="Vector: pBluescript SK(+); Site 1: SstI; Site 2:
XhoI; cDNA was inserted into lambda uni-ZAP XR vector at 5'
end with SstI and 3' end with XhoI site. Callus was
induced on 2N6 media for 30 days and cultured for 36hrs on
regenerated media"

Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1516 AATTAAAAAAGTAAAA 1537
Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 79
LOCUS CN545550/c 22 bp mRNA linear EST 30-APR-2004
DEFINITION EST 17494 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
clone B3CS00RL003D05 3', mRNA sequence.
ACCESSION CN545550
VERSION CN545550.1 GI:46910175
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosida; Vitaceae; Vitis.
1 (bases 1 to 22)
Abbal,P., Agasee,A., Ageorges,A., Atanasova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Komleu,C. and Terrier,N.

TITLE
JOURNAL
COMMENT
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
source
1..22
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL003D05"
/dev_stage="ripening stage"
/clone_lib="Ripe Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
SfiI; Site_2: SfiI; Oriented library"

Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1516 AATTAAAAAAGTAAAA 1537
Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 80
LOCUS A2310066/c 22 bp DNA linear GSS 29-SEP-2000
DEFINITION IM001BD18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M001BD18 R, genomic survey sequence.
ACCESSION A2310066
VERSION A2310066.1 GI:10351682
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0018 row: D column: 18
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
location/Qualifiers
1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"

/clone="UUGC1M0018D18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1516 AATTAAAAAAAGTAAAA 1537
Db 22 AAAAAAAAAAAAAAAAAA 1

RESULT 81
A2316361 22 bp DNA linear GSS 29-SEP-2000
LOCUS
DEFINITION 1M0034116F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0034116 F, genomic survey sequence.
ACCESSION A2316361
VERSION A2316361.1 GI:10364110
KEYWORDS
SOURCE GSS.
ORGANISM Mus musculus (house mouse)
MUS musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah
Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0034 row: 1 column: 16
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

FEATURES
source 1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0034116"

/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1516 AATTAAAAAAAGTAAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 22

RESULT 82
A2317017 22 bp DNA linear GSS 29-SEP-2000
LOCUS
DEFINITION 1M0035P09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0035P09 F, genomic survey sequence.
ACCESSION A2317017
VERSION A2317017.1 GI:10365400
KEYWORDS
SOURCE GSS.
ORGANISM Mus musculus (house mouse)
MUS musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah
Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0035 row: 1 column: 09
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

FEATURES
source 1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0035P09"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1523 AAAAAAAAAAGTAAAGCGAAG 1544
DB 22 AAAAAAAAAAAAAAAAAAGCGCGG 1

RESULT 83
LOCUS AZ351527 22 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0089507R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0089507 R, genomic survey sequence.
ACCESSION AZ351527
VERSION AZ351527.1 GI:10430764
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0089 row: E column: 07
Seq primer: CACACAGGAAACGCTATACAC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

FEATURES
source 1..22
Location/Qualifiers

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0089507"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/lab_lib="Mouse 10kb plasmid UUGC1M library"

/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1516 AATTAAAAAAAAAAGTAAA 1537
DB 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 84
LOCUS AZ357630 22 bp DNA linear GSS 02-OCT-2000
DEFINITION 1M0099M15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0099M15 F, genomic survey sequence.
ACCESSION AZ357630
VERSION AZ357630.1 GI:10471318
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0099 row: M column: 15
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

FEATURES
source 1..22
Location/Qualifiers

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0099M15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/lab_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1516 AATTAAAAAAAGTAAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 22

RESULT 85
LOCUS A2388103 22 bp DNA linear GSS 02-OCT-2000
DEFINITION M0147N14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0147N14 R, genomic survey sequence.
ACCESSION A2388103
VERSION A2388103.1 GI:10501811
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenan,E., Pedersen,T.,
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D., Weis,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0147 row: N column: 14
Seq primer: CACACAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

FEATURES

1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0147N14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv, Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1516 AATTAAAAAAAGTAAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 22

RESULT 86
LOCUS A2401908/c 22 bp DNA linear GSS 03-OCT-2000
DEFINITION M0168P24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0168P24 R, genomic survey sequence.
ACCESSION A2401908
VERSION A2401908.1 GI:10516982
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenan,E., Pedersen,T.,
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D., Weis,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0168 row: P column: 24
Seq primer: CACACAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

FEATURES

1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0168P24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gblAF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1516 AATTAAAAAAGTAAAA 1537
Db 22 AAAAAAAAAAAAAAAAAA 1

RESULT 87
A2424307 22 bp DNA linear GSS 03-OCT-2000
LOCUS 1M0203A24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0203A24 R, genomic survey sequence.

ACCESSION A2424307
VERSION A2424307.1 GI:10548320
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0203 row: A column: 24
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.

FEATURES
Location/Qualifiers

1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0203A24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gblAF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1516 AATTAAAAAAGTAAAA 1537
Db 22 AAAAAAAAAAAAAAAAAA 1

RESULT 88
A2428818 22 bp DNA linear GSS 03-OCT-2000
LOCUS 1M0212A05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0212A05 R, genomic survey sequence.

ACCESSION A2428818
VERSION A2428818.1 GI:10552831
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0212 row: A column: 05
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.

FEATURES
Location/Qualifiers

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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0212A05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1516 AATTAAAAAGTAAAA 1537
Db 22 AAAAAAAAAAAAAAAAAA 1

RESULT 89
AZ459654/c 22 bp DNA linear GSS 04-OCT-2000
LOCUS 1M0272E24F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
DEFINITION clone UGCGIM0272E24 R, genomic survey sequence.
ACCESSION AZ459654
VERSION AZ459654.1 GI:10617779
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
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Unpublished (2000)
Contact: Robert B. Weiss
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0264 row: G column: 12
Seq primer: CACACAGCAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.

FEATURES

Source

1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGIM0272E24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGIM library"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
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Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1516 AATTAAAAAGTAAAA 1537
Db 22 AAAAAAAAAAAAAAAAAA 1

RESULT 90
AZ463503/c 22 bp DNA linear GSS 04-OCT-2000
LOCUS 1M0272E24F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
DEFINITION clone UGCGIM0272E24 F, genomic survey sequence.
ACCESSION AZ463503
VERSION AZ463503.1 GI:10621628
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
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Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0272 row: E column: 24
Seq primer: CGTTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 22.

FEATURES

Source

1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGIM0272E24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGIM library"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
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Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1516 AATTAATTAATTAATTAATTAATTA 1537
Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 91
AZ463652/c
LOCUS 22 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0272E12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0272E12 R, genomic survey sequence.
ACCESSION AZ463652
VERSION AZ463652.1 GI:10621777
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellily, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

REFERENCE
AUTHORS Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
TITLE Unpublished (2000)

JOURNAL
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0272 row: E column: 12
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.

FEATURES
SOURCE Location/Qualifiers

1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0272E12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
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Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1516 AATTAATTAATTAATTAATTAATTA 1537
Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 92
AZ582403
LOCUS 22 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0374J1SR Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0374J1S R, genomic survey sequence.
ACCESSION AZ582403
VERSION AZ582403.1 GI:11701249
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellily, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

REFERENCE
AUTHORS Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
TITLE Unpublished (2000)

JOURNAL
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0374 row: J column: 15
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.

FEATURES
SOURCE Location/Qualifiers

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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
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ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1516 AATTAAAAAAGTAAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 22

RESULT 93
AZ607658 22 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0430A13F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
DEFINITION clone UUGCIM0430A13 F, genomic survey sequence.
ACCESSION AZ607658
VERSION
KEYWORDS
SOURCE GSS.
ORGANISM Mus musculus (house mouse)

REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rielly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

JOURNAL
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0430 row: A column: 13
Seq primer: CGTTGTAAACGACGCCACT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

FEATURES

SOURCE

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
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Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1516 AATTAAAAAAGTAAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 22

RESULT 94
AZ654691 22 bp DNA linear GSS 14-DEC-2000
LOCUS 1M0529D05F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
DEFINITION clone UUGCIM0529D05 F, genomic survey sequence.
ACCESSION AZ654691
VERSION
KEYWORDS
SOURCE GSS.
ORGANISM Mus musculus (house mouse)

REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rielly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weiss, R.
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0529 row: D column: 05
Seq primer: CGTTGTAAACGACGCCACT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

FEATURES

SOURCE

1. .22

/organism="Mus musculus"
/mol_type="genomic DNA"
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/db_xref="taxon:10090"
/clone="UUGCIM0529D05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
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ligated to the blunt ends in high molar excess. The
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Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1516 AATTAAAAAAGTAAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 22

RESULT 95
LOCUS A2760533 22 bp DNA linear GSS 16-FEB-2001
DEFINITION IM0554A24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0554A24 F, genomic survey sequence.
A2760533
A2760533.1 GI:12868477
GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

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JOURNAL Unpublished (2000)

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84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0554 row: A column: 24

Seq primer: CGTGTAAACGACGCCACGT
Class: plasmid ends
High quality sequence stop: 22.

FEATURES
source Location/Qualifiers

1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0554A24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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was blunt end-repaired with T4 DNA polymerase and T4
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10.5 kb range using preparative agarose gel

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Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1516 AATTAAAAAAGTAAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 22

RESULT 96
LOCUS A2779844/c 22 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0016112R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0016112 R, genomic survey sequence.
A2779844
A2779844.1 GI:12910910
GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah
Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0016 row: I column: 12

Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.

FEATURES
source Location/Qualifiers

1..22
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC2M0016112"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1516 AATTAAAAAAGTAAAA 1537
Db 22 AAAAAAAAAAAAAAAAAA 1

RESULT 97
AZ785019/c 22 bp DNA linear GSS 16-FEB-2001
LOCUS 2M0028E04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0028E04 R, genomic survey sequence.
ACCESSION AZ785019
VERSION AZ785019.1 GI:12921341
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Jellam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0028 row: E column: 04
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

FEATURES
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/organism="Mus musculus"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0028E04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
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adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g14732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1516 AATTAAAAAAGTAAAA 1537
Db 22 AAAAAAAAAAAAAAAAAA 1

RESULT 98
AZ787098/c 22 bp DNA linear GSS 16-FEB-2001
LOCUS 2M0033A05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0033A05 F, genomic survey sequence.
ACCESSION AZ787098
VERSION AZ787098.1 GI:12925520
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Jellam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0033 row: A column: 05
Seq primer: CGTTGTAACGACGCCACT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

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/strain="C57BL/6J"
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/clone="UUGC2M0033A05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g14732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1516 AATTAAAAAAGTAAAA 1537
DB 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 99
A2787606/c 22 bp DNA linear GSS 16-FEB-2001
LOCUS 2M0034G12F Mouse 10kb plasmid UGCG1M library Mus musculus genomic
DEFINITION clone UGCG2M0034G12 F, genomic survey sequence.
ACCESSION A2787606
VERSION A2787606.1 GI:12926565
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellily, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiser, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0034 row: G column: 12
Seq primer: CGTGTAAACGACGCCACGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

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/strain="C57BL/6J"
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/sex="Male"
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/clone_lib="Mouse 10kb plasmid UGCG1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1516 AATTAAAAAAGTAAAA 1537
DB 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 100
A2792704/c 22 bp DNA linear GSS 16-FEB-2001
LOCUS 2M0045A24F Mouse 10kb plasmid UGCG1M library Mus musculus genomic
DEFINITION clone UGCG2M0045A24 F, genomic survey sequence.
ACCESSION A2792704
VERSION A2792704.1 GI:12936911
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellily, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiser, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0045 row: A column: 24
Seq primer: CGTGTAAACGACGCCACGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

FEATURES
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/organism="Mus musculus"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCG1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
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polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and

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adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Db 1516 AATTAAAAAGTAAAA 1537
22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 101
A2810674/c 22 bp DNA linear GSS 20-FEB-2001
LOCUS A2810674
DEFINITION 2M0G7E19F Mouse 10kb plasmid UGCG1M library Mus musculus genomic
clone UUGC2M0076E19 F, genomic survey sequence.
ACCESSION A2810674
VERSION A2810674.1 GI:12978158
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Rellly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von
Niederhausen,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0076 row: E column: 19
Seq primer: CGTGTAAACGACGCCGACG
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

FEATURES
source
1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0076E19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
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electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Db 1516 AATTAAAAAGTAAAA 1537
22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 102
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LOCUS A2820439/c
DEFINITION 2M0G92K13F Mouse 10kb plasmid UGCG1M library Mus musculus genomic
clone UUGC2M0092K13 R, genomic survey sequence.
ACCESSION A2820439
VERSION A2820439.1 GI:12990443
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Rellly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von
Niederhausen,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
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Unpublished (2000)
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0092 row: K column: 13
Seq primer: CACACAGAAACGACTATGAC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

FEATURES
source
1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0092K13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

	Query Match	1.1%	Score 15.6;	DB 1;	Length 22;
	Best Local Similarity	81.8%	Pred. No. 54;		
	Matches 18;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0.
OY	1516 AATTAAAAAAAAAAGTAAAA	1537			
Db	22 AAAAAAAAAAAAAAAAAAAAAA	1			

RESULT	105
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DEFINITION	22 bp DNA linear GSS 27-APR-2001
ACCESSION	U00207D13 Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0207D13 R, genomic survey sequence.
VERSION	AZ946102
KEYWORDS	AZ946102.1 GI:13812911
SOURCE	GSS.
ORGANISM	Mus musculus (house mouse)
	Mus musculus

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 22)	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Ismail, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellay, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A. and Wright, D., Weiss, R.	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts	Unpublished (2000)	Contact: Robert B. Weiss

JOURNAL COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0207 row: D column: 13
Seq primer: CACACGAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.

FEATURES

SOURCE

Location/Qualifiers

1. 22

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/mol_type="Genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="U8C2M0207D13"

/sex="Female"

/lab_host="E. coli Strain XL10-Gold, T1-resistant, F-"

/clone_1lb="Mouse 10kb plasmid U8C2M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnarep/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g114732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

Best local Similarity 81.8%; Pred. No. 54;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy      1516 AATTTAAAAAAAAAAAAAGTAAAA 1537
        || || || || || || || || || ||
Db       1 AAAAAAAAAAAAAAAAAAAAAA 22

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RESULT	106
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DEFINITION	22 bp DNA linear GSS 13-DEC-2000
ACCESSION	TAl31B09P
VERSION	TA131B09P.sheared genomic DNA clone 131b09, forward sequence,
KEYWORDS	genomic survey sequence.
SOURCE	AT464164.1 GI:11834427
	GSS.
	Trypanosoma brucei

REFERENCE	AUTHORS	TITLE	JOURNAL
1 (bases 1 to 22)	Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Aktin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S. B., Rajandream, M. A. and Barrell, B. G.	Direct Submission	
	Submitted (10-DEC-2000)	Trypanosoma brucei genome sequencing	

COMMENT

Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of *Trypanosoma brucei* (TREU927/4 GMTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaubin and B. Barrell, Oxford University Press, 1999).

Email: mslayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES		Location/Qualifiers
source		1..22
		/organism="Trypanosoma brucei"
		/mol_type="genomic DNA"
		/strain="TREU927"
		/db_xref="taxon:5691"
		/clone="131b09"
Query Match		1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity		81.8%; Pred. No. 54;
Matches	18; Conservative	0; Mismatches 4; Indels 0; Gaps 0;
QY	1516 AATTAAAAAAAAAAGTAAA	1537
db	1 AAAAAAAAAAAAAAAAAAAAAA	22

RESULT	107
LOCUS	TA329F10P
DEFINITION	TA329F10P 22 bp DNA linear GSS 13-DEC-2000
ACCESSION	T. brucei sheared genomic DNA clone 329f10, forward sequence,
VERSION	AL492691
KEYWORDS	AL492691.1 GI:11868830
SOURCE	GSS.
ORGANISM	Trypanosoma brucei
	Trypanosoma brucei
	Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
	Trypanosoma.
REFERENCE	1 (bases 1 to 22)
AUTHORS	Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
	Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,

TITLE	Melville, S.E., Rajandream, M.A. and Barrett, B.G.
JOURNAL	Direct Submission Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk
COMMENT	Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTac 10.1) was mechanically sheared to give a tight size distribution (4 kb) . The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999). Email: nelsayed@tigr.org Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/ . Location/Qualifiers
FEATURES	1..22 /organism="Trypanosoma brucei" /mol_type="genomic DNA" /strain="TREU927" /db_xref="taxon:5691" /clone="329f10"
Source	
Query Match	1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity	81.8%; Pred. No. 54;
Matches	18; Conservative 0; Mismatches 4; Indels 0; Gaps 0
Or	1516 AATTAAAAAAGTAAAA 1537 1 AAAAAAAAAAAAAAAAAA 22
Db	
RESULT 108	
LOCUS	TA35C120/c
DEFINITION	TA35C120 22 bp DNA linear GSS 13-DEC-2000
ACCESSION	T. brucei sheared genomic DNA clone 35c12, reverse sequence,
VERSION	AL454256
KEYWORDS	genomic survey sequence.
SOURCE	AL454256.1 GI:11855060
ORGANISM	GSS.
REFERENCE	Trypanosoma brucei
AUTHORS	Trypanosoma brucei
COMMENT	Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma. 1 (bases 1 to 22) Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G. Direct Submission Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk
TITLE	Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTac 10.1) was mechanically sheared to give a tight size distribution (4 kb) . The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999). Email: nelsayed@tigr.org Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/ . Location/Qualifiers
JOURNAL	
COMMENT	1..22 /organism="Trypanosoma brucei" /mol_type="genomic DNA" /strain="TREU927"
FEATURES	
Source	

		/db xref="taxon:5691"			
		/clone="j35c12"			
Query Match	1.1%;	Score 15.6;	DB 1;	Length 22;	
Best Local Similarity	81.8%;	Pred. No. 54;			
Matches 18;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;	
Oy	1516	AATTAAAAAAGTAAAA	1537		
Db	22	AAAAAAAAAAAAAAAAAAAA	1		
RESULT 109					
LOCUS	TA380A07P	22 bp	DNA	linear	GSS 13-DEC-20000
DEFINITION	T. brucei sheared genomic DNA clone 380a07, forward sequence,				
ACCESSION	AL497713				
KEYWORDS	AL497713.1	GI:11873435			
SOURCE	GSS.				
ORGANISM	Trypanosoma brucei				
	Trypanosoma brucei				
	Eukaryote; Euglenozoa; Kinetoplastida; Trypanosomatidae;				
REFERENCE	1 (bases 1 to 22)				
AUTHORS	Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.				
TITLE	Direct Submission				
JOURNAL	Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre. The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk				
COMMENT	Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GMTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).				
FEATURES	Email: nh@sanger.ac.uk				
source	Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.				
	Location/Qualifiers				
	1..22				
	/organism="Trypanosoma brucei"				
	/mol_type="genomic DNA"				
	/strain="TREU927"				
	/db_xref="taxon:5691"				
	/clone="380a07"				
Query Match	1.1%;	Score 15.6;	DB 1;	Length 22;	
Best Local Similarity	81.8%;	Pred. No. 54;			
Matches 18;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;	
Oy	1516	AATTAAAAAAGTAAAA	1537		
Db	1	AAAAAAAAAAAAAAAAAAAA	22		
RESULT 110					
LOCUS	AG194579	22 bp	DNA	linear	GSS 06-MAR-2004
DEFINITION	Pan troglodytes DNA, clone: RP43-072N05.T1, genomic survey sequence.				
ACCESSION	AG194579				
VERSION	AG194579.1	GI:45226755			
KEYWORDS	GSS.				
SOURCE	Pan troglodytes (chimpanzee)				
ORGANISM	Pan troglodytes				
	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				

```

REFERENCE      Mammalia; Eutheria; Primates; Carnivora; Hominoidea; Pan.
AUTHORS        Park H., Kim Y., Kim S., Han Y., Woo T., Park K., Eun C.J.,
                Hoon S.T., Chu M., Kim H., Joo S., Kim C., Song W. and Yoo H.
TITLE          BAC end sequences of Library RP-43
JOURNAL        Unpublished
REFERENCE      2 (bases 1 to 22)
AUTHORS        Park H., Kim Y., Kim S., Han Y., Woo T., Park K., Eun C.J.,
                Hoon S.T., Chu M., Kim H., Joo S., Kim C., Song W. and Yoo H.
TITLE          Direct Submission
JOURNAL        Submitted (07-JUN-2002) Hong-Seog Park, Korea Research Institute of
                Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);
                52, Oun-dong, Yusong-gu, Taejeon 305-335, Korea
                (E-mail:redstone@mail.krrib.re.kr, URL:http://phs.grc.krrib.re.kr/,
                Tel:82-42-866-7181, Fax:82-42-860-4409)
COMMENT        Clones are derived from the chimpanzee BAC library RP-43 This BAC
                end was generated during the R&D process and may have higher chances
                of clone tracking errors.
PRIMERS
Sequencing: TV
LIBRARY
Vector       : pBACE3.6
R.Site 1     : EcoRI
R.Site 2     : EcoRI
Location/Qualifiers
1..22
/oranism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-072N05-TV"
/bex="male"
/cell_type="lymphocytes"
/clone_id="RP-43 Chimpanzee Male BAC Library"

Query Match      1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. NO. 54;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1516 AATTAAAAAAAAAAGTAA 1537
Db      1 AAAAAAAAAAAAAAAAAAAAA 22

RESULT 111
CF334610/c      19 bp mRNA linear EST 18-AUG-2003
LOCUS           JMT-03-P13.b1 ACJMT-overexpressing transgenic rice plasmid cDNA
DEFINITION      library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
                 JMT-03-P13, mRNA sequence.
ACCESSION       CF334610
VERSION         CF334610.1 GI:33817556
KEYWORDS        EST.
SOURCE          Oryza sativa (japonica cultivar-group)
ORGANISM        Oryza sativa (japonica cultivar-group)
EXTRACT         Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                 Ehrhartoidae; Oryzaceae; Oryza.
REFERENCE       1 (bases 1 to 19)
AUTHORS         Kim U.S., Jun K.M., Cheong P.J., Kim M.U., Lee T.H., Shin Y.C.,
                 Song S.I., Kim U.K., Kim Y.-K. and Nahm B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT        Contact: Nahm B.H.
                 Genomics and Genetics Institute, Greengene Biotech Inc.; Division
                 of Bioscience and Bioinformatics, Myoung University
                 Yongin, Kyonggi, Korea
                 Tel: 82 31 330 6193
                 Fax: 82 31 321 6355
                 Email: bhnahmgbio.com, bhnahm@bio.myongji.ac.kr.
                 Location/Qualifiers
FEATURES             1..19
                     /oranism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"

```

Query Match	1.1%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 53;	
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY 1515 TAAATTAAAAA 1531	
Db 19 TAAATAAAAA 3	
RESULT 112	
CL680297/c	20 bp DNA linear GSS 09-JUN-2004
LOCUS	
DEFINITION	PR10128C.G05 2 - PR10128C.BR (20) Note: Recurring String Mixed
ACCESSION	pacificus foemid library of P. pacificus var. California Pristionchus
VERSION	CL680297
KEYWORDS	CL680297.1 GI:50187127
SOURCE	GSS.
ORGANISM	Pristionchus pacificus
REFERENCE	Pristionchus pacificus
AUTHORS	Eukaryote; Metazoa; Nematoda; Chromadorea; Diplogasterida;
TITLE	Neodiplogasteridae; Pristionchus.
JOURNAL	1 (bases 1 to 20)
COMMENT	Srinivasan J., Otto G.W., Kahlow U., Geisler R. and Sommer R.J. AppaB: an AcceB database for the nematode satellite organism Pristionchus pacificus Nucleic Acids Res. 32 (1), D421-D422 (2004)
FEATURES	
Source	Contact: Sommer RJ
	Evolutionary Biology
	Max-Planck-Institute for Developmental Biology
	Spemannstr. 37-39, Tuebingen D-72076, Germany
	Tel.: 00497071601371
	Fax: 00497071601498
	Email: ralf.sommer@tuebingen.mpg.de
	This library was generated at Caltech, Pasadena, USA and end
	sequenced at Vancouver, Canada.
	Seq Primer: T7
	Class: foemid ends.
	Location/Qualifiers
	1. 20
	/organism="Pristionchus pacificus"
	/mol_type="genomic DNA"
	/strain="California"
	/db_xref="taxon:54126"
	/clone_lib="Mixed stage foemid library of P. pacificus
	var. California"
	/note="Vector: pepifos-5 Fosmid vector"
Query Match	1.1%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 56;	
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY 1521 AAAAAAAGTAAAA 1537	
Db 20 AAAAAAAGAAAA 4	
RESULT 113	
CF319122/c	21 bp mRNA linear EST 15-AUG-2003
CF319122	

DEFINITION HD--09-107.g1 OsHDA1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone

COMMENT HD--09-107, mRNA sequence.

ACCESSION CF319122.1 GI:33690883

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzoideae; Oryza.

REFERENCE

AUTHORS

1 (bases 1 to 21)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

CONTACT: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 320 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

LOCATION/Qualifiers

1..21

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="HD-09-107"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 2 weeks"

/lab_host="E.coli DH10B"

/clone_lib="OsHDA1-overexpressing transgenic rice plasmid cDNA library (HD)"

/note="Vector: pCR4-TOPO, Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 1.1%; Score 15.4; DB 1; Length 21;

Best Local Similarity 94.1%; Pred. No. 59;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1521 AAAAAAAAAAGTAAA 1537

Db 17 AAAAAAAAAAATAAAA 1

RESULT 114

T49097

LOCUS T49097 25 bp mRNA linear EST 06-FEB-1995

DEFINITION yb08h08.g1 Stratiogene placenta (#937225) Homo sapiens cDNA clone IMAGE:70623 3' similar to gb:K62744 CLASS II HISTOCOMPATIBILITY ANTIGEN, M ALPHA CHAIN (HUMAN), mRNA sequence.

ACCESSION T49097

VERSION T49097.1 GI:650957

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 25)

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chapell,B., Chisoe,S., Dietrich,N., Dubuque,T., Favello,A., Gish,W., Hawtin,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Marini,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevaaskis,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M.

Generation and analysis of 280,000 human expressed sequence tags

Genome Res. 6 (9), 807-828 (1996)

MEDLINE

97044478

PUBMED

8889549

Other ESTs: yb08h08.r1

CONTACT: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High galley sequence stops: 1

High galley sequence stops: 1

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.

Trace considered overall poor quality

Seq primer: -21m13

High quality sequence stop: 1.

LOCATION/Qualifiers

1..25

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="GDB:491520"

/db_xref="taxon:9606"

/clone="IMAGE:70623"

/sex="male"

/lab_host="SOLR cells (kanamycin resistant)"

/clone_lib="Stratiogene placenta (#937225)"

/note="Organ: placenta; Vector: pluescript SK-, Site 1: EcoRI, Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Caucasian. Average insert size: 1.2 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GATTGGCAGCAG 3' -3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3' "

Query Match 1.1%; Score 15.4; DB 1; Length 25;

Best Local Similarity 76.0%; Pred. No. 69;

Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Cy 1302 TCTATTTTATTTTCAGACG 1326

Db 1 TTTTCTTTTCTTTTAAAGAA 25

RESULT 115

AL038460

LOCUS AL038460 20 bp mRNA linear EST 06-JUL-2004

DEFINITION DKFZP56B2246.r1 566 (synonym: hfkd2) Homo sapiens cDNA clone DKFZP56B2246, mRNA sequence.

ACCESSION AL038460

VERSION AL038460.1 GI:49682131

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 20)

Ottewaelder,B., Obermaier,B., Mewes,H.W., Gassenhuber,J. and Wiemann,S.

EST (Ottewaelder, et al.)

Unpublished (1999)

CONTACT: MIPS

MIPS

Ingolstaedter Landstr.1, D-85764 Neubherg, Germany.

LOCATION/Qualifiers

1..20

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="DKFZP56B2246"

/tissue_type="kidney"

/dev_stage="fetal"

/lab_host="X1-2blue"

/clone_lib="566 (synonym: hfkd2)"

/note="Vector: pAMP1, Site 1: NotI, Site 2: SalI"

Query Match 1.1%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 63;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1518 TTTAAAAAAGTAAAA 1537
 Db 1 TCAAAAAAAAAAAAAA 20

RESULT 116
 CF298018/c
 LOCUS CF298018/c
 DEFINITION 7LEAF--01-D19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--01-D19, mRNA sequence.

ACCESSION CF298018
 VERSION CF298018.1 GI:33669779
 KEYWORDS
 SOURCE
 ORGANISM Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 20)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 TITLE
 JOURNAL
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongsin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
 Location/Qualifiers

FEATURES
 source 1..20
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="7LEAF--01-D19"
 /tissue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.1%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 63;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1516 AATTAAAAAAGTAA 1535
 Db 20 AATCAAAAAAAAAAAAAA 1

RESULT 117
 CF339443
 LOCUS CF339443
 DEFINITION RC11--04-003.g1 Regenerated callus lambda phage cDNA library (RC11) Oryza sativa (japonica cultivar-group) cDNA clone RC11--04-003, mRNA sequence.

ACCESSION CF339443
 VERSION CF339443.1 GI:33827271
 KEYWORDS
 SOURCE Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE 1 (bases 1 to 20)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 TITLE
 JOURNAL
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongsin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
 Location/Qualifiers

FEATURES
 source 1..20
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="RC11--04-003"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli SOLR"
 /clone_lib="Regenerated callus lambda phage cDNA library (RC11)"
 /note="Vector: pBluescript SK(+); Site_1: SstI; Site_2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SstI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

Query Match 1.1%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 63;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 424 GTGGCGGCTCGCGCGC 443
 Db 1 GCGGCGGCGAGCGCGCGC 20

RESULT 118
 A0661013/c
 LOCUS A0661013/c
 DEFINITION A0661013 CSEORAN09 Sus scrofa cDNA clone C0000935_H04, mRNA sequence.
 ACCESSION A0661013
 VERSION A0661013.1 GI:49345046
 KEYWORDS
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.

REFERENCE 1 (bases 1 to 21)
 Anderson,S.T., Finlayson,H.A. and Archibald,A.L.
 Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle
 Unpublished (2004)
 TITLE
 JOURNAL
 COMMENT Contact: Anderson SI
 Genomics and Bioinformatics
 Roslin Institute
 Roslin, Midlothian, EH25 9PS, UNITED KINGDOM

Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross match with the -minscore 20 and -mismatch 12 options. Vector:pBluescriptII(KS+) R. Site 1: EcoRI R. Site 2: NotI Description: Normalised library constructed from pooled tissue from day 30 placentas. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.

FEATURES
 source 1..21
 /organism="Sus scrofa"
 /mol_type="mRNA"
 /db_xref="taxon:9823"


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/clone="C0000935.H04"
/tissue_type="placenta"
/clone_id="CSER0AN09"
/notes="Vector: pBluescriptII(KS+); Site_1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pooled tissue from day 30 placentas."

Query Match 1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 66;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1518 TGTATATTAATAAAAAAAAA 1531
DB 20 TTTTATTAATAAAAAAAAA 1

RESULT 119
AL038582 AL038582 21 bp mRNA linear EST 06-JUL-2004
LOCUS DKFZP566F0946.r1.566 (synonym: hfkcd2) Homo sapiens cDNA clone
DEFINITION DKFZP566F0946, mRNA sequence.
ACCESSION AL038582
VERSION AL038582.1 GI:49682163
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 21)
Ostenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
Wiemann, S.
EST (Ostenwaelder, et al.)
TITLE Unpublished (1999)
JOURNAL Contact: MIPS
COMMENT MIPS

FEATURES
source
1..21
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP566F0946"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_idb="566 (synonym: hfkcd2)"
/notes="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match 1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 66;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1518 TTTAAAAAAGTAAAA 1537
DB 1 TCAAAAAAAAAAAAAAAAAA 20

RESULT 120
AL038627 AL038627 21 bp mRNA linear EST 06-JUL-2004
LOCUS DKFZP566H2046.r1.566 (synonym: hfkcd2) Homo sapiens cDNA clone
DEFINITION DKFZP566H2046, mRNA sequence.
ACCESSION AL038627
VERSION AL038627.1 GI:49682173
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 21)
Ostenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
Wiemann, S.
EST (Ostenwaelder, et al.)
TITLE
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JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS
FEATURES Location/Qualifiers
source
1..21
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP566H2046"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_idb="566 (synonym: hfkcd2)"
/notes="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match 1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 66;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1518 TTTAAAAAAGTAAAA 1537
DB 1 TCAAAAAAAAAAAAAAAAAA 20

RESULT 121
AL038839 AL038839 21 bp mRNA linear EST 06-JUL-2004
LOCUS DKFZP566P1346.r1.566 (synonym: hfkcd2) Homo sapiens cDNA clone
DEFINITION DKFZP566P1346, mRNA sequence.
ACCESSION AL038839
VERSION AL038839.1 GI:49682218
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 21)
Ostenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
Wiemann, S.
EST (Ostenwaelder, et al.)
TITLE Unpublished (1999)
JOURNAL Contact: MIPS
COMMENT MIPS

FEATURES Location/Qualifiers
source
1..21
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP566P1346"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_idb="566 (synonym: hfkcd2)"
/notes="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match 1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 66;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1518 TTTAAAAAAGTAAAA 1537
DB 1 TCAAAAAAAAAAAAAAAAAA 20

RESULT 122
CF330439 CF330439 21 bp mRNA linear EST 18-AUG-2003
LOCUS NACL--06-C12.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION NACL--06-C12.b1 Rice callus plasmid cDNA library (NACL) Oryza
sequence.
ACCESSION CF330439
```

VERSION CE330439.1 GI:33809110
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretidae; Oryzae; Oryza.
REFERENCE 1 (bases 1 to 21)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
TITLE Unpublished (2003)
JOURNAL Contact: Nahm B.H.
COMMENT Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--06-C12"
/issue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 66;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1512 TGTTAATTATTAATAAAAAA 1531
||||| |||||||
21 TGTATTAATAAAAAA 2

RESULT 123
CN763587 21 bp mRNA linear EST 20-MAY-2004
LOCUS ID0AAA7BH12RM1 ApMS Acyrthosiphon pisum cDNA clone ID0AAA7BH12 5',
DEFINITION mRNA sequence.
ACCESSION CN763587
VERSION CN763587.1 GI:47537510
KEYWORDS EST.
SOURCE Acyrthosiphon pisum (pea aphid)
ORGANISM Acyrthosiphon pisum
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preygota;
Neoptera; Paraneoptera; Hemiptera; Sternorhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrotrichini; Acyrthosiphina.
REFERENCE 1 (bases 1 to 21)
Hunter,W., Martinez-Torres,D., Rabhe,Y., Sabater-Munoz,B.,
Stern,D., Tagu,D. and Wincker,P.
An expressed sequence tags database for the pea aphid Acyrthosiphon
pisum
Unpublished (2004)
JOURNAL Contact: D. Tagu
COMMENT INRA Rennes
UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France
Tel: +33-2.23.48.51.65
Fax: +33-2.23.48.51.50
Risk of contamination by bacterial sequences from obligatory
(Buchnera) or facultative endosymbionts. These sequences were
obtained in the frame of the International Consortium of Aphid
Genomics in collaboration with Genoscope
PCR Primers
FORWARD: CAGGAAACAGCTATGACC

FEATURES Plate: 7 row: H column: 12.
SOURCE Location/Qualifiers
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/organism="Acyrthosiphon pisum"
/mol_type="mRNA"
/cultivar="developmentstage"
/db_xref="taxon:7029"
/clone="ID0AAA7BH12"
/issue_type="whole insect"
/dev_stage="nymphs and adults (parthenogenetic females)"
/lab_host="Xrl-Blue"
/clone_lib="ApMS"
/note="Vector: pBS-SK minus; Site_1: EcoRI; Site_2: XhoI;
Sample name: ID0AAA; Plant growth place: Department of
Ecology & Evolutionary Biology, Princeton University;
Soil conditions: Soil; Sowing date: 01/06/1999;
Harvesting date: 01/06/1999; Stress date: no stress;
Description: Aphids inoculated on one-week old *Vicia faba*
under non-sterile conditions. All parthenogenetic stages
and both winged and wingless adults were collected for
library construction. ; experimental condition: long
photoperiod (16-hr light/8-hr dark at 18 c)"

Query Match 1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 66;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1512 TGTTAATTATTAATAAAAAA 1531
||||| |||||||
21 TGTATTAATAAAAAA 21

RESULT 124
AZ393269 21 bp DNA linear GSS 03-OCT-2000
LOCUS AZ393269
DEFINITION IM0156F13F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
clone UGCGIM0156F13 F, genomic survey sequence.
ACCESSION AZ393269
VERSION AZ393269.1 GI:10508341
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Rellly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0156 row: F column: 13
Seq primer: CGTGTAAACGACGCGCACT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGIM0156F13"
/sex="Male"

/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone.lib="Mouse 10kb plasmid UGCM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (g14732114|gbl|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 66;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1339 AATTCTATATTTTATTTT 1358
Db 1 AATTAGTATTTTATTTT 20

RESULT 125

AZ625662 21 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0465C23F Mouse 10kb plasmid UGCM library Mus musculus genomic
DEFINITION clone UGCM10465C23 F, genomic survey sequence.

ACCESSION AZ625662
VERSION 1
KEYWORDS GSS:
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)
Dunn, D., Moyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.

AUTHORS Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE Unpublished (2000)

JOURNAL Contact: Robert B. Weiss
University of Utah Genome Center

COMMENT Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0465 row: C column: 23
Seq primer: CGTGTAAACACACGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers

FEATURES
source 1. 21

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCM10465C23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone.lib="Mouse 10kb plasmid UGCM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (g14732114|gbl|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 66;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1301 ATCTATTTTATTTTCA 1320
Db 20 AATATTTTTTTTTTTT 1

RESULT 126

CF300172 23 bp mRNA linear EST 15-AUG-2003
LOCUS 7LEAF--04-H15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone 7LEAF--04-H15, mRNA
sequence.

ACCESSION CF300172
VERSION 1
KEYWORDS EST:
SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehmerioideae; Oryzoae; Oryza.

REFERENCE 1 (bases 1 to 23)
Kim, J.-S., Jun, K.-M., Cheong, P.-J., Kim, M.-J., Lee, T.-H., Shin, Y.-C.,
Song, S.-I., Kim, J.-K., Kim, Y.-K., and Nahm, B.-H.

AUTHORS Large-scale Sequencing Analysis of Rice ESTs

TITLE Unpublished (2003)

JOURNAL Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University

COMMENT Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source 1. 23
Location/Qualifiers

/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--04-H15"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E. coli DH10B"
/clone.lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO. Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.1%; Score 15.2; DB 1; Length 23;
Best Local Similarity 85.0%; Pred. No. 72;

	Matches	17; Conservative	0; Mismatches	3; Indels	0; Gaps
Qy	1248	TTTTTTTGTTTTAAACA	1267		
Db	1	TTTTTTTTTTTTTAAATA	20		

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 2, 2004, 12:41:55 ; Search time 7 Seconds
(without alignments)
3.802 Million cell updates/sec

Title: US-10-643-432-12

Perfect score: 1401

Sequence: 1 ccgcccgaggggagcgag.....cataactatctctctgtc 1401

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 482 seqs, 9499 residues

Total number of hits satisfying chosen parameters: 964

Minimum DB seq length: 8

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 491 summaries

Database : rge12.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18.6	1.3	25	1	AX042782
2	18.2	1.3	25	1	AR370697
3	18.2	1.3	25	1	AX117632
4	18.2	1.3	25	1	AX692829
5	18.2	1.3	25	1	AX692830
6	18.2	1.3	25	1	AX692831
7	17.8	1.3	25	1	AX825106
8	17.2	1.2	24	1	AR431307
9	16.8	1.2	21	1	AR253000
10	16.8	1.2	21	1	AX825103
11	16.8	1.2	21	1	AX825104
12	16.8	1.2	21	1	AX825105
13	16.8	1.2	21	1	AX825151
14	16.8	1.2	24	1	AR261539
15	16.6	1.2	23	1	AO1996
16	16.6	1.2	23	1	AO6442
17	16.4	1.2	19	1	AR294636
18	16.2	1.2	21	1	AR084566
19	16.2	1.2	21	1	AR084578
20	16.2	1.2	21	1	AR084579
21	16.2	1.2	21	1	AR084582
22	16.2	1.2	21	1	AR093142
23	16.2	1.2	21	1	AR093142
24	16.2	1.2	21	1	AR279103
25	16.2	1.2	21	1	AX383931
26	16.2	1.2	21	1	AX713257
27	16.2	1.2	21	1	AX825110
28	16.2	1.2	21	1	AX825114
29	16.2	1.2	21	1	AX825118
30	16.2	1.2	21	1	AX825122
31	16.2	1.2	21	1	AX825138
32	16.2	1.2	21	1	AX825154
33	16.2	1.2	22	1	BD085544

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C 35	15.8	1.1	20	1	A40126	ACCESSION:A40126
C 36	15.8	1.1	20	1	AR139961	ACCESSION:AR139961
C 37	15.8	1.1	20	1	AR140280	ACCESSION:AR140280
C 38	15.8	1.1	20	1	AR140558	ACCESSION:AR140558
C 39	15.8	1.1	20	1	AR182885	ACCESSION:AR182885
C 40	15.8	1.1	20	1	AX104051	ACCESSION:AX104051
C 41	15.8	1.1	20	1	AX281587	ACCESSION:AX281587
C 42	15.8	1.1	20	1	AX355382	ACCESSION:AX355382
C 43	15.8	1.1	20	1	AX547104	ACCESSION:AX547104
C 44	15.8	1.1	20	1	BD069976	ACCESSION:BD069976
C 45	15.8	1.1	21	1	AR084563	ACCESSION:AR084563
C 46	15.8	1.1	21	1	AR084567	ACCESSION:AR084567
C 47	15.8	1.1	21	1	CO830490	ACCESSION:CO830490
C 48	15.8	1.1	21	1	CO830492	ACCESSION:CO830492
C 49	15.8	1.1	21	1	AR242257	ACCESSION:AR242257
C 50	15.8	1.1	21	1	AR242262	ACCESSION:AR242262
C 51	15.8	1.1	21	1	AX825107	ACCESSION:AX825107
C 52	15.8	1.1	21	1	AX825108	ACCESSION:AX825108
C 53	15.8	1.1	21	1	AX825109	ACCESSION:AX825109
C 54	15.8	1.1	21	1	AX825111	ACCESSION:AX825111
C 55	15.8	1.1	21	1	AX825112	ACCESSION:AX825112
C 56	15.8	1.1	21	1	AX825113	ACCESSION:AX825113
C 57	15.8	1.1	21	1	AX825115	ACCESSION:AX825115
C 58	15.8	1.1	21	1	AX825116	ACCESSION:AX825116
C 59	15.8	1.1	21	1	AX825117	ACCESSION:AX825117
C 60	15.8	1.1	21	1	AX825152	ACCESSION:AX825152
C 61	15.8	1.1	21	1	AX825153	ACCESSION:AX825153
C 62	15.8	1.1	21	1	AX825163	ACCESSION:AX825163
C 63	15.8	1.1	22	1	AX658499	ACCESSION:AX658499
C 64	15.6	1.1	22	1	AR164336	ACCESSION:AR164336
C 65	15.6	1.1	22	1	I31828	ACCESSION:I31828
C 66	15.6	1.1	22	1	169425	ACCESSION:169425
C 67	15.4	1.1	17	1	BD254424	ACCESSION:BD254424
C 68	15.4	1.1	17	1	AR187058	ACCESSION:AR187058
C 69	15.4	1.1	17	1	AR286187	ACCESSION:AR286187
C 70	15.4	1.1	17	1	AR323668	ACCESSION:AR323668
C 71	15.4	1.1	17	1	AR398177	ACCESSION:AR398177
C 72	15.4	1.1	18	1	AX804693	ACCESSION:AX804693
C 73	15.4	1.1	20	1	AB8305	ACCESSION:AB8305
C 74	15.4	1.1	20	1	A90272	ACCESSION:A90272
C 75	15.4	1.1	20	1	AX356277	ACCESSION:AX356277
C 76	15.4	1.1	20	1	BD065818	ACCESSION:BD065818
C 77	15.4	1.1	21	1	AX118267	ACCESSION:AX118267
C 78	15.2	1.1	20	1	AR092032	ACCESSION:AR092032
C 79	15.2	1.1	20	1	AR112167	ACCESSION:AR112167
C 80	15.2	1.1	20	1	AR149209	ACCESSION:AR149209
C 81	15.2	1.1	20	1	BD229218	ACCESSION:BD229218
C 82	15.2	1.1	20	1	AR309844	ACCESSION:AR309844
C 83	15.2	1.1	20	1	AR349470	ACCESSION:AR349470
C 84	15.2	1.1	20	1	AX298541	ACCESSION:AX298541
C 85	15.2	1.1	20	1	AX404077	ACCESSION:AX404077
C 86	15.2	1.1	20	1	AX488408	ACCESSION:AX488408
C 87	15.2	1.1	20	1	AX770111	ACCESSION:AX770111
C 88	15.2	1.1	20	1	BD143136	ACCESSION:BD143136
C 89	15.2	1.1	21	1	AX825106	ACCESSION:AX825106
C 90	15.2	1.1	21	1	A20525	ACCESSION:A20525
C 91	15.2	1.1	21	1	A20526	ACCESSION:A20526
C 92	15.2	1.1	21	1	A20531	ACCESSION:A20531
C 93	15.2	1.1	21	1	A20532	ACCESSION:A20532
C 94	15.2	1.1	21	1	AR143626	ACCESSION:AR143626
C 95	15.2	1.1	21	1	AR157200	ACCESSION:AR157200
C 96	15.2	1.1	21	1	E08187	ACCESSION:E08187
C 97	15.2	1.1	21	1	AR437180	ACCESSION:AR437180
C 98	15.2	1.1	21	1	AX825119	ACCESSION:AX825119
C 99	15.2	1.1	21	1	AX825120	ACCESSION:AX825120
C 100	15.2	1.1	21	1	AX825121	ACCESSION:AX825121
C 101	15.2	1.1	21	1	AX825135	ACCESSION:AX825135
C 102	15.2	1.1	21	1	AX825136	ACCESSION:AX825136
C 103	15.2	1.1	21	1	AX825137	ACCESSION:AX825137
C 104	15.2	1.1	21	1	AX825138	ACCESSION:AX825138
C 105	15.2	1.1	21	1	AX825155	ACCESSION:AX825155
C 106	15.2	1.1	21	1	AX825159	ACCESSION:AX825159

107	15.2	1.1	21	1	BD00680	ACCESSION:BD00680	C 180	14.8	1.1	19	1	AR11960	ACCESSION:AR11960
108	15.2	1.1	21	1	BD023735	ACCESSION:BD023735	C 181	14.8	1.1	19	1	AR11970	ACCESSION:AR11970
109	15.2	1.1	25	1	AX117632	ACCESSION:AX117632	C 182	14.8	1.1	19	1	AR12483	ACCESSION:AR12483
C 110	15	1.1	17	1	AR187059	ACCESSION:AR187059	C 183	14.8	1.1	19	1	AR12484	ACCESSION:AR12484
C 111	15	1.1	17	1	AR187060	ACCESSION:AR187060	C 184	14.8	1.1	19	1	AR12485	ACCESSION:AR12485
C 112	15	1.1	17	1	AR323669	ACCESSION:AR323669	C 185	14.8	1.1	19	1	AR12486	ACCESSION:AR12486
C 113	15	1.1	17	1	AR323670	ACCESSION:AR323670	C 186	14.8	1.1	19	1	AR12487	ACCESSION:AR12487
C 114	15	1.1	17	1	AR753821	ACCESSION:AR753821	C 187	14.8	1.1	19	1	AR12488	ACCESSION:AR12488
C 115	15	1.1	17	1	AX753822	ACCESSION:AX753822	C 188	14.8	1.1	19	1	AR12489	ACCESSION:AR12489
C 116	15	1.1	17	1	AX753823	ACCESSION:AX753823	C 189	14.8	1.1	19	1	AR124850	ACCESSION:AR124850
C 117	15	1.1	19	1	AR102020	ACCESSION:AR102020	C 190	14.8	1.1	19	1	AR124854	ACCESSION:AR124854
C 118	15	1.1	19	1	AR134802	ACCESSION:AR134802	C 191	14.8	1.1	19	1	AR124856	ACCESSION:AR124856
C 119	15	1.1	19	1	AR352460	ACCESSION:AR352460	C 192	14.8	1.1	19	1	AR124857	ACCESSION:AR124857
C 120	15	1.1	20	1	E28098	ACCESSION:E28098	C 193	14.8	1.1	19	1	AR124867	ACCESSION:AR124867
C 121	15	1.1	20	1	AR294700	ACCESSION:AR294700	C 194	14.8	1.1	19	1	AR135291	ACCESSION:AR135291
C 122	15	1.1	20	1	AR307942	ACCESSION:AR307942	C 195	14.8	1.1	19	1	AR135292	ACCESSION:AR135292
C 123	15	1.1	20	1	AX048446	ACCESSION:AX048446	C 196	14.8	1.1	19	1	AR135293	ACCESSION:AR135293
C 124	15	1.1	21	1	AX804844	ACCESSION:AX804844	C 197	14.8	1.1	19	1	AR135294	ACCESSION:AR135294
C 125	14.8	1.1	18	1	AR034896	ACCESSION:AR034896	C 198	14.8	1.1	19	1	AR135295	ACCESSION:AR135295
C 126	14.8	1.1	18	1	AR034899	ACCESSION:AR034899	C 199	14.8	1.1	19	1	AR135296	ACCESSION:AR135296
C 127	14.8	1.1	18	1	AR058305	ACCESSION:AR058305	C 200	14.8	1.1	19	1	AR135297	ACCESSION:AR135297
C 128	14.8	1.1	18	1	AR097579	ACCESSION:AR097579	C 201	14.8	1.1	19	1	AR135298	ACCESSION:AR135298
C 129	14.8	1.1	18	1	AR101834	ACCESSION:AR101834	C 202	14.8	1.1	19	1	AR135302	ACCESSION:AR135302
C 130	14.8	1.1	18	1	AR106506	ACCESSION:AR106506	C 203	14.8	1.1	19	1	AR135304	ACCESSION:AR135304
C 131	14.8	1.1	18	1	AR106909	ACCESSION:AR106909	C 204	14.8	1.1	19	1	AR135305	ACCESSION:AR135305
C 132	14.8	1.1	18	1	BD222596	ACCESSION:BD222596	C 205	14.8	1.1	19	1	AR135315	ACCESSION:AR135315
C 133	14.8	1.1	18	1	E28535	ACCESSION:E28535	C 206	14.8	1.1	19	1	AR141898	ACCESSION:AR141898
C 134	14.8	1.1	18	1	E28536	ACCESSION:E28536	C 207	14.8	1.1	19	1	AR153863	ACCESSION:AR153863
C 135	14.8	1.1	18	1	179509	ACCESSION:179509	C 208	14.8	1.1	19	1	AR164173	ACCESSION:AR164173
C 136	14.8	1.1	18	1	AR196702	ACCESSION:AR196702	C 209	14.8	1.1	19	1	BD196900	ACCESSION:BD196900
C 137	14.8	1.1	18	1	AR196704	ACCESSION:AR196704	C 210	14.8	1.1	19	1	BD196911	ACCESSION:BD196911
C 138	14.8	1.1	18	1	AR215435	ACCESSION:AR215435	C 211	14.8	1.1	19	1	BD274438	ACCESSION:BD274438
C 139	14.8	1.1	18	1	AR222464	ACCESSION:AR222464	C 212	14.8	1.1	19	1	BD274439	ACCESSION:BD274439
C 140	14.8	1.1	18	1	AR412363	ACCESSION:AR412363	C 213	14.8	1.1	19	1	BD274440	ACCESSION:BD274440
C 141	14.8	1.1	18	1	AR473365	ACCESSION:AR473365	C 214	14.8	1.1	19	1	BD274441	ACCESSION:BD274441
C 142	14.8	1.1	18	1	AR487019	ACCESSION:AR487019	C 215	14.8	1.1	19	1	BD274449	ACCESSION:BD274449
C 143	14.8	1.1	18	1	AR487020	ACCESSION:AR487020	C 216	14.8	1.1	19	1	AR205798	ACCESSION:AR205798
C 144	14.8	1.1	18	1	AX004875	ACCESSION:AX004875	C 217	14.8	1.1	19	1	AR205799	ACCESSION:AR205799
C 145	14.8	1.1	18	1	AX004879	ACCESSION:AX004879	C 218	14.8	1.1	19	1	AR205800	ACCESSION:AR205800
C 146	14.8	1.1	18	1	AX008117	ACCESSION:AX008117	C 219	14.8	1.1	19	1	AR205801	ACCESSION:AR205801
C 147	14.8	1.1	18	1	AX008118	ACCESSION:AX008118	C 220	14.8	1.1	19	1	AR205809	ACCESSION:AR205809
C 148	14.8	1.1	18	1	AX008122	ACCESSION:AX008122	C 221	14.8	1.1	19	1	AR213490	ACCESSION:AR213490
C 149	14.8	1.1	18	1	AX008123	ACCESSION:AX008123	C 222	14.8	1.1	19	1	AR213491	ACCESSION:AR213491
C 150	14.8	1.1	18	1	AX028843	ACCESSION:AX028843	C 223	14.8	1.1	19	1	AR213492	ACCESSION:AR213492
C 151	14.8	1.1	18	1	AX047271	ACCESSION:AX047271	C 224	14.8	1.1	19	1	AR213493	ACCESSION:AR213493
C 152	14.8	1.1	18	1	AX047273	ACCESSION:AX047273	C 225	14.8	1.1	19	1	AR213494	ACCESSION:AR213494
C 153	14.8	1.1	18	1	AX104721	ACCESSION:AX104721	C 226	14.8	1.1	19	1	AR213495	ACCESSION:AR213495
C 154	14.8	1.1	18	1	AX104747	ACCESSION:AX104747	C 227	14.8	1.1	19	1	AR213496	ACCESSION:AR213496
C 155	14.8	1.1	18	1	AX106551	ACCESSION:AX106551	C 228	14.8	1.1	19	1	AR213497	ACCESSION:AR213497
C 156	14.8	1.1	18	1	AX108642	ACCESSION:AX108642	C 229	14.8	1.1	19	1	AR213501	ACCESSION:AR213501
C 157	14.8	1.1	18	1	AX266883	ACCESSION:AX266883	C 230	14.8	1.1	19	1	AR213502	ACCESSION:AR213502
C 158	14.8	1.1	18	1	AX355809	ACCESSION:AX355809	C 231	14.8	1.1	19	1	AR213503	ACCESSION:AR213503
C 159	14.8	1.1	18	1	AX547774	ACCESSION:AX547774	C 232	14.8	1.1	19	1	AR213512	ACCESSION:AR213512
C 160	14.8	1.1	18	1	AX547800	ACCESSION:AX547800	C 233	14.8	1.1	19	1	AR223465	ACCESSION:AR223465
C 161	14.8	1.1	18	1	AX814716	ACCESSION:AX814716	C 234	14.8	1.1	19	1	AR223463	ACCESSION:AR223463
C 162	14.8	1.1	18	1	AX814723	ACCESSION:AX814723	C 235	14.8	1.1	19	1	AR225557	ACCESSION:AR225557
C 163	14.8	1.1	18	1	AX814724	ACCESSION:AX814724	C 236	14.8	1.1	19	1	AR321589	ACCESSION:AR321589
C 164	14.8	1.1	18	1	AX814725	ACCESSION:AX814725	C 237	14.8	1.1	19	1	AR335804	ACCESSION:AR335804
C 165	14.8	1.1	18	1	AX814736	ACCESSION:AX814736	C 238	14.8	1.1	19	1	AR335805	ACCESSION:AR335805
C 166	14.8	1.1	18	1	BD085545	ACCESSION:BD085545	C 239	14.8	1.1	19	1	AR335806	ACCESSION:AR335806
C 167	14.8	1.1	19	1	A68209	ACCESSION:A68209	C 240	14.8	1.1	19	1	AR357447	ACCESSION:AR357447
C 168	14.8	1.1	19	1	AR048767	ACCESSION:AR048767	C 241	14.8	1.1	19	1	AR359177	ACCESSION:AR359177
C 169	14.8	1.1	19	1	AR113371	ACCESSION:AR113371	C 242	14.8	1.1	19	1	AR359178	ACCESSION:AR359178
C 170	14.8	1.1	19	1	AR111946	ACCESSION:AR111946	C 243	14.8	1.1	19	1	AR403601	ACCESSION:AR403601
C 171	14.8	1.1	19	1	AR111947	ACCESSION:AR111947	C 244	14.8	1.1	19	1	AR403602	ACCESSION:AR403602
C 172	14.8	1.1	19	1	AR111948	ACCESSION:AR111948	C 245	14.8	1.1	19	1	AR403603	ACCESSION:AR403603
C 173	14.8	1.1	19	1	AR111949	ACCESSION:AR111949	C 246	14.8	1.1	19	1	AR403604	ACCESSION:AR403604
C 174	14.8	1.1	19	1	AR111950	ACCESSION:AR111950	C 247	14.8	1.1	19	1	AR403605	ACCESSION:AR403605
C 175	14.8	1.1	19	1	AR111951	ACCESSION:AR111951	C 248	14.8	1.1	19	1	AR403606	ACCESSION:AR403606
C 176	14.8	1.1	19	1	AR111952	ACCESSION:AR111952	C 249	14.8	1.1	19	1	AR403607	ACCESSION:AR403607
C 177	14.8	1.1	19	1	AR111953	ACCESSION:AR111953	C 250	14.8	1.1	19	1	AR403608	ACCESSION:AR403608
C 178	14.8	1.1	19	1	AR111957	ACCESSION:AR111957	C 251	14.8	1.1	19	1	AR403612	ACCESSION:AR403612
C 179	14.8	1.1	19	1	AR111959	ACCESSION:AR111959	C 252	14.8	1.1	19	1	AR403613	ACCESSION:AR403613

C 253	14.8	1.1	19	1	AR403614	ACCESSION:AR403614
C 254	14.8	1.1	19	1	AR403623	ACCESSION:AR403623
C 255	14.8	1.1	19	1	AR413338	ACCESSION:AR413338
C 256	14.8	1.1	19	1	AR432616	ACCESSION:AR432616
C 257	14.8	1.1	19	1	AR432617	ACCESSION:AR432617
C 258	14.8	1.1	19	1	AR451262	ACCESSION:AR451262
C 259	14.8	1.1	19	1	AR451282	ACCESSION:AR451282
C 260	14.8	1.1	19	1	AX059378	ACCESSION:AX059378
C 261	14.8	1.1	19	1	AX132398	ACCESSION:AX132398
C 262	14.8	1.1	19	1	AX226133	ACCESSION:AX226133
C 263	14.8	1.1	19	1	AX349249	ACCESSION:AX349249
C 264	14.8	1.1	19	1	BD087505	ACCESSION:BD087505
C 265	14.8	1.1	20	1	AR030917	ACCESSION:AR030917
C 266	14.8	1.1	20	1	AR064875	ACCESSION:AR064875
C 267	14.8	1.1	20	1	AR080000	ACCESSION:AR080000
C 268	14.8	1.1	20	1	AR085926	ACCESSION:AR085926
C 269	14.8	1.1	20	1	AR087520	ACCESSION:AR087520
C 270	14.8	1.1	20	1	AR093312	ACCESSION:AR093312
C 271	14.8	1.1	20	1	AR118970	ACCESSION:AR118970
C 272	14.8	1.1	20	1	AR121540	ACCESSION:AR121540
C 273	14.8	1.1	20	1	AR121692	ACCESSION:AR121692
C 274	14.8	1.1	20	1	AR123335	ACCESSION:AR123335
C 275	14.8	1.1	20	1	AR139960	ACCESSION:AR139960
C 276	14.8	1.1	20	1	AR139962	ACCESSION:AR139962
C 277	14.8	1.1	20	1	AR140279	ACCESSION:AR140279
C 278	14.8	1.1	20	1	AR140281	ACCESSION:AR140281
C 279	14.8	1.1	20	1	AR140557	ACCESSION:AR140557
C 280	14.8	1.1	20	1	AR140559	ACCESSION:AR140559
C 281	14.8	1.1	20	1	AR141070	ACCESSION:AR141070
C 282	14.8	1.1	20	1	AR154115	ACCESSION:AR154115
C 283	14.8	1.1	20	1	AR164658	ACCESSION:AR164658
C 284	14.8	1.1	20	1	BD218101	ACCESSION:BD218101
C 285	14.8	1.1	20	1	BD234126	ACCESSION:BD234126
C 286	14.8	1.1	20	1	CQ759610	ACCESSION:CQ759610
C 287	14.8	1.1	20	1	E12676	ACCESSION:E12676
C 288	14.8	1.1	20	1	I28309	ACCESSION:I28309
C 289	14.8	1.1	20	1	I36180	ACCESSION:I36180
C 290	14.8	1.1	20	1	I47310	ACCESSION:I47310
C 291	14.8	1.1	20	1	AR213738	ACCESSION:AR213738
C 292	14.8	1.1	20	1	AR222466	ACCESSION:AR222466
C 293	14.8	1.1	20	1	AR231312	ACCESSION:AR231312
C 294	14.8	1.1	20	1	AR236083	ACCESSION:AR236083
C 295	14.8	1.1	20	1	AR274394	ACCESSION:AR274394
C 296	14.8	1.1	20	1	AR343047	ACCESSION:AR343047
C 297	14.8	1.1	20	1	AR344936	ACCESSION:AR344936
C 298	14.8	1.1	20	1	AR365970	ACCESSION:AR365970
C 299	14.8	1.1	20	1	AR382312	ACCESSION:AR382312
C 300	14.8	1.1	20	1	AR429653	ACCESSION:AR429653
C 301	14.8	1.1	20	1	AR447441	ACCESSION:AR447441
C 302	14.8	1.1	20	1	AR451990	ACCESSION:AR451990
C 303	14.8	1.1	20	1	AR454776	ACCESSION:AR454776
C 304	14.8	1.1	20	1	AR488890	ACCESSION:AR488890
C 305	14.8	1.1	20	1	AR489044	ACCESSION:AR489044
C 306	14.8	1.1	20	1	AR494116	ACCESSION:AR494116
C 307	14.8	1.1	20	1	AR494728	ACCESSION:AR494728
C 308	14.8	1.1	20	1	AX004876	ACCESSION:AX004876
C 309	14.8	1.1	20	1	AX045779	ACCESSION:AX045779
C 310	14.8	1.1	20	1	AX045787	ACCESSION:AX045787
C 311	14.8	1.1	20	1	AX045790	ACCESSION:AX045790
C 312	14.8	1.1	20	1	AX056597	ACCESSION:AX056597
C 313	14.8	1.1	20	1	AX056597	ACCESSION:AX056597
C 314	14.8	1.1	20	1	AX104034	ACCESSION:AX104034
C 315	14.8	1.1	20	1	AX104364	ACCESSION:AX104364
C 316	14.8	1.1	20	1	AX104368	ACCESSION:AX104368
C 317	14.8	1.1	20	1	AX196224	ACCESSION:AX196224
C 318	14.8	1.1	20	1	AX196239	ACCESSION:AX196239
C 319	14.8	1.1	20	1	AX354974	ACCESSION:AX354974
C 320	14.8	1.1	20	1	AX355810	ACCESSION:AX355810
C 321	14.8	1.1	20	1	AX355811	ACCESSION:AX355811
C 322	14.8	1.1	20	1	AX440125	ACCESSION:AX440125
C 323	14.8	1.1	20	1	AX440140	ACCESSION:AX440140
C 324	14.8	1.1	20	1	AX465311	ACCESSION:AX465311
C 325	14.8	1.1	20	1	AX465326	ACCESSION:AX465326
C 326	14.8	1.1	20	1	AX524879	ACCESSION:AX524879
C 327	14.8	1.1	20	1	AX547087	ACCESSION:AX547087
C 328	14.8	1.1	20	1	AX547417	ACCESSION:AX547417
C 329	14.8	1.1	20	1	AX547421	ACCESSION:AX547421
C 330	14.8	1.1	20	1	AX556124	ACCESSION:AX556124
C 331	14.8	1.1	20	1	AX556139	ACCESSION:AX556139
C 332	14.8	1.1	20	1	AX664307	ACCESSION:AX664307
C 333	14.8	1.1	20	1	AX664308	ACCESSION:AX664308
C 334	14.8	1.1	20	1	AX708893	ACCESSION:AX708893
C 335	14.8	1.1	20	1	AX741040	ACCESSION:AX741040
C 336	14.8	1.1	20	1	AX741052	ACCESSION:AX741052
C 337	14.8	1.1	20	1	BD008523	ACCESSION:BD008523
C 338	14.8	1.1	20	1	BD080522	ACCESSION:BD080522
C 339	14.8	1.1	20	1	BD107450	ACCESSION:BD107450
C 340	14.8	1.1	20	1	BD174543	ACCESSION:BD174543
C 341	14.8	1.1	21	1	AR080294	ACCESSION:AR080294
C 342	14.8	1.1	21	1	AR084521	ACCESSION:AR084521
C 343	14.8	1.1	21	1	AR084524	ACCESSION:AR084524
C 344	14.8	1.1	21	1	AR095412	ACCESSION:AR095412
C 345	14.8	1.1	21	1	AR103542	ACCESSION:AR103542
C 346	14.8	1.1	21	1	AR118155	ACCESSION:AR118155
C 347	14.8	1.1	21	1	AR153849	ACCESSION:AR153849
C 348	14.8	1.1	21	1	BD224108	ACCESSION:BD224108
C 349	14.8	1.1	21	1	CQ846797	ACCESSION:CQ846797
C 350	14.8	1.1	21	1	I36166	ACCESSION:I36166
C 351	14.8	1.1	21	1	I65744	ACCESSION:I65744
C 352	14.8	1.1	21	1	I84433	ACCESSION:I84433
C 353	14.8	1.1	21	1	AR322245	ACCESSION:AR322245
C 354	14.8	1.1	21	1	AR452591	ACCESSION:AR452591
C 355	14.8	1.1	21	1	AR104720	ACCESSION:AR104720
C 356	14.8	1.1	21	1	AX355812	ACCESSION:AX355812
C 357	14.8	1.1	21	1	AX547773	ACCESSION:AX547773
C 358	14.8	1.1	21	1	AX825123	ACCESSION:AX825123
C 359	14.8	1.1	21	1	AX825124	ACCESSION:AX825124
C 360	14.8	1.1	21	1	AX825125	ACCESSION:AX825125
C 361	14.8	1.1	21	1	AX825126	ACCESSION:AX825126
C 362	14.8	1.1	21	1	AX825127	ACCESSION:AX825127
C 363	14.8	1.1	21	1	AX825128	ACCESSION:AX825128
C 364	14.8	1.1	21	1	AX825129	ACCESSION:AX825129
C 365	14.8	1.1	21	1	AX825130	ACCESSION:AX825130
C 366	14.8	1.1	21	1	AX825131	ACCESSION:AX825131
C 367	14.8	1.1	21	1	AX825132	ACCESSION:AX825132
C 368	14.8	1.1	21	1	AX825133	ACCESSION:AX825133
C 369	14.8	1.1	21	1	AX825134	ACCESSION:AX825134
C 370	14.8	1.1	21	1	AX825139	ACCESSION:AX825139
C 371	14.8	1.1	21	1	AX825140	ACCESSION:AX825140
C 372	14.8	1.1	21	1	AX825141	ACCESSION:AX825141
C 373	14.8	1.1	21	1	AX825142	ACCESSION:AX825142
C 374	14.8	1.1	21	1	AX825143	ACCESSION:AX825143
C 375	14.8	1.1	21	1	AX825144	ACCESSION:AX825144
C 376	14.8	1.1	21	1	AX825145	ACCESSION:AX825145
C 377	14.8	1.1	21	1	AX825146	ACCESSION:AX825146
C 378	14.8	1.1	21	1	AX825147	ACCESSION:AX825147
C 379	14.8	1.1	21	1	AX825148	ACCESSION:AX825148
C 380	14.8	1.1	21	1	AX825149	ACCESSION:AX825149
C 381	14.8	1.1	21	1	AX825150	ACCESSION:AX825150
C 382	14.8	1.1	21	1	AX825156	ACCESSION:AX825156
C 383	14.8	1.1	21	1	AX825157	ACCESSION:AX825157
C 384	14.8	1.1	21	1	AX825158	ACCESSION:AX825158
C 385	14.8	1.1	21	1	AX825160	ACCESSION:AX825160
C 386	14.8	1.1	21	1	AX825161	ACCESSION:AX825161
C 387	14.8	1.1	21	1	AX825162	ACCESSION:AX825162
C 388	14.8	1.1	21	1	AX825164	ACCESSION:AX825164
C 389	14.8	1.1	21	1	AX825165	ACCESSION:AX825165
C 390	14.8	1.1	21	1	AX825166	ACCESSION:AX825166
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C 392	14.8	1.1	21	1	BD087491	ACCESSION:BD087491
C 393	14.8	1.1	22	1	BD129772	ACCESSION:BD129772
C 394	14.6	1.0	19	1	A79657	ACCESSION:A79657
C 395	14.6	1.0	19	1	AR147331	ACCESSION:AR147331
C 396	14.6	1.0	19	1	AX825107	ACCESSION:AX825107
C 397	14.6	1.0	21	1	AX825117	ACCESSION:AX825117
C 398	14.6	1.0	22	1	BD085544	ACCESSION:BD085544

C 399	14.6	1.0	25	1	AX692829	ACCESSION:AX692829
C 400	14.4	1.0	17	1	AR089217	ACCESSION:AR089217
C 401	14.4	1.0	17	1	BD201511	ACCESSION:BD201511
C 402	14.4	1.0	17	1	BD201512	ACCESSION:BD201512
C 403	14.4	1.0	17	1	BD258338	ACCESSION:BD258338
C 404	14.4	1.0	17	1	BD258339	ACCESSION:BD258339
C 405	14.4	1.0	17	1	CQ616719	ACCESSION:CQ616719
C 406	14.4	1.0	17	1	CQ616720	ACCESSION:CQ616720
C 407	14.4	1.0	17	1	CO617530	ACCESSION:CO617530
C 408	14.4	1.0	17	1	CO617531	ACCESSION:CO617531
C 409	14.4	1.0	17	1	AR187057	ACCESSION:AR187057
C 410	14.4	1.0	17	1	AR285940	ACCESSION:AR285940
C 411	14.4	1.0	17	1	AR323667	ACCESSION:AR323667
C 412	14.4	1.0	17	1	AR397930	ACCESSION:AR397930
C 413	14.4	1.0	17	1	AR457782	ACCESSION:AR457782
C 414	14.4	1.0	17	1	AR457783	ACCESSION:AR457783
C 415	14.4	1.0	17	1	AR458593	ACCESSION:AR458593
C 416	14.4	1.0	17	1	AR458594	ACCESSION:AR458594
C 417	14.4	1.0	17	1	AX674744	ACCESSION:AX674744
C 418	14.4	1.0	17	1	AX729555	ACCESSION:AX729555
C 419	14.4	1.0	17	1	AX730083	ACCESSION:AX730083
C 420	14.4	1.0	17	1	AX761696	ACCESSION:AX761696
C 421	14.4	1.0	18	1	AB9378	ACCESSION:AB9378
C 422	14.4	1.0	18	1	AR106885	ACCESSION:AR106885
C 423	14.4	1.0	18	1	AX662307	ACCESSION:AX662307
C 424	14.4	1.0	18	1	BD066891	ACCESSION:BD066891
C 425	14.4	1.0	18	1	BD096088	ACCESSION:BD096088
C 426	14.4	1.0	20	1	AX0129	ACCESSION:AX0129
C 427	14.4	1.0	20	1	BD244919	ACCESSION:BD244919
C 428	14.4	1.0	20	1	AR298254	ACCESSION:AR298254
C 429	14.4	1.0	20	1	AR315939	ACCESSION:AR315939
C 430	14.4	1.0	20	1	AR491020	ACCESSION:AR491020
C 431	14.4	1.0	20	1	AX048436	ACCESSION:AX048436
C 432	14.4	1.0	20	1	AX053082	ACCESSION:AX053082
C 433	14.4	1.0	20	1	AX053091	ACCESSION:AX053091
C 434	14.4	1.0	20	1	AX184293	ACCESSION:AX184293
C 435	14.4	1.0	20	1	AX546302	ACCESSION:AX546302
C 436	14.4	1.0	20	1	AX546392	ACCESSION:AX546392
C 437	14.2	1.0	19	1	AB8414	ACCESSION:AB8414
C 438	14.2	1.0	19	1	AG0381	ACCESSION:AG0381
C 439	14.2	1.0	19	1	BD184608	ACCESSION:BD184608
C 440	14.2	1.0	19	1	AR294423	ACCESSION:AR294423
C 441	14.2	1.0	19	1	AX132831	ACCESSION:AX132831
C 442	14.2	1.0	19	1	AX352893	ACCESSION:AX352893
C 443	14.2	1.0	19	1	AX362738	ACCESSION:AX362738
C 444	14.2	1.0	19	1	AX742755	ACCESSION:AX742755
C 445	14.2	1.0	19	1	BD065927	ACCESSION:BD065927
C 446	14.2	1.0	20	1	AA0129	ACCESSION:AA0129
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C 449	14.2	1.0	20	1	AR086304	ACCESSION:AR086304
C 450	14.2	1.0	20	1	AR086311	ACCESSION:AR086311
C 451	14.2	1.0	20	1	AR129739	ACCESSION:AR129739
C 452	14.2	1.0	20	1	AR142677	ACCESSION:AR142677
C 453	14.2	1.0	20	1	AR158717	ACCESSION:AR158717
C 454	14.2	1.0	20	1	AR158718	ACCESSION:AR158718
C 455	14.2	1.0	20	1	AR163731	ACCESSION:AR163731
C 456	14.2	1.0	20	1	AR169510	ACCESSION:AR169510
C 457	14.2	1.0	20	1	AR176870	ACCESSION:AR176870
C 458	14.2	1.0	20	1	AR176877	ACCESSION:AR176877
C 459	14.2	1.0	20	1	EO5497	ACCESSION:EO5497
C 460	14.2	1.0	20	1	E28096	ACCESSION:E28096
C 461	14.2	1.0	20	1	E44159	ACCESSION:E44159
C 462	14.2	1.0	20	1	ES9328	ACCESSION:ES9328
C 463	14.2	1.0	20	1	II7092	ACCESSION:II7092
C 464	14.2	1.0	20	1	II6387	ACCESSION:II6387
C 465	14.2	1.0	20	1	AR200176	ACCESSION:AR200176
C 466	14.2	1.0	20	1	AR224778	ACCESSION:AR224778
C 467	14.2	1.0	20	1	AR307902	ACCESSION:AR307902
C 468	14.2	1.0	20	1	AR313596	ACCESSION:AR313596
C 469	14.2	1.0	20	1	AR314906	ACCESSION:AR314906
C 470	14.2	1.0	20	1	AR371268	ACCESSION:AR371268
C 471	14.2	1.0	20	1	AR428075	ACCESSION:AR428075

472	14.2	1.0	20	1	AR489489	ACCESSION:AR489489
473	14.2	1.0	20	1	AR491100	ACCESSION:AR491100
474	14.2	1.0	20	1	AX078001	ACCESSION:AX078001
475	14.2	1.0	20	1	AX078001	ACCESSION:AX078001
476	14.2	1.0	20	1	AX137428	ACCESSION:AX137428
477	14.2	1.0	20	1	AX293619	ACCESSION:AX293619
478	14.2	1.0	20	1	AX298452	ACCESSION:AX298452
479	14.2	1.0	20	1	AX452909	ACCESSION:AX452909
480	14.2	1.0	20	1	AX462672	ACCESSION:AX462672
481	14.2	1.0	20	1	AX462737	ACCESSION:AX462737
482	14.2	1.0	20	1	AX750458	ACCESSION:AX750458
483	14.2	1.0	20	1	AX785487	ACCESSION:AX785487
484	14.2	1.0	20	1	AX804971	ACCESSION:AX804971
485	14.2	1.0	20	1	BD003450	ACCESSION:BD003450
486	14.2	1.0	20	1	BD056369	ACCESSION:BD056369
487	14.2	1.0	20	1	BD056371	ACCESSION:BD056371
488	14.2	1.0	20	1	BD089539	ACCESSION:BD089539
489	14.2	1.0	20	1	BD161924	ACCESSION:BD161924
C 490	14.2	1.0	20	1	S4717654	ACCESSION:S4717654
C 491	14.2	1.0	20	1	AB068086	ACCESSION:AB068086

ALIGNMENTS

RESULT 1
AX042782
DEFINITION Sequence 348 from Patent WO0065088.
ACCESSION AX042782
VERSION AX042782.1 GI:11341390

SOURCE
ORGANISM
synthetic construct
artificial sequences.

REFERENCE
AUTHORS Ulfendahl, P. J. and Wong, K. C.
TITLE Primers for identifying typing or classifying nucleic acids
JOURNML Patent: WO 0065088-A 348 02-NOV-2000;
Amerham Pharmacia Biotech AB (SE)

FEATURES
source
1..25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="HLA-B Homozygote Primer Sequence"

Query Match 1.3%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 15;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1308 TTTTATTTTACAGACAGATCAT 1332
Db 1 TTTTATTTTACAGACAGATCTT 25

RESULT 2
AR370697/c
LOCUS AR370697 25 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 10 from patent US 6395275.
ACCESSION AR370697
VERSION AR370697.1 GI:34607513

KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.

REFERENCE
AUTHORS Barbas, C. F., Burton, D. R. and Lerner, R. A.
TITLE Synthetic human neutralizing monoclonal antibodies to human
immunodeficiency virus

JOURNAL Patent: US 6395275-A 10 28-MAY-2002;
FEATURES
source
1..25
Location/Qualifiers

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/organism="unknown"
/mol_type="genomic DNA"

Query Match      1.3%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy      1089 AAGGTTCTCTAGCTCACTTC 1111
Db      24 AAGGTTCTCTCTGTCAAGCTTC 2

RESULT 3
AX117632/c
LOCUS      AX117632      25 bp      DNA      linear      PAT 11-MAY-2001
DEFINITION Sequence 2755 from Patent WO0129262.
ACCESSION  AX117632
VERSION     AX117632.1. GI:14034583
KEYWORDS
SOURCE      .
ORGANISM    synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Picoult-Newburg, L. and Pohl, M.
TITLE       Genotyping reagents, kits and methods of use thereof
JOURNAL     Patent: WO 0129262-A 2755 26-APR-2001;
            Orchid Biosciences, Inc. (US)
FEATURES
SOURCE      1..25
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="primer"

Query Match      1.3%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy      1303 CTATTTTATTTTTCAGACAC 1325
Db      25 CTTTCTTTTCTTTTTCAGACAC 3

RESULT 4
AX692829
LOCUS      AX692829      25 bp      DNA      linear      PAT 31-MAR-2003
DEFINITION Sequence 5561 from Patent EP1281758.
ACCESSION  AX692829
VERSION     AX692829.1 GI:29415792
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1
AUTHORS     Shannon, M., Gu, Y. and Nguyen, C.T.
TITLE       Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
JOURNAL     Patent: EP 1281758-A 5561 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES
SOURCE      1..25
            location/Qualifiers
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            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      1.3%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy      1306 TTTTCTTATTTTCAGACACAGA 1328
Db      3 TTTTCTTATTTTTCAGACACAGA 25
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RESULT 5
AX692830
LOCUS      AX692830      25 bp      DNA      linear      PAT 31-MAR-2003
DEFINITION Sequence 5562 from Patent EP1281758.
ACCESSION  AX692830
VERSION     AX692830.1 GI:29415793
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1
AUTHORS     Shannon, M., Gu, Y. and Nguyen, C.T.
TITLE       Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
JOURNAL     Patent: EP 1281758-A 5562 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES
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            /mol_type="unassigned DNA"
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Query Match      1.3%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy      1306 TTTTCTTATTTTCAGACACAGA 1328
Db      2 TTTTCTTATTTTTCAGACACAGA 24

RESULT 6
AX692831
LOCUS      AX692831      25 bp      DNA      linear      PAT 31-MAR-2003
DEFINITION Sequence 5563 from Patent EP1281758.
ACCESSION  AX692831
VERSION     AX692831.1 GI:29415794
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1
AUTHORS     Shannon, M., Gu, Y. and Nguyen, C.T.
TITLE       Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
JOURNAL     Patent: EP 1281758-A 5563 05-FEB-2003;
            Aeomica, Inc. (US)
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Query Match      1.3%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy      1306 TTTTCTTATTTTCAGACACAGA 1328
Db      1 TTTTCTTATTTTTCAGACACAGA 23

RESULT 7
AX825106/c
LOCUS      AX825106      21 bp      DNA      linear      PAT 11-DEC-2003
DEFINITION Sequence 4 from Patent WO03072818.
ACCESSION  AX825106
VERSION     AX825106.1 GI:39750835
KEYWORDS
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SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 4 04-SEP-2003;
Degussa Bioactives GmbH (DE)
LOCATION/Qualifiers
FEATURES
source 1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
misc_binding 1
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modified_base 3
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Best Local Similarity 90.5%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1517 ATTAAAAAAGTAAAA 1537
Db 21 ATTAAAAAAGTAAAA 1
RESULT 8
AR431307/c 24 bp DNA linear PAT 18-DEC-2003
LOCUS AR431307
DEFINITION Sequence 1 from patent US 6651008.
ACCESSION AR431307
VERSION AR431307.1 GI:40193275
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Valsberg, E.A., Adams, C.L., Sabry, J.H. and Crompton, A.M.
TITLE Database system including computer code for predictive cellular
bioinformatics
JOURNAL Patent: US 6651008-A 1 18-NOV-2003;
LOCATION/Qualifiers
FEATURES
source 1. .24
/organism="unknown"
/mol_type="genomic DNA"
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Best Local Similarity 86.4%; Pred. No. 36;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1516 AATTAAAAAAGTAAAA 1537
Db 24 AATTAAAAAAGTAAAA 3

RESULT 9
AR253000/c 21 bp DNA linear PAT 20-DEC-2002
LOCUS AR253000
DEFINITION Sequence 100 from patent US 6479236.
ACCESSION AR253000
VERSION AR253000.1 GI:27301349
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Penny, L. and Galvin, M.
TITLE Genotyping the human UDP-glucuronosyltransferase 1 (UGT1) gene
JOURNAL Patent: US 6479236-A 100 12-NOV-2002;
LOCATION/Qualifiers
FEATURES
source 1. .21
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.2%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 53;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 344 CCTGCCGCCGCCGAGAG 363
Db 21 CCAGCACGCCGCCGAGAG 2
RESULT 10
AX825103/c 21 bp DNA linear PAT 11-DEC-2003
LOCUS AX825103
DEFINITION Sequence 1 from Patent WO03072818.
ACCESSION AX825103
VERSION AX825103.1 GI:39750832
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 1 04-SEP-2003;
Degussa Bioactives GmbH (DE)
LOCATION/Qualifiers
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source 1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
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/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
misc_binding 1
/bound_moiety="Biotin"
modified_base 3
/note="LNA-T (Locked Nucleic Acid)"
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Query Match 1.2%; Score 16.8; DB 1; Length 21;

Best Local Similarity 90.0%; Pred. No. 53;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 11
AX825104/c 21 bp DNA linear PAT 11-DEC-2003
LOCUS AX825104
DEFINITION Sequence 3 from Patent WO03072818.
ACCESSION AX825104
VERSION AX825104.1 GI:39750833
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNML Patent: WO 03072818-A 2 04-SEP-2003;
Degussa Bioactives GmbH (DE)
location/Qualifiers

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Sequenz:Capture-Oligonukleotid"
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misc_binding 1
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Query Match 1.2%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 53;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1518 TTTAAAAAAAAGTAAA 1537
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20 TTTAAAAAAAAGTAAA 1

RESULT 12
AX825105/c 21 bp DNA linear PAT 11-DEC-2003
LOCUS AX825105
DEFINITION Sequence 3 from Patent WO03072818.
ACCESSION AX825105
VERSION AX825105.1 GI:39750834
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids

JOURNML Patent: WO 03072818-A 3 04-SEP-2003;
Degussa Bioactives GmbH (DE)
location/Qualifiers

FEATURES 1..21
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/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
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/bound_moiety="Biotin"
misc_binding 1
/note="LNA-T (Locked Nucleic Acid) "
modified_base 3
/mod_base=OTHER
modified_base 6
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modified_base 18
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER

Query Match 1.2%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 53;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1518 TTTAAAAAAAAGTAAA 1537
|||||
20 TTTAAAAAAAAGTAAA 1

RESULT 13
AX825151/c 21 bp DNA linear PAT 11-DEC-2003
LOCUS AX825151
DEFINITION Sequence 49 from Patent WO03072818.
ACCESSION AX825151
VERSION AX825151.1 GI:39750880
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNML Patent: WO 03072818-A 49 04-SEP-2003;
Degussa Bioactives GmbH (DE)
location/Qualifiers

FEATURES 1..21
source 1.
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/db_xref="taxon:32630"
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Sequenz:Capture-Oligonukleotid"
1
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misc_binding 1
/note="LNA-T (Locked Nucleic Acid) "
modified_base 3
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modified_base 6
/note="LNA-T (Locked Nucleic Acid) "
modified_base 9
/note="LNA-T (Locked Nucleic Acid) "
modified_base 12
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER

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/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
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modified_base
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modified_base
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18
/mod_base=OTHER

Query Match
Best Local Similarity 90.0%; Pred. No. 53;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1518 TTTAAAAAAAGTAAAA 1537
Db 21 TTTAAAAAAAGTAAAA 2

RESULT 14
AR261539 24 bp DNA linear PAT 29-JAN-2003
LOCUS AR261539 Sequence 6 from patent US 6322971.
DEFINITION AR261539
ACCESSION AR261539.1 GI:28072607
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Chetverin,A.B. and Kramer,F.R.
TITLE Oligonucleotide arrays and their use for sorting, isolating,
sequencing, and manipulating nucleic acids
JOURNAL Patent: US 6322971-A 6 27-NOV-2001;
FEATURES
Source 1. 24
/mol_type="genomic DNA"

Query Match
Best Local Similarity 90.0%; Pred. No. 46;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1518 TTTAAAAAAAGTAAAA 1537
Db 2 TTTAAAAAAAGTAAAA 21

RESULT 15
A01996 23 bp DNA linear PAT 21-MAY-1993
LOCUS A01996 Reverse complement.
DEFINITION A01996
ACCESSION A01996
VERSION A01996.1 GI:344528
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 23)
AUTHORS
JOURNAL Patent: WO 8404538-A 24 22-NOV-1984;
FEATURES
Source 1. 23
/mol_type="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 82.6%; Pred. No. 55;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1248 TTTGTTTGTATTATCAT 1270
Db 1 TTTGTTTGTATTATCAT 23
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RESULT 16
A06442 23 bp DNA linear PAT 21-MAY-1993
LOCUS A06442 Reverse complement, duplicate.
DEFINITION A06442
ACCESSION A06442.1 GI:411262
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 23)
AUTHORS Edens,L., Russell,S.W., Visser,C. and Vertips,C.T.
TITLE Improvements in the expression of newly introduced genes in yeast
cells
JOURNAL Patent: EP 0129268-A 25 27-DEC-1984;
FEATURES
Source UNILEVER NV; UNILEVER PLC
Location/Qualifiers
1. 23
/mol_type="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 82.6%; Pred. No. 55;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1248 TTTGTTTGTATTATCAT 1270
Db 1 TTTGTTTGTATTATCAT 23

RESULT 17
AR294636 19 bp DNA linear PAT 12-JUN-2003
LOCUS AR294636 Sequence 6371 from patent US 6537751.
DEFINITION AR294636
ACCESSION AR294636
VERSION AR294636.1 GI:31681920
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 6371 25-MAR-2003;
FEATURES
Source 1. 19
/mol_type="genomic DNA"

Query Match
Best Local Similarity 94.4%; Pred. No. 75;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1480 ATTCCAGCTATACATTAA 1497
Db 1 ATTCCAGCTATACATTAA 18

RESULT 18
AR084566 21 bp DNA linear PAT 01-SEP-2000
LOCUS AR084566/c
DEFINITION AR084566 Sequence 55 from patent US 5981185.
ACCESSION AR084566
VERSION AR084566.1 GI:10011337
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
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AUTHORS Watson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
 TITLE Oligonucleotide repeat arrays
 JOURNAL Patent: US 5981185-A 55 09-NOV-1999;
 FEATURES Location/Qualifiers
 SOURCE 1..21
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 1.2%; Score 16.2; DB 1; Length 21;
 Best Local Similarity 85.7%; Pred. No. 76;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 424 GTGGCGGCTGCGCGCGCGCGC 444
 |||||
 21 GCGCGCGCGCGCGCGCGCGC 1

RESULT 19
 AR084578/c AR084578 21 bp DNA linear PAT 01-SEP-2000
 LOCUS Sequence 67 from patent US 5981185.
 DEFINITION AR084578
 ACCESSION AR084578.1 GI:10011349
 VERSION
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.

REFERENCE 1 (bases 1 to 21)
 AUTHORS Watson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
 TITLE Oligonucleotide repeat arrays
 JOURNAL Patent: US 5981185-A 67 09-NOV-1999;
 FEATURES Location/Qualifiers
 SOURCE 1..21
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 1.2%; Score 16.2; DB 1; Length 21;
 Best Local Similarity 85.7%; Pred. No. 76;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 426 GCGCGCTGCGCGCGCGCGC 446
 |||||
 21 GCGCGCGCGCGCGCGCGCGC 1

RESULT 20
 AR084579 AR084579 21 bp DNA linear PAT 01-SEP-2000
 LOCUS Sequence 68 from patent US 5981185.
 DEFINITION AR084579
 ACCESSION AR084579.1 GI:10011350
 VERSION
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.

REFERENCE 1 (bases 1 to 21)
 AUTHORS Watson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
 TITLE Oligonucleotide repeat arrays
 JOURNAL Patent: US 5981185-A 68 09-NOV-1999;
 FEATURES Location/Qualifiers
 SOURCE 1..21
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 1.2%; Score 16.2; DB 1; Length 21;
 Best Local Similarity 85.7%; Pred. No. 76;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 424 GTGGCGGCTGCGCGCGCGCGC 444
 |||||
 1 GCGCGCGCGCGCGCGCGCGC 21

RESULT 21
 AR084582 AR084582 21 bp DNA linear PAT 01-SEP-2000
 LOCUS Sequence 71 from patent US 5981185.
 DEFINITION AR084582
 ACCESSION AR084582.1 GI:10011353
 VERSION
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.

REFERENCE 1 (bases 1 to 21)
 AUTHORS Watson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
 TITLE Oligonucleotide repeat arrays
 JOURNAL Patent: US 5981185-A 71 09-NOV-1999;
 FEATURES Location/Qualifiers
 SOURCE 1..21
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 1.2%; Score 16.2; DB 1; Length 21;
 Best Local Similarity 85.7%; Pred. No. 76;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 426 GCGCGCTGCGCGCGCGCGC 446
 |||||
 1 GCGCGCGCGCGCGCGCGCGC 21

RESULT 22
 AR093142 AR093142 21 bp DNA linear PAT 08-SEP-2000
 LOCUS Sequence 11 from patent US 5998596.
 DEFINITION AR093142
 ACCESSION AR093142.1 GI:10019894
 VERSION
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.

REFERENCE 1 (bases 1 to 21)
 AUTHORS Bergan,R. and Neckers,L.
 TITLE Inhibition of protein kinase activity by aptameric action of oligonucleotides
 JOURNAL Patent: US 5998596-A 11 07-DEC-1999;
 FEATURES Location/Qualifiers
 SOURCE 1..21
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 1.2%; Score 16.2; DB 1; Length 21;
 Best Local Similarity 85.7%; Pred. No. 76;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 426 GCGCGCTGCGCGCGCGCGC 446
 |||||
 1 GCGCGCGCGCGCGCGCGCGC 21

RESULT 23
 C0830491 C0830491 21 bp DNA linear PAT 12-JUL-2004
 LOCUS Sequence 3 from Patent WO2004055153.
 DEFINITION C0830491
 ACCESSION C0830491.1 GI:50250831
 VERSION
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 Unclassified.

REFERENCE 1
 AUTHORS Schluesener,H. and Wendel,H.P.
 TITLE Devices coated with substances that mediate the adhesion of biological material
 JOURNAL Patent: WO 2004055153-A 3 01-JUL-2004;
 Eberhard-Karls-Universitaet Tuebingen (DE)

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FEATURES
  source
    1. .21
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="Nukleotidesequenz"

Query Match
  1.2%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 76;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 424 GTGGCGCGTGGCGCGCGCGC 444
Db 1 GCGGCGCGCGCGCGCGCGC 21

RESULT 24
LOCUS AR279103 21 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 236 from patent US 6514694.
ACCESSION AR279103
VERSION AR279103.1 GI:29713746
KEYWORDS
SOURCE
  ORGANISM
    Unknown.
  REFERENCE
    1 (bases 1 to 21)
      AUTHORS
        Milhausen,M.J.
      TITLE
        Methods for the detection of encysted parasites
      JOURNAL
        Patent: US 6514694-A 236 04-FEB-2003;
      FEATURES
        Location/Qualifiers
          1. .21
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match
  1.2%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 76;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 996 TTCTGTGAGATTAACGCTG 1016
Db 1 TGCTGTGAGATTAATGCTG 21

RESULT 25
LOCUS AX383931 21 bp DNA linear PAT 19-MAR-2002
DEFINITION Sequence 34 from Patent WO0214546.
ACCESSION AX383931
VERSION AX383931.1 GI:19577502
KEYWORDS
SOURCE
  ORGANISM
    Plasmodium falciparum (malaria parasite P. falciparum)
  REFERENCE
    1
      AUTHORS
        Fritzsche,M.
      TITLE
        Use of microbial dna sequences for the identification of human
        diseases
      JOURNAL
        Patent: WO 0214546-A 34 21-FEB-2002;
      FEATURES
        Location/Qualifiers
          1. .21
            /organism="Plasmodium falciparum"
            /mol_type="unassigned DNA"
            /db_xref="taxon:5833"

Query Match
  1.2%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 76;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1509 TACTGTTAATTAATAAAAAA 1529
Db 21 TATTTTATTTAATAAAAAA 1
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RESULT 26
LOCUS AX713257 21 bp DNA linear PAT 11-APR-2003
DEFINITION Sequence 143 from Patent WO03018837.
ACCESSION AX713257
VERSION AX713257.1 GI:29823846
KEYWORDS
  ORGANISM
    synthetic construct
    synthetic construct
    artificial sequences.
  REFERENCE
    1
      Wasmuth,S., Schnakenberg,E. and Luetig,M.
      TITLE
        Method and diagnostic kit for the molecular diagnosis of
        pharmacologically relevant genes
      JOURNAL
        Patent: WO 03018837-A 143 06-MAR-2003;
      FEATURES
        Location/Qualifiers
          1. .21
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Oligonukleotid"

Query Match
  1.2%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 76;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1248 TTTGTTTGTTTTATATCAG 1268
Db 21 TTTTATTAATTTTATATCAG 1

RESULT 27
LOCUS AX825110 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 8 from Patent WO03072818.
ACCESSION AX825110
VERSION AX825110.1 GI:39750839
KEYWORDS
SOURCE
  ORGANISM
    synthetic construct
    synthetic construct
    artificial sequences.
  REFERENCE
    1
      Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
      TITLE
        Method for sorting single-stranded nucleic acids
      JOURNAL
        Patent: WO 03072818-A 8 04-SEP-2003;
      FEATURES
        Location/Qualifiers
          1. .21
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Beschreibung der kuenstlichen
            Sequenz: Capture-Oligonukleotid"
          1
            /bound_moiety="Biotin"
          3
            /note="LNA-T (Locked Nucleic Acid)"
            /mod_base=OTHER
          6
            /note="LNA-T (Locked Nucleic Acid)"
            /mod_base=OTHER
          9
            /note="LNA-T (Locked Nucleic Acid)"
            /mod_base=OTHER
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            /note="LNA-T (Locked Nucleic Acid)"
            /mod_base=OTHER
          15
            /note="LNA-T (Locked Nucleic Acid)"
            /mod_base=OTHER
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	modified_base	18	/note="LNA-T (Locked Nucleic Acid)" /mod_base=OTHER	
Query Match		1.2%; Score 16.2; DB 1; Length 21;		
Best Local Similarity	85.7%;	Pred. No. 76;		
Matches	18; Conservative	0; Mismatches	3; Indels	0; Gaps
Oy	1517 ATTAAAAAAAAAAAAAGTAAAA	1537		
Dn	21 AGTAAAAAAAAAAAAAAAAAAAAAA	1		
RESULT 28				
AX825114/c		21 bp	DNA	linear PAT 11-DEC-2003
LOCUS	AX825114			
DEFINITION	Sequence 12 from Patent WO03072818.			
ACCESSION	AX825114			
VERSION	AX825114.1	GI:39750843		
KEYWORDS				
SOURCE				
ORGANISM				
synthetic construct				
artificial sequences.				
REFERENCE				
1				
AUTHORS	Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.			
TITLE	Method for sorting single-stranded nucleic acids			
JOURNAL	Patent: WO 03072818-A 12 04-SBP-2003;			
DEGENSA Bioactives GmbH (DE)				
location/Qualifiers				
FEATURES				
source				
1..21				
/organism="synthetic construct"				
/mol_type="unassigned DNA"				
/db_xref="taxon:32630"				
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1				
/bound_molecyl="Biotin"				
3				
/note="LNA-T (Locked Nucleic Acid)"				
6				
/mod_base=OTHER				
modified_base				
9				
/note="LNA-T (Locked Nucleic Acid)"				
12				
/mod_base=OTHER				
modified_base				
15				
/note="LNA-T (Locked Nucleic Acid)"				
18				
/mod_base=OTHER				
modified_base				
18				
/note="LNA-T (Locked Nucleic Acid)"				
/mod_base=OTHER				
Query Match		1.2%; Score 16.2; DB 1; Length 21;		
Best Local Similarity	85.7%;	Pred. No. 76;		
Matches	18; Conservative	0; Mismatches	3; Indels	0; Gaps
Oy	1517 ATTAAAAAAAAAAAAAGTAAAA	1537		
Dn	21 AGTAAAAAAAAAAAAAAAAAAAAAA	1		
RESULT 29				
AX825118/c		21 bp	DNA	linear PAT 11-DEC-2003
LOCUS	AX825118			
DEFINITION	Sequence 16 from Patent WO03072818.			
ACCESSION	AX825118			
VERSION	AX825118.1	GI:39750847		
KEYWORDS				
SOURCE				
synthetic construct				

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ORGANISM      synthetic construct
              artificial sequences.
REFERENCE     1.
AUTHORS      Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE        Method for sorting single-stranded nucleic acids
JOURNAL      Patent: WO 03072818-A 16 04-SEP-2003;
              Degussa Bioactives GmbH (DE)
FEATURES
  source      Location/Qualifiers
              1..21
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                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Beschreibung der kuenstlichen
                Sequenz:Capture-Oligonukleotid"
  misc_binding
    1
    /bound_moiety="Biotin"
  modified_base
    3
    /note="UNA-T (Locked Nucleic Acid)"
  modified_base
    6
    /note="UNA-T (Locked Nucleic Acid)"
  modified_base
    9
    /note="UNA-T (Locked Nucleic Acid)"
  modified_base
    12
    /note="UNA-T (Locked Nucleic Acid)"
  modified_base
    15
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  modified_base
    18
    /note="UNA-T (Locked Nucleic Acid)"
  modified_base
    21
    /note="UNA-T (Locked Nucleic Acid)"
  modified_base
    24
    /mod_base=OTHER

Query Match      1.2%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 76;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy      1516 AATTAAGTAAAGTAA 1536
Db      21 AATTAAGTAAAGTAA 1

RESULT 30
AX825122/c 21 bp DNA linear PAT 11-DEC-2003
LOCUS      AX825122
DEFINITION Sequence 20 from Patent WO03072818.
ACCESSION  AX825122
VERSION     AX825122.1 GI:39750851
KEYWORDS
SOURCE
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 20 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES
  source      Location/Qualifiers
              1..21
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Beschreibung der kuenstlichen
                Sequenz:Capture-Oligonukleotid"
  misc_binding
    1
    /bound_moiety="Biotin"
  modified_base
    3
    /note="UNA-T (Locked Nucleic Acid)"
  modified_base
    6
    /mod_base=OTHER
  modified_base
    9
    /note="UNA-T (Locked Nucleic Acid)"
  modified_base
    12
    /note="UNA-T (Locked Nucleic Acid)"
  modified_base
    15
    /mod_base=OTHER
  modified_base
    18
    /note="UNA-T (Locked Nucleic Acid)"
  modified_base
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    /note="UNA-T (Locked Nucleic Acid)"
  modified_base
    24
    /mod_base=OTHER

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      modified_base      9 /mod_base=OTHER
                           /note="LNA-T (Locked Nucleic Acid)"
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      modified_base      15 /mod_base=OTHER
                           /note="LNA-T (Locked Nucleic Acid)"
      modified_base      18 /mod_base=OTHER
                           /note="LNA-T (Locked Nucleic Acid)"
                           /mod_base=OTHER

Query Match      1.2%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 76;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1517 ATTAAGTAAAAAGTAAAA 1537
Db      21 ATCAAAAAAAAAAAAAAAAA 1

RESULT 31
LOCUS      AX825138/c      21 bp      DNA      linear      PAT 11-DEC-2003
DEFINITION      Sequence 36 from Patent WO03072818.
ACCESSION      AX825138
VERSION      AX825138.1 GI:39750867
KEYWORDS
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE      1
AUTHORS      Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE      Method for sorting single-stranded nucleic acids
JOURNAL      Patent: WO 03072818-A 36 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
            Location/Qualifiers
FEATURES
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        1..21
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Beschreibung der kuenstlichen
            Sequenz: Capture-Oligonukleotid"
    misc_binding
        1
            /bound_moiety="Biotin"
    modified_base
        3 /note="LNA-T (Locked Nucleic Acid)"
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        6 /note="LNA-T (Locked Nucleic Acid)"
            /mod_base=OTHER
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            /mod_base=OTHER
    modified_base
        18 /note="LNA-T (Locked Nucleic Acid)"
            /mod_base=OTHER
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Query Match      1.2%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 76;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1517 ATTAAGTAAAAAGTAAAA 1537
Db      21 ATGAAAAAAAAAAAAAAAAA 1
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                           /note="LNA-T (Locked Nucleic Acid)"
      modified_base      15 /mod_base=OTHER
                           /note="LNA-T (Locked Nucleic Acid)"
      modified_base      18 /mod_base=OTHER
                           /note="LNA-T (Locked Nucleic Acid)"
                           /mod_base=OTHER

Query Match      1.2%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 76;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1517 ATTAAGTAAAAAGTAAAA 1537
Db      21 ATTAAGTAAAAAGTAAAA 1

RESULT 32
LOCUS      AX825154/c      21 bp      DNA      linear      PAT 11-DEC-2003
DEFINITION      Sequence 52 from Patent WO03072818.
ACCESSION      AX825154
VERSION      AX825154.1 GI:39750883
KEYWORDS
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE      1
AUTHORS      Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE      Method for sorting single-stranded nucleic acids
JOURNAL      Patent: WO 03072818-A 52 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
            Location/Qualifiers
FEATURES
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            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
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            Sequenz: Capture-Oligonukleotid"
    misc_binding
        1
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    modified_base
        3 /note="LNA-T (Locked Nucleic Acid)"
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        6 /note="LNA-T (Locked Nucleic Acid)"
            /mod_base=OTHER
    modified_base
        9 /note="LNA-T (Locked Nucleic Acid)"
            /mod_base=OTHER
    modified_base
        12 /note="LNA-T (Locked Nucleic Acid)"
            /mod_base=OTHER
    modified_base
        15 /note="LNA-T (Locked Nucleic Acid)"
            /mod_base=OTHER
    modified_base
        18 /note="LNA-T (Locked Nucleic Acid)"
            /mod_base=OTHER
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Query Match      1.2%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 76;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1517 ATTAAGTAAAAAGTAAAA 1537
Db      21 ATTAAGTAAAAAGTAAAA 1

RESULT 33
LOCUS      BD085544      22 bp      RNA      linear      PAT 27-AUG-2002
DEFINITION      Method of comparison and detection of RNA amount and DNA amount.
ACCESSION      BD085544
VERSION      BD085544.1 GI:22631154
KEYWORDS      JP 2001333800-A/1.
SOURCE      Homo sapiens (human)
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 22)
            Shimada,K.
AUTHORS      Method of comparison and detection of RNA amount and DNA amount
            Patent: JP 2001333800-A 1 04-DEC-2001;
            UNITECH CO LTD
COMMENT      OS Homo sapiens (human)
            PN JP 2001333800-A/1
            PD 04-DEC-2001
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PF 30-MAY-2000 JP 2000160324
PI KAO RI SHIMADA
PC C1201/68.C12N15/09.G01N3/50.C12N15/00
CC Method of comparison and detection of RNA amount and DNA CC
FH Key Location/Qualifiers
FT source 1..22
/organism="Homo sapiens (human)".
location/Qualifiers
1..22
/organism="Homo sapiens"
/mol_type="genomic RNA"
/db_xref="taxon:9606"

FEATURES
Source

Query Match 1.2%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 73;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1517 ATTAAAAAAGTAAAG 1537
DB 2 ATCAAAAAAAAAAAAAA 22

RESULT 34
ARJ15696/c ARJ15696 20 bp DNA linear PAT 12-JUN-2003
LOCUS Sequence 6233 from patent US 6559294.
ACCESSION ARJ15696
VERSION ARJ15696.1 GI:31709122
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Grifflais, R., Holsbeth, S.K., Zagursky, R.J., Metcalf, B.J., Peek, J.A.,
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 6233 06-MAY-2003;
FEATURES Location/Qualifiers
Source 1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1109 TTCCATTTTCCCCC 1124
DB 17 TTCCATTTTCCCCC 2

RESULT 35
A40126 A40126 20 bp DNA linear PAT 05-MAR-1997
LOCUS Sequence 2 from Patent WO9423026.
ACCESSION A40126
VERSION A40126.1 GI:2296284
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 20)
AUTHORS Vasseur, M., Blumentfeld, M., Megueni, S. and Poddevin, B.
TITLE STABLE AND SEMI-STABLE OLIGONUCLEOTIDES, METHOD OF PREPARATION AND APPLICATIONS
JOURNAL Patent: WO 9423026-A 2 13-OCT-1994;
COMMENT GENSER (PR)
Other publication AU 6432094 941024
Other publication FR 2703053 940930.
FEATURES Location/Qualifiers
Source 1..20
/organism="unidentified"

/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 1.1%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAAGTAAAG 1538
DB 1 AAAAAAAAAAAGCAAG 19

RESULT 36
ARJ39961/c ARJ39961 20 bp DNA linear PAT 16-JUN-2001
LOCUS Sequence 33 from patent US 6207417.
ACCESSION ARJ39961
VERSION ARJ39961.1 GI:14482457
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Zeebo, K.M., Bosseiman, R.A., Suggs, S.V. and Martin, F.H.
TITLE DNA encoding stem cell factor
JOURNAL Patent: US 6207417-A 33 27-MAR-2001;
FEATURES Location/Qualifiers
Source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1519 TAAAAAAGTAAAG 1537
DB 19 TAAAAAAGTAAAG 1

RESULT 37
ARJ40280/c ARJ40280 20 bp DNA linear PAT 16-JUN-2001
LOCUS Sequence 33 from patent US 6207454.
ACCESSION ARJ40280
VERSION ARJ40280.1 GI:14482776
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Zeebo, K.M., Bosseiman, R.A., Suggs, S.V. and Martin, F.H.
TITLE Method for enhancing the efficiency of gene transfer with stem cell factor (SCF) polypeptide
JOURNAL Patent: US 6207454-A 33 27-MAR-2001;
FEATURES Location/Qualifiers
Source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1519 TAAAAAAGTAAAG 1537
DB 19 TAAAAAAGTAAAG 1

RESULT 38
ARJ40558/c ARJ40558 20 bp DNA linear PAT 16-JUN-2001
LOCUS Sequence 33 from patent US 6207802.

ACCESSION ARI40558
VERSION ARI40558.1 GI:14483054
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Zeebo,K.M., BosseIman,R.A., Suggs,S.V. and Martin,F.H.
TITLE Stem cell factor and compositions
JOURNAL Patent: US 6207802-A 33 27-MAR-2001;
FEATURES
Source 1..20
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.1%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1519 TAAATAAAAAAAAAAGTAAAA 1537
Db 19 TAAATAAAAAAAAAAAAAA 1
RESULT 39
LOCUS ARI82885 20 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 57 from patent US 6339068.
ACCESSION ARI82885
VERSION ARI82885.1 GI:20226092
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Krieg,A.M., Davis,H.L., Wu,T. and Schorr,J.
TITLE Vectors and methods for immunization or therapeutic protocols
JOURNAL Patent: US 6339068-A 57 15-JAN-2002;
FEATURES
Source 1..20
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.1%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 426 GCGCGCTGCGCGCGCGCG 444
Db 1 GCGCGCGCGCGCGCGCGCG 19
RESULT 40
LOCUS AXI04051 20 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 243 from Patent WO0122972.
ACCESSION AXI04051
VERSION AXI04051.1 GI:13920248
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 243 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
Source 1..20
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 1.1%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 426 GCGCGCTGCGCGCGCGCG 444
Db 1 GCGCGCGCGCGCGCGCGCG 19

RESULT 41
LOCUS AX281587 20 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 10 from Patent WO0177305.
ACCESSION AX281587
VERSION AX281587.1 GI:16608838
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Andersson,L., Luthman,H. and Marklund,S.
TITLE Variants of the human amp-activated protein kinase gamma 3 subunit
JOURNAL Patent: WO 0177305-A 10 18-OCT-2001;
Arexis AB (SE)
FEATURES
Source 1..20
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetically generated primer"

Query Match 1.1%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 423 AGTGGCGGCTGCGCGCGCG 441
Db 1 AGTGGCGGCTGCGCGCGCG 19

RESULT 42
LOCUS AX35382 20 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 410 from Patent WO0197843.
ACCESSION AX35382
VERSION AX35382.1 GI:18620050
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Weiner,G. and Hartmann,G.
TITLE Methods for enhancing antibody-induced cell lysis and treating
JOURNAL Patent: WO 0197843-A 410 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES
Source 1..20
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide-phosphodiester backbone"

Query Match 1.1%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 426 GCGCGCTGCGCGCGCGCG 444
Db 1 GCGCGCGCGCGCGCGCGCG 19

RESULT 43
LOCUS AX547104 20 bp DNA linear PAT 01-MAR-2003
DEFINITION Sequence 243 from Patent WO02053141.
ACCESSION AX547104
VERSION AX547104.1 GI:25812248
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.
REFERENCE
1 Bratzler, R.L.
AUTHORS Inhibition of angiogenesis by nucleic acids
TITLE Patent: WO 02053141-A 243 11-JUL-2002;
JOURNAL Coley Pharmaceutical Group, Inc. (US)
FEATURES
SOURCE
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"

Query Match 1.1%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 426 GCGCGCTGCGCGCGCGCG 444
|||||
Db 1 GCGCGCGCGCGCGCGCGCG 19

RESULT 44
LOCUS BD069976 20 bp DNA linear PAT 27-AUG-2002
DEFINITION Use of nucleic acids containing unmethylated CPG dinucleotide in the treatment of LPS-associated disorders.
ACCESSION BD069976
VERSION BD069976
KEYWORDS JP 2001513776-A/65.
SOURCE
ORGANISM
synthetic construct
artificial construct
artificial sequences.
REFERENCE
1 (bases 1 to 20)
AUTHORS Schwartz, D.A. and Krieg, A.M.
TITLE Use of nucleic acids containing unmethylated CPG dinucleotide in the treatment of LPS-associated disorders
JOURNAL Patent: JP 2001513776-A 65 04-SEP-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION
FEATURES
SOURCE
OS Artificial Sequence
PN JP 2001513776-A/65
PD 04-SEP-2001
PF 25-FEB-1998 JP 1998537810
PR 28-FEB-1997 US 60/039405
PI DAVID A SCHWARTZ, ARTHUR M KRIEG
PC A61K49/00, C07H21/02, C07H21/04, A01N43/04
CC synthetic oligonucleotide
FH key
FT source
1. .20
Location/Qualifiers
1. .20
Location/Qualifiers
/organism="Artificial Sequence".
1. .20
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.1%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 426 GCGCGCTGCGCGCGCGCG 444
|||||
Db 1 GCGCGCGCGCGCGCGCGCG 19

RESULT 45
LOCUS AR084563/c 21 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 52 from patent US 5981185.
ACCESSION AR084563
VERSION AR084563.1 GI:10011334
KEYWORDS
SOURCE
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 21)
AUTHORS Matsun, R.S., Coassin, P.J., Rampal, J.B. and Caskey, C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 52 09-NOV-1999;
FEATURES
SOURCE
1. .21
Location/Qualifiers
1. .21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 97;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 426 GCGCGCTGCGCGCGCGCG 444
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Db 20 GCGCGCGCGCGCGCGCGCG 2

RESULT 46
LOCUS AR084567 21 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 56 from patent US 5981185.
ACCESSION AR084567
VERSION AR084567.1 GI:10011338
KEYWORDS
SOURCE
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 21)
AUTHORS Matsun, R.S., Coassin, P.J., Rampal, J.B. and Caskey, C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 56 09-NOV-1999;
FEATURES
SOURCE
1. .21
Location/Qualifiers
1. .21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 97;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 426 GCGCGCTGCGCGCGCGCG 444
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Db 2 GCGCGCGCGCGCGCGCGCG 20

RESULT 47
LOCUS CQ830490/c 21 bp DNA linear PAT 12-JUL-2004
DEFINITION Sequence 2 from Patent WO2004055153.
ACCESSION CQ830490
VERSION CQ830490.1 GI:50250830
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.
REFERENCE
1 Schluesener, H. and Wendel, H.P.
AUTHORS Devices coated with substances that mediate the adhesion of biological material
TITLE Patent: WO 2004055153-A 2 01-JUL-2004;
JOURNAL Eberhard-Karls-Universitaet Tuebingen (DE)

FEATURES	Location/Qualifiers
source	1. .21

Query Match	1.1%	Score 15.8;	DB 1;	Length 21;
Best Local Similarity	89.5%;	Pred. No. 97;		
Matches 17; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

QY	426	GCGCGCTGCGCGCGCGCG	444
Db	20	GCGCGCGCGCGCGCGCG	2

RESULT	48				
LOCUS	CO830492				
DEFINITION	CO830492	21 bp	DNA		
ACCESSION	Sequence	4	from Patent WO2004055153.		linear
VERSION	CO830492				
KEYWORDS	CO830492.1	GI:50250832			
SOURCE			synthetic construct		

AUTHORS	Schuesener, H. and Wendel, H. P.
TITLE	Devices coated with substances that mediate the adhesion of biological material
JOURNAL	Patent: WO 200405513-A 4 01-JUL-2004;
FEATURES	Eberhard-Karls-Universitaet Tuebingen (DE)
source	Location/Qualifiers 1. .21

Query Match	1.1%	Score 15.8;	DB 1;	Length 21;
Best Local Similarity	89.5%;	Pred. No. 97;		
Matches 17; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

Qy 426 GCGGCTGCGGCGCGGCG 444
Db 2 GCGGCGCGCGGCGCGGCG 20

RESULT	49				
LOCUS	AR242257				
DEFINITION	AR242257	21 bp	DNA		
ACCESSION	Sequence	20	from patent US 6472173.		
VERSION	AR242257				
KEYWORDS	AR242257.1	GI:27286080			
SOURCE	Unknown.				
ORGANISM	Unknown.				
				linear	PAT 20-DEC-2007

REFERENCE	1 (bases 1 to 21)
AUTHORS	Ford, J. and Yeung, G.
TITLE	Chemokine receptor obtained from a cDNA library of fetal liver-spleen
JOURNAL	Patent: US 6472173-A 20 29-OCT-2002;
FEATURES	Location/Qualifiers
source	1..21

QY 569 CAGCAGGGGGCGCGTAGG 587

Db 1 CAGCAGGTGCTGGCGTAGG 19

RESULT	50		
AR242262/c			
LOCUS	AR242262	21 bp	DNA
DEFINITION	Sequence 25 from patent US 6472173.		linear
ACCESSION	AR242262		
VERSION	AR242262.1	GI:2728085	
KEYWORDS			
SOURCE	Unknown.		

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TITLE      Chemokine receptor obtained from a cDNA library of fetal
JOURNAL    liver-spleen
FEATURES   Patent: US 6472173-A 25 29-OCT-2002;
SOURCE      Location/Qualifiers
            1..21
            /organism="unknown"
            /mol_type="genomic DNA"

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Query Match	1.1%;	Score 15.8;	DB 1;	Length 21;
Best Local Similarity	89.5%;	Pred. No. 97;		
Matches 17; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

QY 569 CAGCAGGGGGCGGCGTAGG 587
|||
Db 21 CAGCAGGTGCTGGCGTAGG 3

[illegible]

DEGUS Bioactives GmbH (DE)
Location/Qualifiers

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/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
1
misc_binding

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modified_base 3 /note="LNA-T (Locked Nucleic Acid)"  
/mod_base=OTHER
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modified_base
9
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

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modified_base
12
/mod_base=OTHER
/note="LNA-T (Locked Nucleic Acid)"

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modified_base
15
/mod_base=OTHER
/note="LNA-T (Locked Nucleic Acid)"
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OT	assess_pertinence!!!

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/NOTE="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 18

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/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

Query Match      1.1%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 97;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      1519 TAAAAAAGTAAAA 1537
Db      19 TAAAAAAGTAAAA 1

RESULT 52
AX825108/c      AX825108      21 bp      DNA      linear      PAT 11-DEC-2003
LOCUS      Sequence 6 from Patent WO03072818.
ACCESSION      AX825108
VERSION      AX825108.1 GI:39750837
KEYWORDS
SOURCE      synthetic construct
ORGANISM      artificial sequences.
REFERENCE      1
AUTHORS      Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE      Method for sorting single-stranded nucleic acids
JOURNAL      Patent: WO 03072818-A 6 04-SEP-2003;
              Degussa Bioactives GmbH (DE)
FEATURES
  source      1..21
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="Beschreibung der kuenstlichen
              Sequenz:Capture-Oligonukleotid"
  misc_binding 1
              /bound_molecly="Biotin"
  modified_base 3
              /note="LNA-T (Locked Nucleic Acid)"
              /mod_base=OTHER
  modified_base 6
              /note="LNA-T (Locked Nucleic Acid)"
              /mod_base=OTHER
  modified_base 9
              /note="LNA-T (Locked Nucleic Acid)"
              /mod_base=OTHER
  modified_base 12
              /note="LNA-T (Locked Nucleic Acid)"
              /mod_base=OTHER
  modified_base 15
              /note="LNA-T (Locked Nucleic Acid)"
              /mod_base=OTHER
  modified_base 18
              /note="LNA-T (Locked Nucleic Acid)"
              /mod_base=OTHER
  modified_base 18
              /note="LNA-T (Locked Nucleic Acid)"
              /mod_base=OTHER

Query Match      1.1%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 97;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      1519 TAAAAAAGTAAAA 1537
Db      19 TAAAAAAGTAAAA 1

RESULT 53
AX825109/c      AX825109      21 bp      DNA      linear      PAT 11-DEC-2003
LOCUS      Sequence 7 from Patent WO03072818.
ACCESSION      AX825109
VERSION      AX825109.1 GI:39750838
KEYWORDS
SOURCE      synthetic construct
ORGANISM      synthetic construct
```

```

artificial sequences.
REFERENCE      1
AUTHORS      Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE      Method for sorting single-stranded nucleic acids
JOURNAL      Patent: WO 03072818-A 7 04-SEP-2003;
              Degussa Bioactives GmbH (DE)
FEATURES
  source      1..21
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="Beschreibung der kuenstlichen
              Sequenz:Capture-Oligonukleotid"
  misc_binding 1
              /bound_molecly="Biotin"
  modified_base 3
              /note="LNA-T (Locked Nucleic Acid)"
              /mod_base=OTHER
  modified_base 6
              /note="LNA-T (Locked Nucleic Acid)"
              /mod_base=OTHER
  modified_base 9
              /note="LNA-T (Locked Nucleic Acid)"
              /mod_base=OTHER
  modified_base 12
              /note="LNA-T (Locked Nucleic Acid)"
              /mod_base=OTHER
  modified_base 15
              /note="LNA-T (Locked Nucleic Acid)"
              /mod_base=OTHER
  modified_base 18
              /note="LNA-T (Locked Nucleic Acid)"
              /mod_base=OTHER
  modified_base 18
              /note="LNA-T (Locked Nucleic Acid)"
              /mod_base=OTHER

Query Match      1.1%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 97;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      1519 TAAAAAAGTAAAA 1537
Db      19 TAAAAAAGTAAAA 1

RESULT 54
AX825111/c      AX825111      21 bp      DNA      linear      PAT 11-DEC-2003
LOCUS      Sequence 9 from Patent WO03072818.
ACCESSION      AX825111
VERSION      AX825111.1 GI:39750840
KEYWORDS
SOURCE      synthetic construct
ORGANISM      synthetic construct
              artificial sequences.
REFERENCE      1
AUTHORS      Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE      Method for sorting single-stranded nucleic acids
JOURNAL      Patent: WO 03072818-A 9 04-SEP-2003;
              Degussa Bioactives GmbH (DE)
FEATURES
  source      1..21
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="Beschreibung der kuenstlichen
              Sequenz:Capture-Oligonukleotid"
  misc_binding 1
              /bound_molecly="Biotin"
  modified_base 3
              /note="LNA-T (Locked Nucleic Acid)"
              /mod_base=OTHER
  modified_base 6
              /note="LNA-T (Locked Nucleic Acid)"
              /mod_base=OTHER
  modified_base 9
              /note="LNA-T (Locked Nucleic Acid)"
              /mod_base=OTHER
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modified_base 9 /note="LNA-T (Locked Nucleic Acid)"
modified_base 12 /mod_base=OTHER
modified_base 15 /note="LNA-T (Locked Nucleic Acid)"
modified_base 18 /mod_base=OTHER
modified_base 18 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
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Query Match 1.1%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 97;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1519 TAAAAAAGTAAAA 1537
Db 19 TAAAAAAGTAAAA 1

RESULT 55
AX825112/c
LOCUS AX825112 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 10 from Patent WO03072818.
ACCESSION AX825112
VERSION AX825112.1 GI:39750841
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
AUTHORS TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 10 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source Location/Qualifiers
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
misc_binding 1
/bound_molecy="Biotin"
modified_base 3 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 6 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 9 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 12 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 15 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 18 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

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misc_binding 1 /bound_molecy="Biotin"
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modified_base 6 /note="LNA-T (Locked Nucleic Acid)"
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modified_base 9 /note="LNA-T (Locked Nucleic Acid)"
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modified_base 12 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 15 /note="LNA-T (Locked Nucleic Acid)"
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modified_base 18 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
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Query Match 1.1%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 97;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1519 TAAAAAAGTAAAA 1537
Db 19 TAAAAAAGTAAAA 1

RESULT 56
AX825113/c
LOCUS AX825113 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 11 from Patent WO03072818.
ACCESSION AX825113
VERSION AX825113.1 GI:39750842
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
AUTHORS TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 11 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source Location/Qualifiers
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
misc_binding 1
/bound_molecy="Biotin"
modified_base 3 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 6 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 9 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 12 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 15 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 18 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

Query Match 1.1%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 97;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1519 TAAAAAAGTAAAA 1537
Db 19 TAAAAAAGTAAAA 1

RESULT 57
AX825115/c
LOCUS AX825115 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 13 from Patent WO03072818.
ACCESSION AX825115
VERSION AX825115.1 GI:39750844
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
AUTHORS TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 13 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source Location/Qualifiers
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"


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misc_binding      /note="Beschreibung der kuenstlichen Sequenz:Capture-Oligonukleotid"
modified_base     1/bound_molecule="Blotin"
                  3/note="LNA-T (Locked Nucleic Acid)"
                  /mod_base=OTHER
modified_base     6/note="LNA-T (Locked Nucleic Acid)"
                  /mod_base=OTHER
modified_base     9/note="LNA-T (Locked Nucleic Acid)"
                  /mod_base=OTHER
modified_base    12/note="LNA-T (Locked Nucleic Acid)"
                  /mod_base=OTHER
modified_base    15/note="LNA-T (Locked Nucleic Acid)"
                  /mod_base=OTHER
modified_base    18/note="LNA-T (Locked Nucleic Acid)"
                  /mod_base=OTHER

Query Match      1.1%; Score 15.8; DB 1; Length 21;
Beet Local Similarity 89.5%; Pred.No. 97;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0.

OY              1519 TAAAAAAGTAAA 1537
Db              19 TAAAAAAAAAAAAAA 1

RESULT 58
AX825116/c      AX825116          21 bp   DNA       linear    PAT 11-DEC-2003
LOCUS           Sequence 14 from Patent WO03072818.
DEFINITION      AX825116
ACCESSION       AX825116
VERSION         AX825116.1 GI:39750845
KEYWORDS        .
SOURCE          synthetic construct
ORGANISM        synthetic construct
                artificial sequences.
REFERENCE       1 Boekamp,D., Dieck,T.H. and Hoppe,H.U.
AUTHORS         Method for sorting single-stranded nucleic acids
TITLE           Patent: WO 03072818-A 14 04-SBP-2003;
JOURNAL         Degussa Bioactives GmbH (DE)
FEATURES        location/Qualifiers
Source          1..21
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                 /mol_type="unassigned DNA"
                 /db_xref="taxon:32630"
                 /note="Beschreibung der kuenstlichen Sequenz:Capture-Oligonukleotid"
                 1/bound_molecule="Blotin"
                 3/note="LNA-T (Locked Nucleic Acid)"
                 /mod_base=OTHER
                 6/note="LNA-T (Locked Nucleic Acid)"
                 /mod_base=OTHER
                 9/note="LNA-T (Locked Nucleic Acid)"
                 /mod_base=OTHER
                 12/note="LNA-T (Locked Nucleic Acid)"
                 /mod_base=OTHER
                 15/note="LNA-T (Locked Nucleic Acid)"
                 /mod_base=OTHER
                 18/mod_base=OTHER
                 /note="LNA-T (Locked Nucleic Acid)"
                 /note="LNA-T (Locked Nucleic Acid)"

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Query Match	1.1%; Score 15.8; DB 1; Length 21;		
Best Local Similarity	89.5%; Pred. No. 97;		
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
Qy	1519 TAAAAAAAAAAGTAA 1537		
Db	19 TAAAAAAAAAAAAAAAA 1		
RESULT 59			
AX825117/c	AX825117	21 bp	DNA
LOCUS	Sequence 15 from Patent WO03072818.		linear
DEFINITION			PAT 11-DEC-2003
ACCESSION	AX825117		
VERSION	AX825117.1	GI:39750846	
KEYWORDS			
SOURCE	synthetic construct		
ORGANISM	synthetic construct		
REFERENCE	artificial sequences.		
AUTHORS	1		
TITLE	Boekenkamp, D., Dieck, T. H. and Hoppe, H. U.		
JOURNAL	Method for sorting single-stranded nucleic acids		
DEPOSIT	Patent: WO 03072818-A 15 04-SEP-2003;		
FEATURES	Degussa Bioactives GmbH (DE)		
source	location/Qualifiers		
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	/organism="synthetic construct"		
	/mol_type="unassigned DNA"		
	/db_xref="taxon:32630"		
	/note="Beschreibung der kuenstlichen		
	Sequenz: Capture-Oligonukleotid"		
	1		
misc_binding	/bound_moiety="Biotin"		
	3		
modified_base	/note="LNA-T (Locked Nucleic Acid)"		
	/mod_base=OTHER		
	6		
modified_base	/note="LNA-T (Locked Nucleic Acid)"		
	/mod_base=OTHER		
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modified_base	/note="LNA-T (Locked Nucleic Acid)"		
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modified_base	/note="LNA-T (Locked Nucleic Acid)"		
	/mod_base=OTHER		
	18		
modified_base	/note="LNA-T (Locked Nucleic Acid)"		
	/mod_base=OTHER		
Query Match	1.1%; Score 15.8; DB 1; Length 21;		
Best Local Similarity	89.5%; Pred. No. 97;		
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
Qy	1519 TAAAAAAAAAAGTAA 1537		
Db	19 TAAAAAAAAAAAAAAAA 1		
RESULT 60			
AX825152/c	AX825152	21 bp	DNA
LOCUS	Sequence 50 from Patent WO03072818.		linear
DEFINITION			PAT 11-DEC-2003
ACCESSION	AX825152		
VERSION	AX825152.1	GI:39750881	
KEYWORDS			
SOURCE	synthetic construct		
ORGANISM	synthetic construct		
	artificial sequences.		

[illegible]

	modified_base	12	/note="LNA-T (Locked Nucleic Acid)" /mod_base=OTHER	
	modified_base	15	/note="LNA-T (Locked Nucleic Acid)" /mod_base=OTHER	
	modified_base	18	/note="LNA-T (Locked Nucleic Acid)" /mod_base=OTHER	
Qy	Query Match	1.1%;	Score 15.8;	DB 1; Length 21; Best Local Similarity 89.5%; Pred. No. 97; Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db	1519 TAAAAAAGTAA	1537		
	20 TAAAAAAAAA	2		
RESULT 62	AX825163/c			
LOCUS	AX825163	21 bp	DNA	linear PAT 11-DEC-2003
DEFINITION	Sequence 61 from Patent WO03072818.			
ACCESSION	AX825163			
VERSION	AX825163.1	GI:39750892		
KEYWORDS	.			
SOURCE	synthetic construct			
ORGANISM	synthetic construct			
REFERENCE	1			
AUTHORS	Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.			
TITLE	Method for sorting single-stranded nucleic acids			
JOURNAL	Patent: WO 03072818-A 61 04-SEP-2003; Degussa Bioactives GmbH (DE)			
FEATURES	location/Qualifiers			
source	1..21			
	/organism="synthetic construct"			
	/mol_type="unassigned DNA"			
	/db_xref="taxon:32630"			
	/note="Beschreibung der kuenstlichen Sequenz:Capture-Oligonukleotid"			
misc_binding	1			
	/bound_moiety="Biotin"			
modified_base	3			
	/note="LNA-T (Locked Nucleic Acid)"			
modified_base	6			
	/mod_base=OTHER			
modified_base	9			
	/note="LNA-T (Locked Nucleic Acid)"			
modified_base	12			
	/mod_base=OTHER			
modified_base	15			
	/note="LNA-T (Locked Nucleic Acid)"			
modified_base	18			
	/mod_base=OTHER			
modified_base	18			
	/note="LNA-T (Locked Nucleic Acid)"			
	/mod_base=OTHER			
Query Match	1.1%;	Score 15.8;	DB 1; Length 21; Best Local Similarity 89.5%; Pred. No. 97; Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
Db	1519 TAAAAAAGTAA	1537		
	21 TAAAAAAAAA	3		

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RESULT 63
LOCUS AX58499 22 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 415 from Patent WO03000928.
ACCESSION AX58499
VERSION AX58499.1 GI:29160856
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Poulsen,H.S., Pedersen,N., Mortensen,S., Sorensen,S.B.,
Petersen,M.W. and Bisner,H.I.
TITLE Methods for identification of cancer cell surface molecules and
cancer specific promoters, and therapeutic uses thereof
JOURNAL Patent: WO 0300928-A 415 03-JAN-2003;
Odin Medical A/S (DK)
FEATURES
SOURCE Location/Qualifiers
1..22
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. No. 93;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 989 GTTCTGTTCTGTGAGAA 1007
Db 2 GTTCTGTCTGTGAGAA 20
RESULT 64
LOCUS AR164336 22 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 19 from patent US 6271369.
ACCESSION AR164336
VERSION AR164336.1 GI:16235464
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS 1 (bases 1 to 22)
Torrence,P.F., Silverman,R.H., Maitra,R.K. and Lesiak,K.
TITLE Chimeric molecules targeted to viral RNAs
JOURNAL Patent: US 6271369-A 19 07-AUG-2001;
LOCATION/Qualifiers
1..22
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 1e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 1516 AATTAAAAAAAGTAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 22
RESULT 65
LOCUS I31828 22 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 19 from patent US 5583032.
ACCESSION I31828
VERSION I31828.1 GI:1822619
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS 1 (bases 1 to 22)
Torrence,P., Silverman,R., Maitra,R. and Lesiak,K.
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TITLE Method of cleaving specific strands of RNA
JOURNAL Patent: US 5583032-A 19 10-DEC-1996;
FEATURES Location/Qualifiers
SOURCE 1..22
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 1e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 1516 AATTAAAAAAAGTAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 22
RESULT 66
LOCUS I69425 22 bp DNA linear PAT 04-FEB-1998
DEFINITION Sequence 19 from patent US 5677289.
ACCESSION I69425
VERSION I69425.1 GI:2831547
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS 1 (bases 1 to 22)
Torrence,P., Silverman,R., Maitra,R. and Lesiak,K.
TITLE Method of cleaving specific strands of RNA and medical treatments
thereby
JOURNAL Patent: US 5677289-A 19 14-OCT-1997;
LOCATION/Qualifiers
1..22
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.1%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 1e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 1516 AATTAAAAAAAGTAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 22
RESULT 67
LOCUS BD254424 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD254424
VERSION BD254424.1 GI:33064194
KEYWORDS
SOURCE JP 2002541795-A/2217.
ORGANISM unidentified
REFERENCE
AUTHORS 1 (bases 1 to 17)
Blatt,L., Zwick,M., Pavco,P. and Mcswigen,J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 2217 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
OS Eukaryote
PN JP 2002541795-A/2217
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGEN PC
C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
C12P21/02,
PC C12P21/02,C12P21/02/A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
C12R1:91),
PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
PC A61K37/02,
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PC (C12N5/00,C12N1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key Location/Qualifiers
FT source 1..17
/organism='Eukaryote'.
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source Location/Qualifiers
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 1.1%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 646 GCCGTGCCGAGCCGCC 662
DB 17 GCCGGCCGAGCCGCC 1

RESULT 68
AR187058/c
LOCUS AR187058 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 2546 from patent US 6346398.
ACCESSION AR187058
VERSION AR187058.1 GI:20233023
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 2546 12-FEB-2002;
FEATURES
source Location/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAAGTAAA 1536
DB 17 AAAAAAAAAAAGTAGA 1

RESULT 69
AR286187
LOCUS AR286187 17 bp RNA linear PAT 10-APR-2003
DEFINITION Sequence 559 from patent US 6528640.
ACCESSION AR286187
VERSION AR286187.1 GI:29723783
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A., Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Synthetic ribonucleic acids with RNase activity
JOURNAL Patent: US 6528640-A 559 04-MAR-2003;
FEATURES
source Location/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 1.1%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1248 TTGTGTTGTTTTTAA 1264
DB 1 TTGTGTTGTTTTTAA 17

RESULT 70
AR323668/c
LOCUS AR323668 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 1070 from patent US 6566127.
ACCESSION AR323668
VERSION AR323668.1 GI:33709476
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 1070 20-MAY-2003;
FEATURES
source Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned RNA"

Query Match 1.1%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAAGTAAA 1536
DB 17 AAAAAAAAAAAGTAGA 1

RESULT 71
AR398177
LOCUS AR398177 17 bp RNA linear PAT 18-DEC-2003
DEFINITION Sequence 558 from patent US 6617438.
ACCESSION AR398177
VERSION AR398177.1 GI:40135776
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A.B., Beaudry,A., Karpeisky,A., Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Oligoribonucleotides with enzymatic activity
JOURNAL Patent: US 6617438-A 558 09-SEP-2003;
FEATURES
source Location/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 1.1%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1248 TTGTGTTGTTTTTAA 1264
DB 1 TTGTGTTGTTTTTAA 17

RESULT 72
AX804693
LOCUS AX804693 18 bp DNA linear PAT 25-NOV-2003
DEFINITION Sequence 861 from Patent WO03060160.
ACCESSION AX804693
VERSION AX804693.1 GI:38521834
KEYWORDS
SOURCE Oreochromis niloticus (Nile tilapia)
ORGANISM Oreochromis niloticus (Nile tilapia); Buteleostomi; Buteleostomi; Metazoa; Chordata; Vertebrata;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes;
Labroidae; Cichlidae; Oreochromis.
REFERENCE
AUTHORS
TITLE
1 Lie,Y., Sietean,A., Hoeyum,M. and Lingaas,F.
Verification of food origin based on nucleic acid pattern
recognition
JOURNAL
Patent: WO 03060160-A 861 24-JUL-2003;
Genomar ASA (NO)
FEATURES
Source
Location/Qualifiers
1..18
/organism="Oreochromis niloticus"
/mol_type="unassigned DNA"
/db_xref="taxon:8128"

Query Match 1.1%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 660 GCGTCAGACTCAGCTCT 676
DB 1 GCGTCAGCTCAGCTCT 17

RESULT 73
A88305
LOCUS A88305 20 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 453 from Patent WO9833904.
ACCESSION A88305
VERSION A88305.1 GI:6736875
KEYWORDS
SOURCE
ORGANISM
unidentified
unclassified.
REFERENCE
AUTHORS
TITLE
1 (bases 1 to 20)
Brysch,W. and Schlingensiepen,K.
AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL
Patent: WO 9833904-A 453 06-AUG-1998;
BIOGNOSTIK GBS (DE); BRYSCH WOLFGANG (DE)
FEATURES
Source
Location/Qualifiers
1..20
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 1.1%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAAGTAAA 1536
DB 4 AAAACAAAAAAGTAAA 20

RESULT 74
A90272
LOCUS A90272 20 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 453 from Patent EP0856579.
ACCESSION A90272
VERSION A90272.1 GI:6738786
KEYWORDS
SOURCE
ORGANISM
unidentified
unclassified.
REFERENCE
AUTHORS
TITLE
1 (bases 1 to 20)
Brysch,W.D. and Schlingensiepen,K.D.
An antisense oligonucleotide preparation method
JOURNAL
Patent: EP 0856579-A 453 05-AUG-1998;
BIOGNOSTIK GBS (DE)
FEATURES
Source
Location/Qualifiers
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/organism="unidentified"
/mol_type="unassigned DNA"

/db_xref="taxon:32644"

Query Match 1.1%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAAGTAAA 1536
DB 4 AAAACAAAAAAGTAAA 20

RESULT 75
AX356277
LOCUS AX356277 20 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 71 from Patent WO0200905.
ACCESSION AX356277
VERSION AX356277.1 GI:18620784
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.
REFERENCE
AUTHORS
TITLE
1 Conner,T.W., Dubois,P., Malven,M. and Masucci,J.D.
Plant regulatory sequences for selective control of gene expression
JOURNAL
Patent: WO 0200905-A 71 03-JAN-2002;
Monsanto Technology LLC (US)
FEATURES
Source
Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic"

Query Match 1.1%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 552 GCGGTGCGTGGCTTCG 568
DB 2 GCGAGTGGTGGCTTCG 18

RESULT 76
BD065818
LOCUS BD065818 20 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD065818
VERSION BD065818.1 GI:22611421
KEYWORDS
SOURCE
ORGANISM
unidentified
unclassified.
REFERENCE
AUTHORS
TITLE
1 (bases 1 to 20)
Schlingensiepen,K.H. and Brysch,W.
An antisense oligonucleotide preparation method
JOURNAL
Patent: JP 2001511000-A 453 07-AUG-2001;
BIOGNOSTIK GEBELTSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
OS Unknown
PN JP 2001511000-A/453
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
Location/Qualifiers
1..20
/organism="Unknown".
FT source

FEATURES
Source
Location/Qualifiers
1..20
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 1.1%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAAGTAAA 1536
DB 4 AAAAAAAAAAAGTAAA 20

RESULT 77
AX118267/c AX118267 21 bp DNA linear PAT 11-MAY-2001
LOCUS Sequence 3390 from Patent WO0129262.
DEFINITION AX118267
ACCESSION AX118267
VERSION AX118267.1 GI:14035218
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Picoult-Newbury, L. and Pohl, M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 3390 26-APR-2001;
Orchid Biosciences, Inc. (US)
LOCATION/Qualifiers
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 1.1%; Score 15.4; DB 1; Length 21;
Best Local Similarity 94.1%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1403 GTGTCAAGATTAAGGTT 1419
DB 21 GTGTCAAGATTAAGGTT 5

RESULT 78
AR092032/c AR092032 20 bp DNA linear PAT 08-SEP-2000
LOCUS Sequence 56 from patent US 5998141.
DEFINITION AR092032
ACCESSION AR092032
VERSION AR092032.1 GI:10018786
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Acton, S. Laurene.
TITLE Intronic and polymorphic SR-BI nucleic acids and uses therefor
JOURNAL Patent: US 5998141-A 56 07-DEC-1999;
LOCATION/Qualifiers
1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1037 GTGGCGCGCGGTGTGTAA 1056
DB 20 GTGGCGCGCGGTGTGTAA 1

RESULT 79
AR112167/c AR112167 20 bp DNA linear PAT 16-MAY-2001
LOCUS Sequence 56 from patent US 6130041.
DEFINITION

ACCESSION AR112167
VERSION AR112167.1 GI:14092067
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Acton, S. Laurene.
TITLE Human intronic and polymorphic SR-BI nucleic acids and uses therefor
JOURNAL Patent: US 6130041-A 56 10-OCT-2000;
LOCATION/Qualifiers
1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1037 GTGGCGCGCGGTGTGTAA 1056
DB 20 GTGGCGCGCGGTGTGTAA 1

RESULT 80
AR149209/c AR149209 20 bp DNA linear PAT 08-AUG-2001
LOCUS Sequence 56 from patent US 6228581.
DEFINITION AR149209
ACCESSION AR149209
VERSION AR149209.1 GI:15113800
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Acton, S. L. and Ordoval, J. M.
TITLE Human intronic and polymorphic SR-BI nucleic acids and uses therefor
JOURNAL Patent: US 6228581-A 56 08-MAY-2001;
LOCATION/Qualifiers
1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1037 GTGGCGCGCGGTGTGTAA 1056
DB 20 GTGGCGCGCGGTGTGTAA 1

RESULT 81
BD229218 BD229218 20 bp DNA linear PAT 17-JUL-2003
LOCUS Genotype determination of human UDP-glucuronosyl transferase 2B4
DEFINITION (UGT2B4), 2B7 (UGT2B7) and 2B15 (UGT2B15) genes.
ACCESSION BD229218
VERSION BD229218.1 GI:33038988
KEYWORDS JP 2002521067-A/90.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 20)
AUTHORS Galvin, M., Miller, A., Penny, L. and Riechy, M.
TITLE Genotype determination of human UDP-glucuronosyl transferase 2B4 (UGT2B4), 2B7 (UGT2B7) and 2B15 (UGT2B15) genes
JOURNAL Patent: JP 2002521067-A 90 16-JUL-2002;
AXIS PHARMACEUTICALS INC
OS Homo sapiens (human)

PN JP 2002521067-A/90
PD 16-JUL-2002
PF 22-JUL-1999 JP 2000562558
PR 28-JUL-1998 US 60/094391
PI MARGARET GALVIN, ANDREW MILLER, LAURA PENNY, MICHAEL RIEDY PC
C12N15/09, C12N15/00, C12Q1/69, C12N15/00, C12N15/00 CC
Genotype determination of human UDP-glucuronosyl transferase CC
2B4 (UGT2B4),
CC 2B7 (UGT2B7) and 2B15 (UGT2B15) genes
FH key Location/Qualifiers
FT source 1..20 /organism='Homo sapiens (human)'.
FEATURES
source 1..20 Location/Qualifiers
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'

Query Match 1.1%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1632 CCTCCCTACCTTTGAAAA 1651
DB 1 CCTGGCTACACTTTGAAAA 20

RESULT 82
AR309844 20 bp DNA linear PAT 12-JUN-2003
LOCUS AR309844
DEFINITION Sequence 4 from patent US 6555670.
ACCESSION AR309844
VERSION AR309844.1 GI:31701953
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Aizawa, A., Kawakami, A. and Kondo, T.
TITLE Testis-specific gene
JOURNAL Patent: US 6555670-A 4 29-APR-2003;
FEATURES Location/Qualifiers
source 1..20 /organism='unknown'
/mol_type='genomic DNA'

Query Match 1.1%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1300 AATCTATTTTATTTTTC 1319
DB 1 AAGCTTTTATTTTTC 20

RESULT 83
AR349470 20 bp DNA linear PAT 17-AUG-2003
LOCUS AR349470
DEFINITION Sequence 92 from patent US 6586175.
ACCESSION AR349470
VERSION AR349470.1 GI:33750263
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Galvin, M., Miller, A., Penny, L. and Riedy, M.
TITLE Genotyping the human udp-glucuronosyltransferase 2B7 (UGT2B7) gene
JOURNAL Patent: US 6586175-A 92 01-JUL-2003;
FEATURES Location/Qualifiers
source 1..20 /organism='unknown'
/mol_type='genomic DNA'

Query Match 1.1%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1632 CCTCCCTACCTTTGAAAA 1651
DB 1 CCTGGCTACACTTTGAAAA 20

RESULT 84
AX298541/c 20 bp DNA linear PAT 26-NOV-2001
LOCUS AX298541/c
DEFINITION Sequence 175 from Patent WO0183749.
ACCESSION AX298541
VERSION AX298541.1 GI:17128531
KEYWORDS
SOURCE Mus sp.
ORGANISM Mus sp.
REFERENCE 1
AUTHORS Bachmanov, A.A., Beauchamp, G.K., Chatterjee, A., de Jong, P.J., Li, S.,
Li, X., Ohmen, J.D., Reed, D.R., Ross, D. and Tordoff, M.G.
TITLE Gene and sequence variation associated with sensing carbohydrate
compounds and other sweeteners
JOURNAL Patent: WO 0183749-A 175 08-NOV-2001;
WARNER-LAMBERT COMPANY (US) ; The Monell Chemical Senses Center
(US)

FEATURES
source 1..20 Location/Qualifiers
/organism='Mus sp.'
/mol_type='unassigned DNA'
/db_xref='taxon:10095'

Query Match 1.1%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 808 CTGAATTTGTGTGTCATC 827
DB 20 CGAATTTGTGTGTCATC 1

RESULT 85
AX404077 20 bp DNA linear PAT 14-JUN-2002
LOCUS AX404077
DEFINITION Sequence 4 from Patent EP1195382.
ACCESSION AX404077
VERSION AX404077.1 GI:21437393
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Aizawa, A., Kawakami, A. and Kondo, T.
TITLE Testis-specific gene
JOURNAL Patent: EP 1195382-A 4 10-APR-2002;
Livestock Improvement Association of Japan, Inc. (JP) ; President
of Gunma University (JP)
FEATURES Location/Qualifiers
source 1..20 /organism='synthetic construct'
/mol_type='unassigned DNA'
/db_xref='taxon:32630'

Query Match 1.1%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1300 AATCTATTTTATTTTTC 1319
DB 1 AAGCTTTTATTTTTC 20

```
RESULT 86
AX488408          20 bp  DNA      linear  PAT 16-AUG-2002
LOCUS              Sequence 5708 from Patent WO02053728.
DEFINITION
ACCESSION          AX488408
VERSION            AX488408.1 GI:22322488
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS            Roemer,T., Jiang,B., Boone,C., Bussey,H. and Ohlsen,K.L.
TITLE              Gene distribution methodologies for drug target discovery
JOURNAL            Patent: WO 02053728-A 5708 11-JUL-2002;
                  Elitza Pharmaceuticals, Inc. (US)
FEATURES
source
1..20
/organism="Candida albicans"
/mol_type="unassigned DNA"
/db_xref="taxon:5476"

Query Match          1.1%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY          727 GCTGTGCTGCTGCTTTGT 746
Db          1 GCTCTCTCTCTGCTGTTGT 20

RESULT 87
AX770111          20 bp  DNA      linear  PAT 02-JUL-2003
LOCUS              Sequence 9 from Patent WO03016562.
DEFINITION
ACCESSION          AX770111
VERSION            AX770111.1 GI:32437689
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS            Glacquel,B.
TITLE              Compositions and methods for detecting multidrug resistant strains
JOURNAL            of M. tuberculosis having mutations in genes of the mutR family
                  Patent: WO 03016562-A 9 27-FEB-2003;
                  INSTITUT PASTEUR (FR)
FEATURES
source
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match          1.1%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY          439 CCGGCGACGATCCGCGCT 458
Db          1 CCGGCGACGATCGCTCGTT 20

RESULT 88
BD143136          20 bp  DNA      linear  PAT 17-JAN-2003
LOCUS              Novel testis-specific gene.
DEFINITION
ACCESSION          BD143136
VERSION            BD143136.1 GI:27848894
KEYWORDS
JUP 2002112777-A/3.
SOURCE
synthetic construct
```

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ORGANISM            synthetic construct
artificial sequences.
REFERENCE
1 (bases 1 to 20)
AUTHORS            Aizawa,A., Kawakami,A. and Kondo,T.
TITLE              Novel testis-specific gene
JOURNAL            Patent: JP 2002112777-A 3 16-APR-2002;
                  KACHIKU KAIRYO JIGYODAN, PRESIDENT OF GUNMA UNIVERSITY
COMMENT
OS Artificial Sequence
PN JP 2002112777-A/3
PD 16-APR-2002
PF 03-OCT-2000 JP 2000303994
PI AKIRA AIZAWA, AKIRO KAWAKAMI, TOSHITAKO KONDO
PC C12N15/09; C07K14/47; C12N15/00
CC Novel testis-specific gene
FH Key
FT source
FT Location/Qualifiers
1..20
/organism="Artificial Sequence".
FEATURES
source
1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match          1.1%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY          1300 AATCTATTTTTTTTAAATTTTC 1319
Db          1 AAGCTTTTTTTTTTTTTTTTC 20

RESULT 89
AX825106          21 bp  DNA      linear  PAT 11-DEC-2003
LOCUS              Sequence 4 from Patent WO03072818.
DEFINITION
ACCESSION          AX825106
VERSION            AX825106.1 GI:39750835
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS            Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE              Method for sorting single-stranded nucleic acids
JOURNAL            Patent: WO 03072818-A 4 04-SEP-2003;
                  Degussa Bioactives GmbH (DE)
FEATURES
source
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
misc_binding
1
/bound_moiety="Biotin"
modified_base
3
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
6
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
9
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
12
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
15
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
18
/note="LNA-T (Locked Nucleic Acid)"
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/mod_base=OTHER

Query Match 1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1246 TCTTGTGTTTGTAT 1265
| | | | | | | | | | | | | | | | | | | | | |
Db 2 TTTTGTGTTTGTAT 21

RESULT 90
A20525 21 bp DNA linear PAT 12-AUG-1994
LOCUS oligonucleotide for the mutagenesis of SA216.
DEFINITION A20525
VERSION A20525.1 GI:583360
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 21)
AUTHORS
TITLE A POLYPEPTIDE
JOURNAL Patent: WO 9104315-A 22 04-APR-1991;
FEATURES
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 597 GGCGGGCGCGTGC 616
| | | | | | | | | | | | | | | | | | | | | |
Db 2 GGCGGGCGCGAGTGC 21

RESULT 91
A20526 21 bp DNA linear PAT 12-AUG-1994
LOCUS oligonucleotide for the mutagenesis of SA216.
DEFINITION A20526
VERSION A20526.1 GI:579020
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 21)
AUTHORS
TITLE A POLYPEPTIDE
JOURNAL Patent: WO 9104315-A 23 04-APR-1991;
FEATURES
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 597 GGCGGGCGCGTGC 616
| | | | | | | | | | | | | | | | | | | | | |
Db 20 GGCGGGCGCGAGTGC 1

RESULT 92
A20531 21 bp DNA linear PAT 12-AUG-1994
LOCUS oligonucleotide for the mutagenesis of SAT216.
DEFINITION

ACCESSION A20531
VERSION A20531.1 GI:583363
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 21)
AUTHORS
TITLE A POLYPEPTIDE
JOURNAL Patent: WO 9104315-A 28 04-APR-1991;
FEATURES
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 597 GGCGGGCGCGTGC 616
| | | | | | | | | | | | | | | | | | | | | |
Db 2 GGCGGGCGCGAGTGC 21

RESULT 93
A20532 21 bp DNA linear PAT 12-AUG-1994
LOCUS oligonucleotide for the mutagenesis of SAT216.
DEFINITION A20532
VERSION A20532.1 GI:579023
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 21)
AUTHORS
TITLE A POLYPEPTIDE
JOURNAL Patent: WO 9104315-A 29 04-APR-1991;
FEATURES
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 597 GGCGGGCGCGTGC 616
| | | | | | | | | | | | | | | | | | | | | |
Db 20 GGCGGGCGCGAGTGC 1

RESULT 94
A20532 21 bp DNA linear PAT 08-AUG-2001
LOCUS Sequence 11 from patent US 6204435.
DEFINITION A20532
VERSION A20532.1 GI:15104912
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Felleisen, J. S., Schnepf, H. Ernest., Narva, K. E., Stockhoff, B. A.,
Schmeltz, J., Loewer, D., Dullum, C. Joseph., Muller-Cohn, J. and
Stamp, L. M.
TITLE Pesticidal toxins and nucleotide sequences which encode these
toxins
JOURNAL Patent: US 6204435-A 11 20-MAR-2001;
FEATURES
source 1..21

/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1630 ATCCTCCCTACCCCTTTGAA 1649
Db 2 ATCCTCCCTACACTTCTTA 21

RESULT 95
AR157200 21 bp DNA linear PAT 08-AUG-2001
LOCUS AR157200
DEFINITION Sequence 11 from patent US 6242669.
ACCESSION AR157200
VERSION AR157200.1 GI:15125904
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Felten, J.S., Schnepf, H. Ernest., Narva, K.E., Stockhoff, B.A.,
Schmeits, J., Loewer, D., Dullum, C. Joseph., Muller-Cohn, J., Stamp, L.,
Morrill, G., and Finstad-Lee, S.
TITLE Pesticidal toxins and nucleotide sequences which encode these
toxins
JOURNAL Patent: US 6242669-A 11 05-JUN-2001;
FEATURES
source Location/Qualifiers
1..21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1630 ATCCTCCCTACCCCTTTGAA 1649
Db 2 ATCCTCCCTACACTTCTTA 21

RESULT 96
E08187 21 bp DNA linear PAT 29-SEP-1997
LOCUS E08187
DEFINITION Primer for isolation of the promoter in rice starch-branching
enzyme.
ACCESSION E08187
VERSION E08187.1 GI:2176308
KEYWORDS JP 1994261767-A/5.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 21)
AUTHORS Baba, T., and Shimada, H.
TITLE NEW RICE PLANT STARCH-BRANCHED ENZYMIC GENE
JOURNAL Patent: JP 1994261767-A 5 20-SEP-1994;
MITSUI GIYOUSAI SHOKUBUTSU BIO KENKUSHO:KK
OS None
OC Artificial sequences.
PN JP 1994261767-A/5
PD 20-SEP-1994
PF 22-OCT-1993 JP 1993265171
PR 29-OCT-1992 JP 92P 291719
PI BABA TARASHI, SHIMADA HIROAKI
PC C12N15/54, A01H5/00, C12N5/10, C12P19/16//A23L1/10, C12N9/10, CC
strandedness: Single;
CC topology: linear;
FH Key Location/Qualifiers
FH 1..21
FT source /organism="Artificial sequences".

FEATURES
source Location/Qualifiers
1..21
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 546 GTGTGTGCGTGTGCGCGT 565
Db 2 GTGTGTGCGTGTGCGCGT 21

RESULT 97
AR437180 21 bp DNA linear PAT 18-DEC-2003
LOCUS AR437180
DEFINITION Sequence 11 from patent US 6656908.
ACCESSION AR437180
VERSION AR437180.1 GI:40202037
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Felten, J.S., Schnepf, H.E., Narva, K.E., Stockhoff, B.A.,
Schmeits, J., Loewer, D., Dullum, C.J., Muller-Cohn, J., Stamp, L.,
Morrill, G., and Finstad-Lee, S.
TITLE Pesticidal toxins and nucleotide sequences which encode these
toxins
JOURNAL Patent: US 6656908-A 11 02-DEC-2003;
FEATURES
source Location/Qualifiers
1..21
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1630 ATCCTCCCTACCCCTTTGAA 1649
Db 2 ATCCTCCCTACACTTCTTA 21

RESULT 98
AX825119 21 bp DNA linear PAT 11-DEC-2003
LOCUS AX825119/c
DEFINITION Sequence 17 from Patent WO03072818.
ACCESSION AX825119
VERSION AX825119.1 GI:39750848
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 17 04-SEP-2003;
Degussa Bioactives GmbH (DB)
FEATURES
source Location/Qualifiers
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
1
misc_binding /bound_moiety="Biotin"
3
modified_base /note="DNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

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modified_base 6 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 9 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 12 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 15 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 18 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
Query Match 1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1518 TTAATAAAAAAAAAAGTAAAA 1537
Db 21 TTAATAAAAAAAAAAAAAAAAA 2

RESULT 99
AX825120/c AX825120 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 18 from Patent WO03072818.
ACCESSION AX825120
VERSION AX825120.1 GI:39750849
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
AUTHORS Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 18 04-SEP-2003;
FEATURES
Source Bioactives GmbH (DE)
Location/Qualifiers
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
modified_base 1 /bound_moiety="Biotin"
misc_binding 3 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 6 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 9 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 12 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 15 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 18 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
Query Match 1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1518 TTAATAAAAAAAAAAGTAAAA 1537
Db 21 TTAATAAAAAAAAAAAAAAAAA 2
```

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Db 20 TCAAAAAAAAAAAAAAAAAA 1

RESULT 100
AX825121/c AX825121 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 19 from Patent WO03072818.
ACCESSION AX825121
VERSION AX825121.1 GI:39750850
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
AUTHORS Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 19 04-SEP-2003;
FEATURES
Source Bioactives GmbH (DE)
Location/Qualifiers
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
misc_binding 1 /bound_moiety="Biotin"
modified_base 3 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 6 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 9 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 12 /note="LNA-T (Locked Nucleic Acid) "
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modified_base 18 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
Query Match 1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1518 TTAATAAAAAAAAAAGTAAAA 1537
Db 20 TCAAAAAAAAAAAAAAAAAA 1

RESULT 101
AX825135/c AX825135 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 33 from Patent WO03072818.
ACCESSION AX825135
VERSION AX825135.1 GI:39750864
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
AUTHORS Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 33 04-SEP-2003;
FEATURES
Source Bioactives GmbH (DE)
Location/Qualifiers
1. .21
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/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
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1 /bound_moiety="Biotin"
modified_base
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modified_base
6 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
9 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
12 /note="LNA-T (Locked Nucleic Acid)"
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modified_base
15 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
18 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

Query Match
1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1518 TTAATAAAAAAAAAAGTAAAA 1537
Db 21 TTGAAAAAAAAAAAAAAAAAAAA 2

RESULT 102
AX825136 21 bp DNA linear PAT 11-DEC-2003
LOCUS AX825136
DEFINITION Sequence 34 from Patent WO03072818.
ACCESSION AX825136
VERSION AX825136.1 GI:39750865
KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1 Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITL Method for sorting single-stranded nucleic acids
JOURN Patent: WO 03072818-A 34 04-SEP-2003;
Degussa Bioactives GmbH (DE)
location/Qualifiers
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/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
1 /bound_moiety="Biotin"
misc_binding
3 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
6 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
9 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
12 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
15 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
18 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

Query Match
1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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18 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base

Query Match
1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1302 TCTATTTTCTTTTATTTTCAG 1321
Db 2 TTTTCTTTTCTTTTCTTCAG 21

RESULT 103
AX825136/c 21 bp DNA linear PAT 11-DEC-2003
LOCUS AX825136
DEFINITION Sequence 34 from Patent WO03072818.
ACCESSION AX825136
VERSION AX825136.1 GI:39750865
KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1 Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITL Method for sorting single-stranded nucleic acids
JOURN Patent: WO 03072818-A 34 04-SEP-2003;
Degussa Bioactives GmbH (DE)
location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
1 /bound_moiety="Biotin"
misc_binding
3 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
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/mod_base=OTHER
modified_base
9 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
12 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
15 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
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/mod_base=OTHER

Query Match
1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1518 TTAATAAAAAAAAAAGTAAAA 1537
Db 20 TGAATAAAAAAAAAAAAAAAAAAA 1

RESULT 104
AX825137 21 bp DNA linear PAT 11-DEC-2003
LOCUS AX825137/c
DEFINITION Sequence 35 from Patent WO03072818.
ACCESSION AX825137
VERSION AX825137.1 GI:39750866
KEYWORDS
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SOURCE      synthetic construct
ORGANISM     synthetic construct
              artificial sequences.
REFERENCE    1
AUTHORS      Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE        Method for sorting single-stranded nucleic acids
JOURNAL      Patent: WO 03072818-A 35 04-SEP-2003;
              Degussa Bioactives GmbH (DE)
FEATURES     source
              1..21
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Beschreibung der kuenstlichen
                Sequenz: Capture-Oligonukleotid"
misc_binding 1
              /bound_moiety="Biotin"
modified_base 3
              /note="LNA-T (Locked Nucleic Acid)"
modified_base 6
              /mod_base=OTHER
modified_base 9
              /note="LNA-T (Locked Nucleic Acid)"
modified_base 12
              /mod_base=OTHER
modified_base 15
              /note="LNA-T (Locked Nucleic Acid)"
modified_base 18
              /note="LNA-T (Locked Nucleic Acid)"
modified_base 18
              /mod_base=OTHER
Query Match 1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 1518 TTTAAAAAAAGTAAAA 1537
| | | | | | | | | | | | | | | | | | | | |
Db 20 TCAAAAAAAAAAAAAAAAAA 1

RESULT 105
AX825155/c 21 bp DNA linear PAT 11-DEC-2003
LOCUS      AX825155
DEFINITION Sequence 53 from Patent WO03072818.
ACCESSION  AX825155
VERSION     AX825155.1 GI:39750884
KEYWORDS
SOURCE      synthetic construct
ORGANISM     synthetic construct
              artificial sequences.
REFERENCE    1
AUTHORS      Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE        Method for sorting single-stranded nucleic acids
JOURNAL      Patent: WO 03072818-A 35 04-SEP-2003;
              Degussa Bioactives GmbH (DE)
FEATURES     Location/Qualifiers
              1..21
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Beschreibung der kuenstlichen
                Sequenz: Capture-Oligonukleotid"
misc_binding 1
              /bound_moiety="Biotin"
modified_base 3
              /note="LNA-T (Locked Nucleic Acid)"
modified_base 6
              /mod_base=OTHER
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/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 9
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modified_base 15
              /note="LNA-T (Locked Nucleic Acid)"
modified_base 18
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modified_base 18
              /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
Query Match 1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 1518 TTTAAAAAAAGTAAAA 1537
| | | | | | | | | | | | | | | | | | | | |
Db 21 TCAAAAAAAAAAAAAAAAAA 2

RESULT 106
AX825159/c 21 bp DNA linear PAT 11-DEC-2003
LOCUS      AX825159
DEFINITION Sequence 57 from Patent WO03072818.
ACCESSION  AX825159
VERSION     AX825159.1 GI:39750888
KEYWORDS
SOURCE      synthetic construct
ORGANISM     synthetic construct
              artificial sequences.
REFERENCE    1
AUTHORS      Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE        Method for sorting single-stranded nucleic acids
JOURNAL      Patent: WO 03072818-A 57 04-SEP-2003;
              Degussa Bioactives GmbH (DE)
FEATURES     Location/Qualifiers
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                /note="Beschreibung der kuenstlichen
                Sequenz: Capture-Oligonukleotid"
misc_binding 1
              /bound_moiety="Biotin"
modified_base 3
              /note="LNA-T (Locked Nucleic Acid)"
modified_base 6
              /mod_base=OTHER
modified_base 9
              /note="LNA-T (Locked Nucleic Acid)"
modified_base 12
              /mod_base=OTHER
modified_base 15
              /note="LNA-T (Locked Nucleic Acid)"
modified_base 18
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modified_base 18
              /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
Query Match 1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 1518 TTTAAAAAAAGTAAAA 1537
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Db 21 TGAATAAAAAAAAAAAAAA 2

RESULT 107
BD008680
LOCUS
DEFINITION Novel pesticidal toxins and nucleotide sequences which encode these toxins.
ACCESSION BD008680
VERSION BD008680.1 GI:18637053
KEYWORDS JP 2001502919-A/8.
SOURCE unidentified
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Fetteelson,J.S., Schnepf,E.H., Narva,K.E., Stochhoff,B.A.,
Schmelts,J.L., Loewer,D., Schwab,G., Dullum,C.J., Cohn,J.M. and
Stamp,L.
TITLE Novel pesticidal toxins and nucleotide sequences which encode these toxins
JOURNAL Patent: JP 2001502919-A 8 06-MAR-2001;
MYCOGEN CORP
OS Unidentified
PN JP 2001502919-A/8
PD 06-MAR-2001
PF 30-OCT-1997 JP 1998520788
PR
PI JERALD S FETTELSON,ERNEST H SCHNEPF,KENNETH E NARVA, PI
BRIAN A STOCCKHOFF,
PI JAMES L SCHMEITS,DAVID LOEWER,GEORGE SCHWAB,
PI CHARLES JOSEPH DULLUM,
PI JUDY MULLER COHN,LISA STAMP
PC C12N15/32,C07K14/325,C12Q1/68,A01N63/00,C12N15/82 CC
Strandedness: Single;
CC Topology: Linear;
FH key Location/Qualifiers
FT source 1..21
location/Qualifiers
1..21
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1630 ATCTCTACCTACCTTTGAA 1649
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Db 2 ATCTCTCTACACTTTCTTA 21

RESULT 108
BD023735 21 bp DNA linear PAT 27-AUG-2002
LOCUS Beta-galactosidase having reversibly inactive lactase activity.
DEFINITION BD023735
ACCESSION BD023735.1 GI:22564958
VERSION JP 2001506136-A/1.
KEYWORDS JP 2001506136-A/1.
SOURCE Eremothecium gossypii (Ashbya gossypii)
ORGANISM Eremothecium gossypii
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Eremothecium.
REFERENCE 1 (bases 1 to 21)
AUTHORS Karatzas,C.N., Turner,J.D., Eino,M., Kabel,J.J. and Amantea,G.F.
TITLE Beta-galactosidase having reversibly inactive lactase activity
JOURNAL Patent: JP 2001506136-A 1 15-MAY-2001;
NEXIA BIOTECHNOLOGIES INC
PN JP 2001506136-A/1
PD 15-MAY-2001
PF 29-DEC-1997 JP 1998529775
PR 31-DEC-1996 US 08/775842

PI COSTAS N KARATZAS,JEFFREY D TURNER,MAHMOUD EINO,JOHN J KABEL,
PI JERALD F AMANTEA
PC C12N15/09,A01K67/027,C12N1/19,C12N9/38//C12N1/19,C12N1:685),
PC (C12N9/38,C12N1:685),C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
FH key Location/Qualifiers
FT source 1..21
location/Qualifiers
1..21
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/mol_type="genomic DNA"
/db_xref="taxon:33169"

Query Match 1.1%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1605 GGTCTCGAGACACTGATG 1624
|||||
Db 1 GGTACCGAGCACTGATGG 20

RESULT 109
AX117632 25 bp DNA linear PAT 11-MAY-2001
LOCUS AX117632
DEFINITION Sequence 2755 from Patent WO0129262.
ACCESSION AX117632
VERSION AX117632.1 GI:14034583
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Picoult-Newburg,J. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 2755 26-APR-2001;
Orchid Biosciences, Inc (US)
FEATURES
source 1..25
location/Qualifiers
1..25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 1.1%; Score 15.2; DB 1; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1511 CTGTTAATTAAAAA 1530
|||||
Db 5 CTCTTAAAAA 24

RESULT 110
AR187059/c 17 bp DNA linear PAT 20-APR-2002
LOCUS AR187059
DEFINITION Sequence 2547 from patent US 6346398.
ACCESSION AR187059
VERSION AR187059.1 GI:20233024
KEYWORDS
SOURCE unknown.
ORGANISM unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Payco,P., Mswiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 2547 12-FEB-2002;
LOCATION/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1520 AAAAAAAAAAAGTA 1534
16 AAAAAAAAAAAGTA 2

RESULT 111
ARI87060/c ARI87060 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 2548 from patent US 6346398.
ACCESSION ARI87060
VERSION ARI87060.1 GI:20233025
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 2548 12-FEB-2002;
FEATURES
source Location/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1520 AAAAAAAAAAAGTA 1534
15 AAAAAAAAAAAGTA 1

RESULT 112
AR323669/c AR323669 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 1071 from patent US 6566127.
ACCESSION AR323669
VERSION AR323669.1 GI:33709477
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 1071 20-MAY-2003;
FEATURES
source Location/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 1.1%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1520 AAAAAAAAAAAGTA 1534
16 AAAAAAAAAAAGTA 2

RESULT 113
AR323670/c AR323670 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 1072 from patent US 6566127.
ACCESSION AR323670
VERSION AR323670.1 GI:33709478

KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 1072 20-MAY-2003;
FEATURES
source Location/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 1.1%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1520 AAAAAAAAAAAGTA 1534
15 AAAAAAAAAAAGTA 1

RESULT 114
AX753821/c AX753821 17 bp DNA linear PAT 23-JUN-2003
DEFINITION Sequence 168 from Patent WO03037931.
ACCESSION AX753821
VERSION AX753821.1 GI:32166518
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE 1
AUTHORS Shannon,M. and Phan,T.
TITLE Human angiomin-like protein 1
JOURNAL Patent: WO 03037931-A 168 08-MAY-2003;
FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.1%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 726 TGGTGTGCTGCTGC 740
17 TGGTGTGCTGCTGC 3

RESULT 115
AX753822/c AX753822 17 bp DNA linear PAT 23-JUN-2003
DEFINITION Sequence 169 from Patent WO03037931.
ACCESSION AX753822
VERSION AX753822.1 GI:32166519
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE 1
AUTHORS Shannon,M. and Phan,T.
TITLE Human angiomin-like protein 1
JOURNAL Patent: WO 03037931-A 169 08-MAY-2003;
FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"

/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.1%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 726 TGCTGTTGCTGCTGC 740
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16 TGCTGTTGCTGCTGC 2

RESULT 116
AX753823/c 17 bp DNA linear PAT 23-JUN-2003
LOCUS AX753823
DEFINITION Sequence 170 from Patent WO03037931.
ACCESSION AX753823
VERSION AX753823.1 GI:32166520
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Shannon, M. and Phan, T.
TITLE Human angiotensin-like protein 1
JOURNAL Patent: WO 03037931-A 170 08-MAY-2003;
Amersham Biosciences SV Corp. (US)
LOCATION/Qualifiers

FEATURES
source 1. 17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.1%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 726 TGCTGTTGCTGCTGC 740
|||||
15 TGCTGTTGCTGCTGC 1

RESULT 117
ARI02020/c 19 bp DNA linear PAT 14-FEB-2001
LOCUS ARI02020
DEFINITION Sequence 18 from patent US 6083731.
ACCESSION ARI02020
VERSION ARI02020.1 GI:12812818
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Croteau, R., Bruce, J., Lupien, S., Lee, and Karp, F.
TITLE Recombinant materials and methods for the production of limonene hydroxylases
JOURNAL Patent: US 6083731-A 18 04-JUL-2000;
FEATURES
source 1. 19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 15; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.7e+02;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1519 TAAATAAAAAAAAAAGTAAAA 1537
:|||||
19 DAAAAAAAAAAAAAAAAAAAAA 1

RESULT 118

ARI34802/c 19 bp DNA linear PAT 16-MAY-2001
LOCUS ARI34802
DEFINITION Sequence 18 from patent US 6194185.
ACCESSION ARI34802
VERSION ARI34802.1 GI:14123707
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Croteau, R., Bruce, J., Lupien, S., Lee, and Karp, F.
TITLE Recombinant materials and methods for production of limonene hydroxylases
JOURNAL Patent: US 6194185-A 18 27-FEB-2001;
FEATURES
source 1. 19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 15; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.7e+02;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1519 TAAATAAAAAAAAAAGTAAAA 1537
:|||||
19 DAAAAAAAAAAAAAAAAAAAAA 1

RESULT 119
AR352460/c 19 bp DNA linear PAT 17-AUG-2003
LOCUS AR352460
DEFINITION Sequence 6 from patent US 6589752.
ACCESSION AR352460
VERSION AR352460.1 GI:33757610
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kong, Y., Chung, J., Y., Bahk, Y., Y., Kang, S., Y., and Cho, S., Y.
TITLE Recombinant antigen of Taenia solium metacercodes
JOURNAL Patent: US 6589752-A 6 08-JUL-2003;
FEATURES
source 1. 19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 15; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1241 CCTCATCTTTGTTT 1255
|||||
18 CCTCATCTTTGTTT 4

RESULT 120
E28098/c 20 bp DNA linear PAT 18-JUN-2001
LOCUS E28098
DEFINITION Method for analyzing DNA fragment.
ACCESSION E28098
VERSION E28098.1 GI:13018323
KEYWORDS JP 1999196874-A/9.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 20)
AUTHORS Hideki, K. and Senshu, U.
TITLE Method for analyzing DNA fragment
JOURNAL Patent: JP 1999196874-A 9 27-JUL-1999;
HITACHI LTD
COMMENT OS Unidentified
FN JP 1999196874-A/9

PD 27-JUL-1999
PF 14-JAN-1998 JP 1998005399
PR HIDEKI KAMIBARA, SENSU UEMATSU
PC C12N15/09, C12Q1/68, G01N27/447, C12N15/00, G01N27/26 CC
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..20 /organism='Unidentified'.
FEATURES
source Location/Qualifiers
1..20 /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 1.1%; Score 15; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.6e+02;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1519 TMAAAAAAAAAAGTAAAA 1537
DB 19 BAAAAAAAAAAAAAAAAAAAA 1

RESULT 121
LOCUS AR294700/c 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 6435 from patent US 6537751.
ACCESSION AR294700
VERSION AR294700.1 GI:31681984
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Cohen, D., Chumakov, I. and Blumenfeld, M.
TITLE Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 6435 25-MAR-2003;
FEATURES
source Location/Qualifiers
1..20 /organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 941 CCTCAGTCACCTTCT 955
DB 16 CCTCAGTCACCTTCT 2

RESULT 122
LOCUS AR307942 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 153 from patent US 6551826.
ACCESSION AR307942
VERSION AR307942.1 GI:3198698
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Watt, A.T.
TITLE Antisense modulation of raiid expression
JOURNAL Patent: US 6551826-A 153 22-APR-2003;
FEATURES
source Location/Qualifiers
1..20 /organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1539 GGAAGCAGCATGTC 1553
DB 6 GGAAGCAGCATGTC 20

RESULT 123
LOCUS AX048446/c 20 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 45 from Patent WO0071747.
ACCESSION AX048446
VERSION AX048446.1 GI:12225610
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Boekenkamp, D., Hoppe, H. U. and Burgeraller, P.
TITLE Detection system for separating constituents of a sample and
production and use of the same
JOURNAL Patent: WO 0071747-A 45 30-NOV-2000;
Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES
source Location/Qualifiers
1..20 /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kunstlichen
Sequenz: Erkennungssystem"

Query Match 1.1%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1517 ATTAATAAAAAAAAAA 1531
DB 16 ATTAATAAAAAAAAAA 2

RESULT 124
LOCUS AX804844/c 21 bp DNA linear PAT 25-NOV-2003
DEFINITION Sequence 1012 from Patent WO03060160.
ACCESSION AX804844
VERSION AX804844.1 GI:38521985
KEYWORDS
SOURCE Oreochromis niloticus (Nile tilapia)
ORGANISM Oreochromis niloticus
REFERENCE 1
AUTHORS Lie, Y., Sieltjan, A., Hoeyum, M. and Lingaas, F.
TITLE Verification of food origin based on nucleic acid pattern
recognition
JOURNAL Patent: WO 03060160-A 1012 24-JUN-2003;
Genomar ASA (NO)
FEATURES
source Location/Qualifiers
1..21 /organism="Oreochromis niloticus"
/mol_type="unassigned DNA"
/db_xref="taxon:8128"

Query Match 1.1%; Score 15; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 735 TGCTGCTTGTGAC 749
|||||

Db 19 TGCTGCTTTGTGAC 5

RESULT 125
AR034896/c
LOCUS AR034896 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 12 from patent US 5869643.
ACCESSION AR034896
VERSION AR034896.1 GI:5950501
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Chatelain,F. and Kumarev,V.
TITLE Process for preparing polynucleotides on a solid support in a tightly packed bed
JOURNAL Patent: US 5869643-A 12 09-FEB-1999;
FEATURES Location/Qualifiers
1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2;

Qy 1520 AAAAAAAAAAGTAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 126
AR034899
LOCUS AR034899 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 18 from patent US 5869643.
ACCESSION AR034899
VERSION AR034899.1 GI:5950504
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Chatelain,F. and Kumarev,V.
TITLE Process for preparing polynucleotides on a solid support in a tightly packed bed
JOURNAL Patent: US 5869643-A 18 09-FEB-1999;
FEATURES Location/Qualifiers
1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2;

Qy 1520 AAAAAAAAAAGTAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 127
AR058305
LOCUS AR058305 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 3 from patent US 5837820.
ACCESSION AR058305
VERSION AR058305.1 GI:5983882
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS De Rose,R., Douce,R., Duval,M., Job,C. and Job,D.

TITLE Seed specific biotinylated protein, SBP65, from leguminous plants
JOURNAL Patent: US 5837820-A 3 17-NOV-1998;
FEATURES Location/Qualifiers
1..18
/organism="unknown"
/mol_type="unassigned DNA"

Qy 1520 AAAAAAAAAAGTAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 128
AR097579/c
LOCUS AR097579 18 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 9 from patent US 6071745.
ACCESSION AR097579
VERSION AR097579.1 GI:12806309
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Lin,C.-I.Patsy., Wallace,R.Bruce., Cossman,J. and French,C.
TITLE Method and formulation for lyophilizing cultured human cells to preserve RNA and DNA contained in cells for use in molecular biology experiments
JOURNAL Patent: US 6071745-A 9 06-JUN-2000;
FEATURES Location/Qualifiers
1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2;

Qy 1520 AAAAAAAAAAGTAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 129
AR101834
LOCUS AR101834 18 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 25 from patent US 6083713.
ACCESSION AR101834
VERSION AR101834.1 GI:12812632
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Manly,S.P., Kozlowski,M.R. and Neve,R.L.
TITLE Cloning and expression of .beta.App-C100 receptor (C100-R)
JOURNAL Patent: US 6083713-A 25 04-JUL-2000;
FEATURES Location/Qualifiers
1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2;

Qy 1520 AAAAAAAAAAGTAA 1537
Db 1 AAAAAAAAAAGAACCA 18

RESULT 130
LOCUS AR106506 18 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 30 from patent US 6107060.
ACCESSION AR106506
VERSION AR106506.1 GI:12821036
KEYWORDS
SOURCE
ORGANISM
Unclassified.
1 (bases 1 to 18)
AUTHORS Keeling,P. and Guan,H.
TITLE Starch encapsulation
JOURNAL Patent: US 6107060-A 30 22-AUG-2000;
FEATURES
Location/Qualifiers
source
1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1520 AAAAAAAAAAAGTAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 131
LOCUS AR106909/c 18 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 70 from patent US 6107092.
ACCESSION AR106909
VERSION AR106909.1 GI:12821439
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
1 (bases 1 to 18)
AUTHORS Cowart,L.M., Bennett,C.Frank. and O'Malley,B.W.
TITLE Antisense modulation of SRA expression
JOURNAL Patent: US 6107092-A 70 22-AUG-2000;
FEATURES
Location/Qualifiers
source
1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1489 ATACATTATTGCAGAAA 1506
Db 18 AAAGTTAATTGCAGAAA 1

RESULT 132
LOCUS BD222596/c 18 bp DNA linear PAT 17-JUL-2003
DEFINITION Aminoxy-modified nucleoside compound and oligomer compound
produced therefrom.
ACCESSION BD222596
VERSION BD222596.1 GI:33032366
KEYWORDS JP 2002522447-A/14.
SOURCE
ORGANISM
synthetic construct
artificial sequences.
1 (bases 1 to 18)
AUTHORS Manoharan,M., Cook,P.D., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified nucleoside compound and oligomer compound
produced therefrom
JOURNAL Patent: JP 2002522447-A 14 23-JUL-2002;

COMMENT
ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002522447-A/14
PD 23-JUL-2002
PF 09-AUG-1999 JP 2000563675
PR 07-AUG-1998 US 09/130973
PI MUTHIAH MANOHARAN,PHILIP DAN COOK,THAZHA P PRAKASH,ANDREW M
PI KAMASAKI
PC C07H19/167,C07H19/067,C07H19/10,C07H19/20,C07H21/02,C12N15/00,
CC C12N15/00
CC Description of Artificial Sequence: antisense sequence FH
Key
FT source
1..18
/organism="Artificial Sequence".
Location/Qualifiers
source
1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1520 AAAAAAAAAAAGTAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 133
LOCUS E28535 18 bp DNA linear PAT 18-JUN-2001
DEFINITION Method for labeling oligonucleotide and utilization thereof.
ACCESSION E28535
VERSION E28535.1 GI:13025387
KEYWORDS JP 1999075880-A/2.
SOURCE
ORGANISM
unidentified
unclassified.
1 (bases 1 to 18)
AUTHORS Kenichi,H., Hiroshi,Y. and Masahide,N.
TITLE Method for labeling oligonucleotide and utilization thereof
JOURNAL Patent: JP 1999075880-A 2 23-MAR-1999;
COMMENT
OS Unidentified
PN JP 1999075880-A/2
PD 23-MAR-1999
PF 10-JUL-1998 JP 1998195719
PR
PI KENICHI HANAKI,HIROSHI YOSHIKURA,MASAHIDE NOZAKI PC
CC C12N15/09,C12Q1/68,G01N33/58,C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key
FT source
1..18
/organism="Unidentified".
Location/Qualifiers
source
1..18
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1520 AAAAAAAAAAAGTAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 134
E28536/c

LOCUS E28536 18 bp DNA linear PAT 18-JUN-2001
DEFINITION Method for labeling oligonucleotide and utilization thereof.
ACCESSION E28536
VERSION E28536.1 GI:13025388
KEYWORDS JP 1999075880-A/3.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 18)
AUTHORS Kenichi,H., Hiroshi,Y. and Maehide,N.
TITLE Method for labeling oligonucleotide and utilization thereof
JOURNAL Patent: JP 1999075880-A 3 23-MAR-1999;
CHEMO SERO THERAPEUT RES INST
OS Unidentified
PN JP 1999075880-A/3
PD 23-MAR-1999
PF 10-JUL-1998 JP 1998195719
PR
PI KENICHI HANAKI,HIROSHI YOSHIKURA,MASAHIDE NOZAKI PC
C12N15/09,C12Q1/68,G01N33/58,C12N15/00
CC Strandedness: Single;
Topology: Linear;
FH Key Location/Qualifiers
FT source 1..18
Location/Qualifiers
1..18
/organism="Unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

LOCUS I79509 18 bp DNA linear PAT 10-JUN-1998
DEFINITION Sequence 16 from patent US 5707807.
ACCESSION I79509
VERSION I79509.1 GI:3207799
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kato,K.
TITLE Molecular indexing for expressed gene analysis
JOURNAL Patent: US 5707807-A 16 13-JAN-1998;
FEATURES
source 1..18
Location/Qualifiers
1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

LOCUS I79509/c 18 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 1167 from patent US 6350934.
ACCESSION ARI96702
FEATURES
source 1..18
Location/Qualifiers
1..18
/organism="unknown"
/mol_type="genomic DNA"

VERSION ARI96702.1 GI:20246139
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Zwick,M.G., Edington,B.E., McSwiggen,J.A., Merlo,P,Ann Owens.,
TITLE Guo,L., Skokut,T.A., Young,S.A., Folkerts,O. and Merlo,D.J.
JOURNAL Nucleic acid encoding delta-9 desaturase
FEATURES Patent: US 6350934-A 1167 26-FEB-2002;
source 1..18
Location/Qualifiers
1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

LOCUS ARI96704/c 18 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 1169 from patent US 6350934.
ACCESSION ARI96704
VERSION ARI96704.1 GI:20246141
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Zwick,M.G., Edington,B.E., McSwiggen,J.A., Merlo,P,Ann Owens.,
TITLE Guo,L., Skokut,T.A., Young,S.A., Folkerts,O. and Merlo,D.J.
JOURNAL Nucleic acid encoding delta-9 desaturase
FEATURES Patent: US 6350934-A 1169 26-FEB-2002;
source 1..18
Location/Qualifiers
1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

LOCUS ARI215435/c 18 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 9 from patent US 6410321.
ACCESSION ARI215435
VERSION ARI215435.1 GI:23313691
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Iln,C.-I.P., Wallace,R.B., Cosman,J. and French,C.
TITLE Method and formulation for lyophilizing cultured human cells to preserve RNA and DNA contained in cells for use in molecular biology experiments
JOURNAL Patent: US 6410321-A 9 25-JUN-2002;
FEATURES
source 1..18
Location/Qualifiers
1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAGTAAA 1537
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 139
LOCUS AR222464 18 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 24 from patent US 6429300.
ACCESSION AR222464
VERSION AR222464.1 GI:23329995
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kurtz,M., Lohse,P. and Wagner,R.
TITLE Peptide acceptor ligation method
JOURNAL Patent: US 6429300-A 24 06-AUG-2002;
FEATURES
Location/Qualifiers
1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAGTAAA 1537
DB 1 AAAAAAAAAAAAAAAAAA 18

RESULT 140
LOCUS AR412363 18 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 14 from patent US 6639062.
ACCESSION AR412363
VERSION AR412363.1 GI:40167473
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Manoharan,M., Cook,P.D., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified nucleosidic compounds and oligomeric compounds prepared therefrom
JOURNAL Patent: US 6639062-A 14 28-OCT-2003;
FEATURES
Location/Qualifiers
1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAGTAAA 1537
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 141
LOCUS AR473365 18 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 9 from patent US 6686460.
ACCESSION AR473365
VERSION AR473365.1 GI:42708816

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 18)
TITLE Lin,C.-I.,P., Wallace,R.B., Cossman,T. and French,C.
METHOD Method and formulation for lyophilizing cultured human cells to preserve RNA and DNA contained in cells for use in molecular biology experiments
JOURNAL Patent: US 6686460-A 9 03-FEB-2004;
FEATURES
Location/Qualifiers
1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAGTAAA 1537
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 142
LOCUS AR487019 18 bp DNA linear PAT 14-MAY-2004
DEFINITION Sequence 6 from patent US 6706476.
ACCESSION AR487019
VERSION AR487019.1 GI:47251966
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Thirstrup,K., Warthoe,P. and Pettersson,N.B.
TITLE Process for amplifying and labeling single stranded cDNA by 5' ligated adaptor mediated amplification
JOURNAL Patent: US 6706476-A 6 16-MAR-2004;
FEATURES
Location/Qualifiers
1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAGTAAA 1537
DB 1 AAAAAAAAAAAAAAAAAA 18

RESULT 143
LOCUS AR487020 18 bp DNA linear PAT 14-MAY-2004
DEFINITION Sequence 7 from patent US 6706476.
ACCESSION AR487020
VERSION AR487020.1 GI:47251967
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Thirstrup,K., Warthoe,P. and Pettersson,N.B.
TITLE Process for amplifying and labeling single stranded cDNA by 5' ligated adaptor mediated amplification
JOURNAL Patent: US 6706476-A 7 16-MAR-2004;
FEATURES
Location/Qualifiers
1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAA 1537
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 144
AX004875/c

LOCUS AX004875 18 bp DNA linear PAT 24-AUG-2000
DEFINITION Sequence 4 from Patent WO910527.
ACCESSION AX004875
VERSION AX004875.1 GI:9928275
KEYWORDS

SOURCE
ORGANISM
synthetic construct
artificial sequences.

REFERENCE
1 Bayer, E. and Schwilz, J.
Method for isolating anionic organic substances from aqueous systems using cationic polymer nanoparticles
Patent: WO 910527-A 4 04-MAR-1999;

JOURNAL
SUBDEUTSCHE KALKSTICKSTOFF (DE); BAYER ERNST (DE)
Location/Qualifiers

FEATURES
source
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="3' palmityl oligonucleotide"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAA 1537
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 145
AX004879/c

LOCUS AX004879 18 bp RNA linear PAT 24-AUG-2000
DEFINITION Sequence 8 from Patent WO910527.
ACCESSION AX004879
VERSION AX004879.1 GI:9928279
KEYWORDS

SOURCE
ORGANISM
synthetic construct
artificial sequences.

REFERENCE
1 Bayer, E. and Schwilz, J.
Method for isolating anionic organic substances from aqueous systems using cationic polymer nanoparticles
Patent: WO 910527-A 8 04-MAR-1999;

JOURNAL
SUBDEUTSCHE KALKSTICKSTOFF (DE); BAYER ERNST (DE)
Location/Qualifiers

FEATURES
source
1. .18
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="2' methyl-modified oligonucleotide"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAA 1537
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 146
AX008117
LOCUS AX008117 18 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 2 from Patent WO9967378.
ACCESSION AX008117
VERSION AX008117.1 GI:9995742
KEYWORDS

SOURCE
ORGANISM
synthetic construct
artificial sequences.

REFERENCE
1 Damha, M.J., Parniak, M.A., Wilds, C., Arion, D., Noronha, A.M. and Borkow, G.
Antisense oligonucleotide constructs based on beta -arabinofuranose and its analogues
Patent: WO 9967378-A 2 29-DEC-1999;

JOURNAL
DAMHA MASSAD JOSE (CA); PARNIAK MICHAEL A (CA); WILDS CHRISTOPHER (CA); UNIV MCGILL (CA); ARION DOMINIQUE (CA); NORONHA ANNE M (CA); BORKOW GADI (IL)
Location/Qualifiers

FEATURES
source
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Use as an oligomer"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAA 1537
DB 1 AAAAAAAAAAAAAAAAAA 18

RESULT 147
AX008118/c

LOCUS AX008118 18 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 3 from Patent WO9967378.
ACCESSION AX008118
VERSION AX008118.1 GI:9995743.
KEYWORDS

SOURCE
ORGANISM
synthetic construct
artificial sequences.

REFERENCE
1 Damha, M.J., Parniak, M.A., Wilds, C., Arion, D., Noronha, A.M. and Borkow, G.
Antisense oligonucleotide constructs based on beta -arabinofuranose and its analogues
Patent: WO 9967378-A 3 29-DEC-1999;

JOURNAL
DAMHA MASSAD JOSE (CA); PARNIAK MICHAEL A (CA); WILDS CHRISTOPHER (CA); UNIV MCGILL (CA); ARION DOMINIQUE (CA); NORONHA ANNE M (CA); BORKOW GADI (IL)
Location/Qualifiers

FEATURES
source
1. .18
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Use as an oligomer"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAA 1537
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 148

AX008122/c
LOCUS AX008122 18 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 7 from Patent WO967378.
ACCESSION AX008122
VERSION AX008122.1 GI:9995747
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS 1 Damha,M.J., Parniak,M.A., Wilds,C., Arion,D., Noronha,A.M. and Borkow,G.
TITLE Antisense oligonucleotide constructs based on beta -arabinoofuranose and its analogues
JOURNALS Patent: WO 9967378-A 7 29-DEC-1999;
DAMHA MASSAD JOSE (CA); PARNIAK MICHAEL A (CA); WILDS CHRISTOPHER (CA); UNIV MCGILL (CA); ARION DOMINIQUE (CA); NORONHA ANNE M (CA); BORKOW GADI (IL)
FEATURES
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Use as an oligomer"
Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAGTAAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1
RESULT 149
AX008123 18 bp DNA linear PAT 06-SEP-2000
LOCUS AX008123
DEFINITION Sequence 8 from Patent WO967378.
ACCESSION AX008123
VERSION AX008123.1 GI:9995748
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS 1 Damha,M.J., Parniak,M.A., Wilds,C., Arion,D., Noronha,A.M. and Borkow,G.
TITLE Antisense oligonucleotide constructs based on beta -arabinoofuranose and its analogues
JOURNALS Patent: WO 9967378-A 8 29-DEC-1999;
DAMHA MASSAD JOSE (CA); PARNIAK MICHAEL A (CA); WILDS CHRISTOPHER (CA); UNIV MCGILL (CA); ARION DOMINIQUE (CA); NORONHA ANNE M (CA); BORKOW GADI (IL)
FEATURES
source 1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Use as an oligomer"
Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAGTAAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1
RESULT 150
AX028843 18 bp DNA linear PAT 24-NOV-2000
LOCUS AX028843/c
DEFINITION Sequence 27 from Patent WO9732023.

ACCESSION AX028843
VERSION AX028843.1 GI:10189946
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS 1 Bruggiera,F., Holton,T.A. and Michael,M.Z.
TITLE Genetic sequences encoding flavonoid pathway enzymes and uses therefor
JOURNALS Patent: WO 9732023-A 27 04-SEP-1997;
FLORIGENE LIMITED (AU); BRUGLIERA FILIPPA (AU); HOLTON TIMOTHY ALBERT (AU); MICHAEL MICHAEL ZENON (AU)
FEATURES
source 1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide"
Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1519 TAAAAAAAAAAGTAAA 1536
Db 18 TAAAAAAAAAAAAAAAAA 1
RESULT 151
AX047271 18 bp DNA linear PAT 15-DEC-2000
LOCUS AX047271
DEFINITION Sequence 21 from Patent WO0068422.
ACCESSION AX047271
VERSION AX047271.1 GI:11876551
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS 1 Muehleger,K., Angerer,B., Seela,F., Ankenbauer,W., Augustin,M., Gumbiowski,K. and Zulauf,M.
TITLE High density labeling of dna with modified or chromophore carrying nucleotides and dna polymerases used
JOURNALS Patent: WO 0068422-A 21 16-NOV-2000;
Roche Diagnostics GmbH (DE)
FEATURES
source 1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="second fragment of SEQ ID NO: 6"
Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAAGTAAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1
RESULT 152
AX047273 18 bp DNA linear PAT 15-DEC-2000
LOCUS AX047273/c
DEFINITION Sequence 23 from Patent WO0068422.
ACCESSION AX047273
VERSION AX047273.1 GI:11876553
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS 1

AUTHORS Muehlegger, K., Angerer, B., Seela, F., Ankenbauer, W., Augustin, M., Gumbrowski, K., and Zulauf, M.
TITLE High density labeling of dna with modified or chromophore carrying nucleotides and dna polymerases used
JOURNAL Patent: WO 0068422-A 23 16-NOV-2000;
Roche Diagnostics GmbH (DE)
FEATURES Location/Qualifiers
SOURCE 1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="second fragment of SEQ ID NO: 6"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAAGTAAA 1537
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 153
LOCUS AX104721/c 18 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 913 from Patent WO0122972.
ACCESSION AX104721
VERSION AX104721.1 GI:13920918
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Krieg, A.M., Schetter, C. and Vollmer, J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 913 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical GmbH (DE)
FEATURES Location/Qualifiers
SOURCE 1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAAGTAAA 1537
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 154
LOCUS AX104747/c 18 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 939 from Patent WO0122972.
ACCESSION AX104747
VERSION AX104747.1 GI:13920944
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Krieg, A.M., Schetter, C. and Vollmer, J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 939 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical GmbH (DE)
FEATURES Location/Qualifiers
SOURCE 1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"

/db_xref="taxon:32630"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAAGTAAA 1537
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 155
LOCUS AX105651/c 18 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 10 from Patent WO0123564.
ACCESSION AX105651
VERSION AX105651.1 GI:13921674
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Stanton, L.W. and Kapoun, A.M.
TITLE Secreted factors
JOURNAL Patent: WO 0123564-A 10 05-APR-2001;
SciOs Inc. (US)
FEATURES Location/Qualifiers
SOURCE 1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAAGTAAA 1537
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 156
LOCUS AX106642/c 18 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 10 from Patent WO0123419.
ACCESSION AX106642
VERSION AX106642.1 GI:13923875
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Stanton, L.W. and Kapoun, A.M.
TITLE Differentially expressed genes
JOURNAL Patent: WO 0123419-A 10 05-APR-2001;
SciOs Inc. (US)
FEATURES Location/Qualifiers
SOURCE 1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAAGTAAA 1537
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 157
AX268883/c 18 bp DNA linear PAT 29-OCT-2001
LOCUS Sequence 84 from Patent WO0174901.
DEFINITION AX268883
ACCESSION AX268883
VERSION GI:16541910
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Stanton, L.W. and White, R.T.
TITLE Secured factors
JOURNAL Patent: WO 0174901-A 84 11-OCT-2001;
SciOs Inc. (US)
FEATURES
source
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligos corresponding to polylinker sequence."

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 158
AX355809/c 18 bp DNA linear PAT 06-FEB-2002
LOCUS Sequence 837 from Patent WO0197843.
DEFINITION AX355809
ACCESSION AX355809
VERSION GI:18620477
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Weiner, G. and Hartmann, G.
TITLE Methods for enhancing antibody-induced cell lysis and treating
JOURNAL Cancer
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES
source
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide-phosphorothioate
backbone"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 159
AX547774/c 18 bp DNA linear PAT 01-MAR-2003
LOCUS AX547774
DEFINITION Sequence 913 from Patent WO02053141.
ACCESSION AX547774
VERSION AX547774.1 GI:25812918
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct

artificial sequences.

REFERENCE
1
AUTHORS Bratzler, R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 913 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
FEATURES
source
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 160
AX547800/c 18 bp DNA linear PAT 01-MAR-2003
LOCUS AX547800
DEFINITION Sequence 939 from Patent WO02053141.
ACCESSION AX547800
VERSION AX547800.1 GI:25812944
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Bratzler, R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 939 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
FEATURES
source
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 161
AX814716/c 18 bp DNA linear PAT 05-DEC-2003
LOCUS AX814716
DEFINITION Sequence 1 from Patent WO03064441.
ACCESSION AX814716
VERSION AX814716.1 GI:39103916
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Damba, M.J. and Parniak, M.A.
TITLE Oligonucleotides comprising alternating segments and uses thereof
JOURNAL Patent: WO 03064441-A 1 07-AUG-2003;
MCGILL UNIVERSITY (CA)
FEATURES
source
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

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/note="Oligonucleotide"
Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 162
AX814723/c 18 bp DNA linear PAT 05-DEC-2003
LOCUS AX814723
DEFINITION Sequence 8 from Patent WO03064441.
ACCESSION AX814723
VERSION AX814723.1 GI:39103922
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Damha,M.J. and Parniak,M.A.
TITLE Oligonucleotides comprising alternating segments and uses thereof
JOURNAL Patent: WO 03064441-A 8 07-AUG-2003;
MCGILL UNIVERSITY (CA)
FEATURES
source 1.18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide"
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/note="Residues 1-3, 7-9, and 13-15 are
2'-O-methyl-D-uridine"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 163
AX814724/c 18 bp DNA linear PAT 05-DEC-2003
LOCUS AX814724
DEFINITION Sequence 9 from Patent WO03064441.
ACCESSION AX814724
VERSION AX814724.1 GI:39103923
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Damha,M.J. and Parniak,M.A.
TITLE Oligonucleotides comprising alternating segments and uses thereof
JOURNAL Patent: WO 03064441-A 9 07-AUG-2003;
MCGILL UNIVERSITY (CA)
FEATURES
source 1.18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide"
/misc_feature 1.15
/note="Residues 1-3, 7-9, and 13-15 are
2'-O-methyl-D-uridine"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 1520 AAAAAAAAAAGTAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 164
AX814725/c 18 bp DNA linear PAT 05-DEC-2003
LOCUS AX814725
DEFINITION Sequence 10 from Patent WO03064441.
ACCESSION AX814725
VERSION AX814725.1 GI:39103924
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Damha,M.J. and Parniak,M.A.
TITLE Oligonucleotides comprising alternating segments and uses thereof
JOURNAL Patent: WO 03064441-A 10 07-AUG-2003;
MCGILL UNIVERSITY (CA)
FEATURES
source 1.18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide"
/misc_feature 1.16
/note="Residues 1-6 and 13-18 are 2'-O-methyl-D-uridine"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 165
AX814736 18 bp RNA linear PAT 05-DEC-2003
LOCUS AX814736
DEFINITION Sequence 21 from Patent WO03064441.
ACCESSION AX814736
VERSION AX814736.1 GI:39103935
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Damha,M.J. and Parniak,M.A.
TITLE Oligonucleotides comprising alternating segments and uses thereof
JOURNAL Patent: WO 03064441-A 21 07-AUG-2003;
MCGILL UNIVERSITY (CA)
FEATURES
source 1.18
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Target RNA oligonucleotide"

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 166
BD085545/c 18 bp RNA linear PAT 27-AUG-2002
LOCUS BD085545
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DEFINITION Method of comparison and detection of RNA amount and DNA amount.
ACCESSION BD085545
VERSION BD085545.1 GI:22631155
KEYWORDS JP 2001333800-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 18)
AUTHORS Shimada, K.
TITLE Method of comparison and detection of RNA amount and DNA amount
JOURNAL Patent: JP 2001333800-A 2 04-DEC-2001;
UNITECH CO LTD
OS Homo sapiens (human)
PN JP 2001333800-A/2
PD 04-DEC-2001
PF 30-MAY-2000 JP 2000160324
PI KAOI SHIMADA
PC C12Q1/68,C12N15/09,G01N33/50,C12N15/00
CC Method of comparison and detection of RNA amount and DNA CC

FEATURES
source
FH Key Location/Qualifiers
FT source 1..18 /organism='Homo sapiens (human)'.
1..18 /organism='Homo sapiens'
/mol_type='genomic RNA'
/db_xref='taxon:9606'

Query Match 1.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2;

OY 1520 AAAAAAAAAAGTAAA 1537
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 167
LOCUS A68209 19 bp DNA linear PAT 06-MAY-1999
DEFINITION Sequence 4 from Patent WO9747636.
ACCESSION A68209
VERSION A68209.1 GI:4759376
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 19)
AUTHORS Collingwood, S.P., Moser, H.E., Altmann, K. and Douglas, M.E.
TITLE INTERMEDIATES FOR OLIGONUCLEOTIDE SYNTHESIS
JOURNAL Patent: WO 9747636-A 4 18-DEC-1997;
CIBA GEIGY AG (CH)
FEATURES
source
1..19 Location/Qualifiers
/organism='unidentified'
/mol_type='unassigned DNA'
/db_xref='taxon:32644'

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2;

OY 1520 AAAAAAAAAAGTAAA 1537
DB 19 AAAAAAAAAAAAAAAAAA 2

RESULT 168
LOCUS AR048767 19 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1 from patent US 5821354.

ACCESSION AR048767
VERSION AR048767.1 GI:5971110
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Leclerc, G. and Martel, R.
TITLE Radiolabeled DNA oligonucleotide and method of preparation
JOURNAL Patent: US 5821354-A 1 13-OCT-1998;
FEATURES
source
1..19 Location/Qualifiers
/organism='unknown'
/mol_type='unassigned DNA'

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2;

OY 1520 AAAAAAAAAAGTAAA 1537
DB 19 AAAAAAAAAAAAAAAAAA 2

RESULT 169
LOCUS AR111371 19 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 1 from patent US 6127124.
ACCESSION AR111371
VERSION AR111371.1 GI:12828219
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Leeds, J.M. and Cummins, L.L.
TITLE Fluorescence based nuclease assay
JOURNAL Patent: US 6127124-A 1 03-OCT-2000;
FEATURES
source
1..19 Location/Qualifiers
/organism='unknown'
/mol_type='unassigned DNA'

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2;

OY 1520 AAAAAAAAAAGTAAA 1537
DB 19 AAAAAAAAAAAAAAAAAA 2

RESULT 170
LOCUS AR111946 19 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 20 from patent US 6127533.
ACCESSION AR111946
VERSION AR111946.1 GI:12828794
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook, P.Dan., Manoharan, M. and Kawasaki, A. Mamoru.
TITLE 2'-O-aminoxy-modified oligonucleotides
JOURNAL Patent: US 6127533-A 20 03-OCT-2000;
FEATURES
source
1..19 Location/Qualifiers
/organism='unknown'
/mol_type='unassigned DNA'

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2;

Matches	16;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
Qy	1520	AAAAAAAAAAAGTAAA	1537						
Db	19	AAAAAAAAAAAAAAAAAAAA	2						
RESULT 171									
LOCUS	AR111947/c		19 bp	DNA		linear		PAT 14-FEB-2001	
DEFINITION	Sequence	21 from patent US 6127533.							
ACCESSION	AR111947								
VERSION	AR111947.1	GI:12828795							
KEYWORDS									
SOURCE	Unknown.								
ORGANISM	Unknown.								
REFERENCE	Unclassified.								
AUTHORS	1 (bases 1 to 19)								
TITLE	Cook, P. Dan., Manoharan, M. and Kawasaki, A. Mamoru.								
JOURNAL	2'-O-aminoxy-modified oligonucleotides								
FEATURES	Patent: US 6127533-A 21 03-OCT-2000;								
source	Location/Qualifiers								
	1..19								
	/organism="unknown"								
	/mol_type="unassigned DNA"								
Query Match		1.1%;	Score 14.8;	DB 1;	Length 19;				
Best Local Similarity		88.9%;	Pred. No. 1.9e+02;						
Matches	16;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
Qy	1520	AAAAAAAAAAAGTAAA	1537						
Db	19	AAAAAAAAAAAAAAAAAAAA	2						
RESULT 172									
LOCUS	AR111948/c		19 bp	DNA		linear		PAT 14-FEB-2001	
DEFINITION	Sequence	22 from patent US 6127533.							
ACCESSION	AR111948								
VERSION	AR111948.1	GI:12828796							
KEYWORDS									
SOURCE	Unknown.								
ORGANISM	Unknown.								
REFERENCE	Unclassified.								
AUTHORS	1 (bases 1 to 19)								
TITLE	Cook, P. Dan., Manoharan, M. and Kawasaki, A. Mamoru.								
JOURNAL	2'-O-aminoxy-modified oligonucleotides								
FEATURES	Patent: US 6127533-A 22 03-OCT-2000;								
source	Location/Qualifiers								
	1..19								
	/organism="unknown"								
	/mol_type="unassigned DNA"								
Query Match		1.1%;	Score 14.8;	DB 1;	Length 19;				
Best Local Similarity		88.9%;	Pred. No. 1.9e+02;						
Matches	16;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
LOCUS	AR111949/c		19 bp	DNA		linear		PAT 14-FEB-2001	
DEFINITION	Sequence	23 from patent US 6127533.							
ACCESSION	AR111949								
VERSION	AR111949.1	GI:12828797							
KEYWORDS									
SOURCE	Unknown.								
ORGANISM	Unknown.								
REFERENCE	Unclassified.								
AUTHORS	1 (bases 1 to 19)								
TITLE	Cook, P. Dan., Manoharan, M. and Kawasaki, A. Mamoru.								
JOURNAL	2'-O-aminoxy-modified oligonucleotides								
FEATURES	Patent: US 6127533-A 22 03-OCT-2000;								
source	Location/Qualifiers								
	1..19								
	/organism="unknown"								
	/mol_type="unassigned DNA"								
Query Match		1.1%;	Score 14.8;	DB 1;	Length 19;				
Best Local Similarity		88.9%;	Pred. No. 1.9e+02;						
Matches	16;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
Qy	1520	AAAAAAAAAAAGTAAA	1537						
Db	19	AAAAAAAAAAAAAAAAAAAA	2						

Query Match	1.1%;	Score 14.8;	DB 1;	Length 19;
Best Local Similarity	88.9%;	Pred. No. 1.9e+02;		
Matches 16;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
<p>REFERENCE</p> <p>ATTHORS Cook, P.Dan., Manoharan, M. and Kawasaki, A. Mamoru.</p> <p>TITLE 2'-O-aminooxy-modified oligonucleotides</p> <p>JOURNAL Patent: US 6127533-A 23 03-OCT-2000;</p> <p>FEATURES Location/Qualifiers</p> <p>1. .19</p> <p>source /organism="unknown"</p> <p>/mol_type="unassigned DNA"</p>				
<p>RESULT 174</p> <p>LOCUS AR111950/c 19 bp DNA linear PAT 14-FEB-2001</p> <p>DEFINITION Sequence 24 from patent US 6127533.</p> <p>ACCESSION AR111950</p> <p>VERSION AR111950.1 GI:12828798</p> <p>KEYWORDS</p> <p>SOURCE Unknown.</p> <p>ORGANISM Unclassified.</p> <p>REFERENCE 1 (bases 1 to 19)</p> <p>ATTHORS Cook, P.Dan., Manoharan, M. and Kawasaki, A. Mamoru.</p> <p>TITLE 2'-O-aminooxy-modified oligonucleotides</p> <p>JOURNAL Patent: US 6127533-A 24 03-OCT-2000;</p> <p>FEATURES Location/Qualifiers</p> <p>1. .19</p> <p>source /organism="unknown"</p> <p>/mol_type="unassigned DNA"</p>				
<p>Query Match</p> <p>Best Local Similarity 88.9%;</p> <p>Matches 16;</p> <p>Conservative 0;</p> <p>Mismatches 2;</p> <p>Indels 0;</p> <p>Gaps 0;</p>				
<p>RESULT 175</p> <p>LOCUS AR111951/c 19 bp DNA linear PAT 14-FEB-2001</p> <p>DEFINITION Sequence 25 from patent US 6127533.</p> <p>ACCESSION AR111951</p> <p>VERSION AR111951.1 GI:12828799</p> <p>KEYWORDS</p> <p>SOURCE Unknown.</p> <p>ORGANISM Unclassified.</p> <p>REFERENCE 1 (bases 1 to 19)</p> <p>ATTHORS Cook, P.Dan., Manoharan, M. and Kawasaki, A. Mamoru.</p> <p>TITLE 2'-O-aminooxy-modified oligonucleotides</p> <p>JOURNAL Patent: US 6127533-A 25 03-OCT-2000;</p> <p>FEATURES Location/Qualifiers</p> <p>1. .19</p> <p>source /organism="unknown"</p> <p>/mol_type="unassigned DNA"</p>				
<p>Query Match</p> <p>Best Local Similarity 88.9%;</p> <p>Matches 16;</p> <p>Conservative 0;</p> <p>Mismatches 2;</p> <p>Indels 0;</p> <p>Gaps 0;</p>				
<p>RESULT 176</p> <p>LOCUS AR111952/c 19 bp DNA linear PAT 14-FEB-2001</p> <p>DEFINITION Sequence 26 from patent US 6127533.</p> <p>ACCESSION AR111952</p> <p>VERSION AR111952.1 GI:12828800</p> <p>KEYWORDS</p> <p>SOURCE Unknown.</p> <p>ORGANISM Unclassified.</p> <p>REFERENCE 1 (bases 1 to 19)</p> <p>ATTHORS Cook, P.Dan., Manoharan, M. and Kawasaki, A. Mamoru.</p> <p>TITLE 2'-O-aminooxy-modified oligonucleotides</p> <p>JOURNAL Patent: US 6127533-A 26 03-OCT-2000;</p> <p>FEATURES Location/Qualifiers</p> <p>1. .19</p> <p>source /organism="unknown"</p> <p>/mol_type="unassigned DNA"</p>				
<p>Query Match</p> <p>Best Local Similarity 88.9%;</p> <p>Matches 16;</p> <p>Conservative 0;</p> <p>Mismatches 2;</p> <p>Indels 0;</p> <p>Gaps 0;</p>				
<p>RESULT 177</p> <p>LOCUS AR111953/c 19 bp DNA linear PAT 14-FEB-2001</p> <p>DEFINITION Sequence 27 from patent US 6127533.</p> <p>ACCESSION AR111953</p> <p>VERSION AR111953.1 GI:12828801</p> <p>KEYWORDS</p> <p>SOURCE Unknown.</p> <p>ORGANISM Unclassified.</p> <p>REFERENCE 1 (bases 1 to 19)</p> <p>ATTHORS Cook, P.Dan., Manoharan, M. and Kawasaki, A. Mamoru.</p> <p>TITLE 2'-O-aminooxy-modified oligonucleotides</p> <p>JOURNAL Patent: US 6127533-A 27 03-OCT-2000;</p> <p>FEATURES Location/Qualifiers</p> <p>1. .19</p> <p>source /organism="unknown"</p> <p>/mol_type="unassigned DNA"</p>				
<p>Query Match</p> <p>Best Local Similarity 88.9%;</p> <p>Matches 16;</p> <p>Conservative 0;</p> <p>Mismatches 2;</p> <p>Indels 0;</p> <p>Gaps 0;</p>				
<p>RESULT 178</p> <p>LOCUS AR111954/c 19 bp DNA linear PAT 14-FEB-2001</p> <p>DEFINITION Sequence 28 from patent US 6127533.</p> <p>ACCESSION AR111954</p> <p>VERSION AR111954.1 GI:12828802</p> <p>KEYWORDS</p> <p>SOURCE Unknown.</p> <p>ORGANISM Unclassified.</p> <p>REFERENCE 1 (bases 1 to 19)</p> <p>ATTHORS Cook, P.Dan., Manoharan, M. and Kawasaki, A. Mamoru.</p> <p>TITLE 2'-O-aminooxy-modified oligonucleotides</p> <p>JOURNAL Patent: US 6127533-A 28 03-OCT-2000;</p> <p>FEATURES Location/Qualifiers</p> <p>1. .19</p> <p>source /organism="unknown"</p> <p>/mol_type="unassigned DNA"</p>				
<p>Query Match</p> <p>Best Local Similarity 88.9%;</p> <p>Matches 16;</p> <p>Conservative 0;</p> <p>Mismatches 2;</p> <p>Indels 0;</p> <p>Gaps 0;</p>				
<p>RESULT 179</p> <p>LOCUS AR111955/c 19 bp DNA linear PAT 14-FEB-2001</p> <p>DEFINITION Sequence 29 from patent US 6127533.</p> <p>ACCESSION AR111955</p> <p>VERSION AR111955.1 GI:12828803</p> <p>KEYWORDS</p> <p>SOURCE Unknown.</p> <p>ORGANISM Unclassified.</p> <p>REFERENCE 1 (bases 1 to 19)</p> <p>ATTHORS Cook, P.Dan., Manoharan, M. and Kawasaki, A. Mamoru.</p> <p>TITLE 2'-O-aminooxy-modified oligonucleotides</p> <p>JOURNAL Patent: US 6127533-A 29 03-OCT-2000;</p> <p>FEATURES Location/Qualifiers</p> <p>1. .19</p> <p>source /organism="unknown"</p> <p>/mol_type="unassigned DNA"</p>				
<p>Query Match</p> <p>Best Local Similarity 88.9%;</p> <p>Matches 16;</p> <p>Conservative 0;</p> <p>Mismatches 2;</p> <p>Indels 0;</p> <p>Gaps 0;</p>				
<p>RESULT 180</p> <p>LOCUS AR111956/c 19 bp DNA linear PAT 14-FEB-2001</p> <p>DEFINITION Sequence 30 from patent US 6127533.</p> <p>ACCESSION AR111956</p> <p>VERSION AR111956.1 GI:12828804</p> <p>KEYWORDS</p> <p>SOURCE Unknown.</p> <p>ORGANISM Unclassified.</p> <p>REFERENCE 1 (bases 1 to 19)</p> <p>ATTHORS Cook, P.Dan., Manoharan, M. and Kawasaki, A. Mamoru.</p> <p>TITLE 2'-O-aminooxy-modified oligonucleotides</p> <p>JOURNAL Patent: US 6127533-A 30 03-OCT-2000;</p> <p>FEATURES Location/Qualifiers</p> <p>1. .19</p> <p>source /organism="unknown"</p> <p>/mol_type="unassigned DNA"</p>				
<p>Query Match</p> <p>Best Local Similarity 88.9%;</p> <p>Matches 16;</p> <p>Conservative 0;</p> <p>Mismatches 2;</p> <p>Indels 0;</p> <p>Gaps 0;</p>				
<p>RESULT 181</p> <p>LOCUS AR111957/c 19 bp DNA linear PAT 14-FEB-2001</p> <p>DEFINITION Sequence 31 from patent US 6127533.</p> <p>ACCESSION AR111957</p> <p>VERSION AR111957.1 GI:12828805</p> <p>KEYWORDS</p> <p>SOURCE Unknown.</p> <p>ORGANISM Unclassified.</p> <p>REFERENCE 1 (bases 1 to 19)</p> <p>ATTHORS Cook, P.Dan., Manoharan, M. and Kawasaki, A. Mamoru.</p> <p>TITLE 2'-O-aminooxy-modified oligonucleotides</p> <p>JOURNAL Patent: US 6127533-A 31 03-OCT-2000;</p> <p>FEATURES Location/Qualifiers</p> <p>1. .19</p> <p>source /organism="unknown"</p> <p>/mol_type="unassigned DNA"</p>				
<p>Query Match</p> <p>Best Local Similarity 88.9%;</p> <p>Matches 16;</p> <p>Conservative 0;</p> <p>Mismatches 2;</p> <p>Indels 0;</p> <p>Gaps 0;</p>				
<p>RESULT 182</p> <p>LOCUS AR111958/c 19 bp DNA linear PAT 14-FEB-2001</p> <p>DEFINITION Sequence 32 from patent US 6127533.</p> <p>ACCESSION AR111958</p> <p>VERSION AR111958.1 GI:12828806</p> <p>KEYWORDS</p> <p>SOURCE Unknown.</p> <p>ORGANISM Unclassified.</p> <p>REFERENCE 1 (bases 1 to 19)</p> <p>ATTHORS Cook, P.Dan., Manoharan, M. and Kawasaki, A. Mamoru.</p> <p>TITLE 2'-O-aminooxy-modified oligonucleotides</p> <p>JOURNAL Patent: US 6127533-A 32 03-OCT-2000;</p> <p>FEATURES Location/Qualifiers</p> <p>1. .19</p> <p>source /organism="unknown"</p> <p>/mol_type="unassigned DNA"</p>				
<p>Query Match</p> <p>Best Local Similarity 88.9%;</p> <p>Matches 16;</p> <p>Conservative 0;</p> <p>Mismatches 2;</p> <p>Indels 0;</p> <p>Gaps 0;</p>				
<p>RESULT 183</p> <p>LOCUS AR111959/c 19 bp DNA linear PAT 14-FEB-2001</p> <p>DEFINITION Sequence 33 from patent US 6127533.</p> <p>ACCESSION AR111959</p> <p>VERSION AR111959.1 GI:12828807</p> <p>KEYWORDS</p> <p>SOURCE Unknown.</p> <p>ORGANISM Unclassified.</p> <p>REFERENCE 1 (bases 1 to 19)</p> <p>ATTHORS Cook, P.Dan., Manoharan, M. and Kawasaki, A. Mamoru.</p> <p>TITLE 2'-O-aminooxy-modified oligonucleotides</p> <p>JOURNAL Patent: US 6127533-A 33 03-OCT-2000;</p> <p>FEATURES</p>				

RESULT 176
LOCUS AR11952/c 19 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 26 from patent US 6127533.
ACCESSION AR11952
VERSION AR11952.1 GI:12828800
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE 2'-O-aminooxy-modified oligonucleotides
JOURNAL Patent: US 6127533-A 26 03-OCT-2000;
FEATURES Location/Qualifiers
source. 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred.No.1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1520 AAAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 177
LOCUS AR11953/c 19 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 27 from patent US 6127533.
ACCESSION AR11953
VERSION AR11953.1 GI:12828801
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE 2'-O-aminooxy-modified oligonucleotides
JOURNAL Patent: US 6127533-A 27 03-OCT-2000;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred.No.1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1520 AAAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 178
LOCUS AR11957/c 19 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 31 from patent US 6127533.
ACCESSION AR11957
VERSION AR11957.1 GI:12828805
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE 2'-O-aminooxy-modified oligonucleotides
JOURNAL Patent: US 6127533-A 31 03-OCT-2000;
FEATURES Location/Qualifiers
source 1..19

/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred.No.1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1520 AAAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 179
LOCUS AR11959/c 19 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 33 from patent US 6127533.
ACCESSION AR11959
VERSION AR11959.1 GI:12828807
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE 2'-O-aminooxy-modified oligonucleotides
JOURNAL Patent: US 6127533-A 33 03-OCT-2000;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred.No.1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1520 AAAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 180
LOCUS AR11960/c 19 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 34 from patent US 6127533.
ACCESSION AR11960
VERSION AR11960.1 GI:12828808
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE 2'-O-aminooxy-modified oligonucleotides
JOURNAL Patent: US 6127533-A 34 03-OCT-2000;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred.No.1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1520 AAAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 181
LOCUS AR11970/c 19 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 44 from patent US 6127533.
ACCESSION AR11970

VERSION AR11970.1 GI:12828618
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook, P. Dan., Manoharan, M. and Kawasaki, A. Mamoru.
TITLE 2'-O-aminooxy-modified oligonucleotides
JOURNAL Patent: US 6172533-A 44 03-OCT-2000;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 182
AR124843/c
LOCUS AR124843 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 20 from patent US 6172209.
ACCESSION AR124843
VERSION AR124843.1 GI:14110204
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan, M.; Cook, P. Dan., Prakash, T. P. and Kawasaki, A. M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 20 09-JAN-2001;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 183
AR124844/c
LOCUS AR124844 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 21 from patent US 6172209.
ACCESSION AR124844
VERSION AR124844.1 GI:14110205
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan, M.; Cook, P. Dan., Prakash, T. P. and Kawasaki, A. M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 21 09-JAN-2001;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 184
AR124845/c
LOCUS AR124845 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 22 from patent US 6172209.
ACCESSION AR124845
VERSION AR124845.1 GI:14110206
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan, M.; Cook, P. Dan., Prakash, T. P. and Kawasaki, A. M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 22 09-JAN-2001;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 185
AR124846/c
LOCUS AR124846 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 23 from patent US 6172209.
ACCESSION AR124846
VERSION AR124846.1 GI:14110207
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan, M.; Cook, P. Dan., Prakash, T. P. and Kawasaki, A. M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 23 09-JAN-2001;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 186
AR124847/c
LOCUS AR124847 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 24 from patent US 6172209.
ACCESSION AR124847
VERSION AR124847.1 GI:14110208
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)

AUTHORS Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 24 09-JAN-2001;
FEATURES Location/Qualifiers
SOURCE 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred.No.1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1520 AAAAAAAAAAAGTAAA 1537
|||||
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 187
ARI24848/c

LOCUS ARI24848 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 25 from patent US 6172209.
ACCESSION ARI24848
VERSION ARI24848.1 GI:14110209
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 25 09-JAN-2001;
FEATURES Location/Qualifiers
SOURCE 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred.No.1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1520 AAAAAAAAAAAGTAAA 1537
|||||
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 188
ARI24849/c

LOCUS ARI24849 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 26 from patent US 6172209.
ACCESSION ARI24849
VERSION ARI24849.1 GI:14110210
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 26 09-JAN-2001;
FEATURES Location/Qualifiers
SOURCE 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred.No.1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1520 AAAAAAAAAAAGTAAA 1537
|||||
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 189
ARI24850/c

LOCUS ARI24850 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 27 from patent US 6172209.
ACCESSION ARI24850
VERSION ARI24850.1 GI:14110211
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 27 09-JAN-2001;
FEATURES Location/Qualifiers
SOURCE 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred.No.1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1520 AAAAAAAAAAAGTAAA 1537
|||||
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 190
ARI24854/c

LOCUS ARI24854 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 31 from patent US 6172209.
ACCESSION ARI24854
VERSION ARI24854.1 GI:14110215
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 31 09-JAN-2001;
FEATURES Location/Qualifiers
SOURCE 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred.No.1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1520 AAAAAAAAAAAGTAAA 1537
|||||
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 191
ARI24856/c

LOCUS ARI24856 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 33 from patent US 6172209.
ACCESSION ARI24856
VERSION ARI24856.1 GI:14110217
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 33 09-JAN-2001;
FEATURES Location/Qualifiers
SOURCE 1..19
/organism="unknown"

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/mol_type="unassigned DNA"
Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1520 AAAAAAAAAAGTAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 192
AR124857/c 19 bp DNA linear PAT 16-MAY-2001
LOCUS AR124857
DEFINITION Sequence 34 from patent US 6172209.
ACCESSION AR124857
VERSION AR124857.1 GI:14110218
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.,Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 34 09-JAN-2001;
FEATURES
Location/Qualifiers
1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1520 AAAAAAAAAAGTAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 193
AR124867/c 19 bp DNA linear PAT 16-MAY-2001
LOCUS AR124867
DEFINITION Sequence 44 from patent US 6172209.
ACCESSION AR124867
VERSION AR124867.1 GI:14110228
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.,Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 44 09-JAN-2001;
FEATURES
Location/Qualifiers
1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1520 AAAAAAAAAAGTAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 194
AR135291/c 19 bp DNA linear PAT 16-MAY-2001
LOCUS AR135291
DEFINITION Sequence 20 from patent US 6194598.
ACCESSION AR135291
VERSION AR135291.1 GI:14124196
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KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.,Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE Aminoxy-modified oligonucleotide synthetic intermediates
JOURNAL Patent: US 6194598-A 20 27-FEB-2001;
FEATURES
Location/Qualifiers
1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1520 AAAAAAAAAAGTAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2
```

```

RESULT 195
AR135292/c 19 bp DNA linear PAT 16-MAY-2001
LOCUS AR135292
DEFINITION Sequence 21 from patent US 6194598.
ACCESSION AR135292
VERSION AR135292.1 GI:14124197
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.,Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE Aminoxy-modified oligonucleotide synthetic intermediates
JOURNAL Patent: US 6194598-A 21 27-FEB-2001;
FEATURES
Location/Qualifiers
1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1520 AAAAAAAAAAGTAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2
```

```

RESULT 196
AR135293/c 19 bp DNA linear PAT 16-MAY-2001
LOCUS AR135293
DEFINITION Sequence 22 from patent US 6194598.
ACCESSION AR135293
VERSION AR135293.1 GI:14124198
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.,Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE Aminoxy-modified oligonucleotide synthetic intermediates
JOURNAL Patent: US 6194598-A 22 27-FEB-2001;
FEATURES
Location/Qualifiers
1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 197
LOCUS AR135294/c 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 23 from patent US 6194598.
ACCESSION AR135294
VERSION AR135294.1 GI:14124199
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE
AUTHORS 1 (bases 1 to 19)
TITLE Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
JOURNAL Aminoxy-modified oligonucleotide synthetic intermediates
FEATURES Patent: US 6194598-A 23 27-FEB-2001;
Location/Qualifiers
1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred.No.1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 198
LOCUS AR135295/c 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 24 from patent US 6194598.
ACCESSION AR135295
VERSION AR135295.1 GI:14124200
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE
AUTHORS 1 (bases 1 to 19)
TITLE Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
JOURNAL Aminoxy-modified oligonucleotide synthetic intermediates
FEATURES Patent: US 6194598-A 24 27-FEB-2001;
Location/Qualifiers
1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred.No.1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 199
LOCUS AR135296/c 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 25 from patent US 6194598.
ACCESSION AR135296
VERSION AR135296.1 GI:14124201
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE
AUTHORS 1 (bases 1 to 19)
TITLE Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.

TITLE Aminoxy-modified oligonucleotide synthetic intermediates
JOURNAL Patent: US 6194598-A 25 27-FEB-2001;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred.No.1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 200
LOCUS AR135297/c 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 26 from patent US 6194598.
ACCESSION AR135297
VERSION AR135297.1 GI:14124202
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE
AUTHORS 1 (bases 1 to 19)
TITLE Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
JOURNAL Aminoxy-modified oligonucleotide synthetic intermediates
FEATURES Patent: US 6194598-A 26 27-FEB-2001;
Location/Qualifiers
1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred.No.1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 201
LOCUS AR135298/c 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 27 from patent US 6194598.
ACCESSION AR135298
VERSION AR135298.1 GI:14124203
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE
AUTHORS 1 (bases 1 to 19)
TITLE Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
JOURNAL Aminoxy-modified oligonucleotide synthetic intermediates
FEATURES Patent: US 6194598-A 27 27-FEB-2001;
Location/Qualifiers
1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred.No.1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 202

AR135302/c
LOCUS AR135302 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 31 from patent US 6194598.
ACCESSION AR135302
VERSION AR135302.1 GI:14124207
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook, P. Dan., Manoharan, M. and Kawasaki, A. Mamoru.
TITLE Aminoxy-modified oligonucleotide synthetic intermediates
JOURNAL Patent: US 6194598-A 31 27-FEB-2001;
FEATURES
source
Location/Qualifiers
1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 203
AR135304/c
LOCUS AR135304 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 33 from patent US 6194598.
ACCESSION AR135304
VERSION AR135304.1 GI:14124209
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook, P. Dan., Manoharan, M. and Kawasaki, A. Mamoru.
TITLE Aminoxy-modified oligonucleotide synthetic intermediates
JOURNAL Patent: US 6194598-A 33 27-FEB-2001;
FEATURES
source
Location/Qualifiers
1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 204
AR135305/c
LOCUS AR135305 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 34 from patent US 6194598.
ACCESSION AR135305
VERSION AR135305.1 GI:14124210
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook, P. Dan., Manoharan, M. and Kawasaki, A. Mamoru.
TITLE Aminoxy-modified oligonucleotide synthetic intermediates
JOURNAL Patent: US 6194598-A 34 27-FEB-2001;
FEATURES
source
Location/Qualifiers
1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 205
AR135315/c
LOCUS AR135315 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 44 from patent US 6194598.
ACCESSION AR135315
VERSION AR135315.1 GI:14124220
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook, P. Dan., Manoharan, M. and Kawasaki, A. Mamoru.
TITLE Aminoxy-modified oligonucleotide synthetic intermediates
JOURNAL Patent: US 6194598-A 44 27-FEB-2001;
FEATURES
source
Location/Qualifiers
1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 206
AR141898/c
LOCUS AR141898 19 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 4 from patent US 6147200.
ACCESSION AR141898
VERSION AR141898.1 GI:15101414
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan, M., Kawasaki, A. M., Cook, P. Dan., Fraser, A. S. and Prakash, T. P.
TITLE 2'-O-acetamido modified monomers and oligomers
JOURNAL Patent: US 6147200-A 4 14-NOV-2000;
FEATURES
source
Location/Qualifiers
1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 207
AR153863/c
LOCUS AR153863 19 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 16 from patent US 6238624.
ACCESSION AR153863
VERSION AR153863.1 GI:15121916

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
SOURCE

Unknown.
Unclassified.
1 (bases 1 to 19)
Heller,M.J., Tu,E., Evans,G.A. and Sosnowski,R.G.
Methods for transport in molecular biological analysis and
diagnostics
Patent: US 6238624-A 16-29-MAY-2001;
Location/Qualifiers
1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred.No.1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAGTAAA 1537
DB 19 AAAAAAAAAAAAAAAAA 2

RESULT 208
AR164173/c 19 bp DNA linear PAT 17-OCT-2001
LOCUS AR164173
DEFINITION Sequence 6 from patent US 6271358.
ACCESSION AR164173
VERSION AR164173.1 GI:16235162
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
SOURCE

Unknown.
Unclassified.
1 (bases 1 to 19)
Manoharan,M., Mohan,V. and Boswell,H.
RNA targeted 2'-modified oligonucleotides that are conformationally
preorganized
Patent: US 6271358-A 6-07-AUG-2001;
Location/Qualifiers
1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred.No.1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAGTAAA 1537
DB 19 AAAAAAAAAAAAAAAAA 2

RESULT 209
BD196900/c 19 bp DNA linear PAT 17-JUL-2003
LOCUS BD196900
DEFINITION Prostatic cancer gene.
ACCESSION BD196900
VERSION BD196900.1 GI:33006670
KEYWORDS JP 2002516657-A/489.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 19)
Cohen,D., Blumenfeld,M., Chumakov,I. and Bougueleret,L.
Prostatic cancer gene
Patent: JP 2002516657-A 489 11-JUN-2002;
GENSET
OS Homo sapiens (human)
PN JP 2002516657-A/489
PD 11-JUN-2002
PF 22-DEC-1998 JP 2000525562
PR 22-DEC-1997 US 08/996306,09-SEP-1998 US 60/099658 PI

DANIEL COHEN,MARTA BLUMENFELD,ILYA CHUMAKOV,LYDIE BOUGUELERET PC
C12N15/09,C12N15/09,A01K67/027,C07K14/47,C07K16/18,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,C12N5/10,C12P21/08,C12Q1/68,G01N33/50 PC
PC C12N5/00,C12N5/00
PC C12N5/00,C12N15/00
CC potential microsequencing oligo for 4-4-187, mis2 FH Key
Location/Qualifiers
FT primer bind 1..19.
Location/Qualifiers
1..19
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred.No.1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1132 ATAGATGTTTAAATTTT 1149
DB 2 ATAGATGTTTAAATTTCT 19

RESULT 211
BD274438/c 19 bp DNA linear PAT 17-JUL-2003
LOCUS BD274438
DEFINITION Oligonucleotides having A-DNA form and B-DNA form conformational

ACCESSION geometry.
BD274438.1 GI:33084206
VERSION BD274438.1
KEYWORDS JP 2002543215-A/15.
SOURCE synthetic construct
ORGANISM artificial construct
artificial sequences.
1 (bases 1 to 19)
REFERENCE Manoharan,M. and Mohan,V.
AUTHORS Oligonucleotides having A-DNA form and B-DNA form confirmational
TITLE
JOURNAL Geometry
Patent: JP 2002543215-A 15 17-DEC-2002;
ISIS PHARMACEUTICALS INC
COMMENT OS Artificial Sequence
PN JP 2002543215-A/15
PD 17-DEC-2002
PR 03-MAY-2000 JP 2000615638
PI MUTHIAH MANOHARAN, VENKATRAMAN MOHAN
PC C07H21/02,A61K48/00,A61P35/00,A61P43/00,C12N15/09,
PC C12N15/00
CC Oligonucleotide
CC 3' - O-MOE linkage
CC 3' - O-MOE linkage
CC 3' - O-MOE linkage
CC 3' - O-MOE linkage
FH Key Location/Qualifiers
FT misc_feature (16) . (17)
FT misc_feature (17) . (18)
FT misc_feature (18) . (19).
FEATURES Location/Qualifiers
source 1..19
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAA 1537
Db 19 AAAAAAAAAAAAAAAAA 2

RESULT 212
BD274439/c
LOCUS BD274439 19 bp DNA linear PAT 17-JUL-2003
DEFINITION Oligonucleotides having A-DNA form and B-DNA form confirmational
geometry.
ACCESSION BD274439
VERSION BD274439.1 GI:33084207
KEYWORDS JP 2002543215-A/16.
SOURCE synthetic construct
ORGANISM artificial construct
artificial sequences.
1 (bases 1 to 19)
REFERENCE Manoharan,M. and Mohan,V.
AUTHORS Oligonucleotides having A-DNA form and B-DNA form confirmational
TITLE
JOURNAL Geometry
Patent: JP 2002543215-A 16 17-DEC-2002;
ISIS PHARMACEUTICALS INC
COMMENT OS Artificial Sequence
PN JP 2002543215-A/16
PD 17-DEC-2002
PR 03-MAY-2000 JP 2000615638
PI MUTHIAH MANOHARAN, VENKATRAMAN MOHAN
PC C07H21/02,A61K48/00,A61P35/00,A61P35/02,A61P43/00,C12N15/09,
PC C12N15/00
CC Oligonucleotide
CC 2' - O-MOE linkage
CC 2' - O-MOE linkage
CC 2' - O-MOE linkage

PH Key Location/Qualifiers
FT misc_feature (16) . (17)
FT misc_feature (17) . (18)
FT misc_feature (18) . (19).
FEATURES Location/Qualifiers
source 1..19
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAA 1537
Db 19 AAAAAAAAAAAAAAAAA 2

RESULT 213
BD274440/c
LOCUS BD274440 19 bp DNA linear PAT 17-JUL-2003
DEFINITION Oligonucleotides having A-DNA form and B-DNA form confirmational
geometry.
ACCESSION BD274440
VERSION BD274440.1 GI:33084208
KEYWORDS JP 2002543215-A/17.
SOURCE synthetic construct
ORGANISM artificial construct
artificial sequences.
1 (bases 1 to 19)
REFERENCE Manoharan,M. and Mohan,V.
AUTHORS Oligonucleotides having A-DNA form and B-DNA form confirmational
TITLE
JOURNAL Geometry
Patent: JP 2002543215-A 17 17-DEC-2002;
ISIS PHARMACEUTICALS INC
COMMENT OS Artificial Sequence
PN JP 2002543215-A/17
PD 17-DEC-2002
PR 03-MAY-2000 JP 2000615638
PI MUTHIAH MANOHARAN, VENKATRAMAN MOHAN
PC C07H21/02,A61K48/00,A61P35/00,A61P35/02,A61P43/00,C12N15/09,
PC C12N15/00
CC Oligonucleotide
CC sub O linkage
CC 3' - O-MOE linkage; sub O linkage
CC 3' - O-MOE linkage; sub O linkage
CC 3' - O-MOE linkage; sub O linkage
CC 3' - O-MOE linkage
FH Key Location/Qualifiers
FT misc_feature (15) . (16)
FT misc_feature (16) . (17)
FT misc_feature (17) . (18)
FT misc_feature (18) . (19)
FT misc_feature (19) . (19).
FEATURES Location/Qualifiers
source 1..19
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAA 1537
Db 19 AAAAAAAAAAAAAAAAA 2

RESULT 214
BD274441/c

LOCUS BD274441 19 bp DNA linear PAT 17-JUL-2003
DEFINITION Oligonucleotides having A-DNA form and B-DNA form conformational geometry.
ACCESSION BD274441.1 GI:33084209
VERSION JP 2002543215-A/18.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan, M. and Mohan, V.
TITLE Oligonucleotides having A-DNA form and B-DNA form conformational geometry
JOURNAL Patent: JP 2002543215-A 18 17-DEC-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002543215-A/18
PD 17-DEC-2002
PF 03-MAY-2000 JP 2000615638
PR 03-MAY-1999 US 09/303586
PI MUTHIAH MANOHARAN, VENKATRAMAN MOHAN

LOCUS BD274449 19 bp DNA linear PAT 17-JUL-2003
DEFINITION Oligonucleotides having A-DNA form and B-DNA form conformational geometry.
ACCESSION BD274449.1 GI:33084217
VERSION JP 2002543215-A/26.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan, M. and Mohan, V.
TITLE Oligonucleotides having A-DNA form and B-DNA form conformational geometry
JOURNAL Patent: JP 2002543215-A 26 17-DEC-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002543215-A/26
PD 17-DEC-2002
PF 03-MAY-2000 JP 2000615638
PR 03-MAY-1999 US 09/303586
PI MUTHIAH MANOHARAN, VENKATRAMAN MOHAN

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

FEATURES
source 1..19
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

PC C07H21/02, A61K48/00, A61P35/00, A61P35/02, A61P43/00, C12N15/09,
PC C12N15/00
CC Oligonucleotide
CC 2'-modified T linkage
CC 2'-modified T linkage
CC 2'-modified T linkage
CC 2'-modified T linkage
FH Key Location/Qualifiers
FT misc_feature (16)..(17)
FT misc_feature (17)..(18)
FT misc_feature (18)..(19)
FT misc_feature (19)..(19).
Location/Qualifiers
source 1..19
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 216
LOCUS AR205798 19 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 15 from patent US 6369209.
ACCESSION AR205798
VERSION AR205798.1 GI:21503472
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan, M. and Mohan, V.
TITLE Oligonucleotides having A-DNA form and B-DNA form conformational geometry
JOURNAL Patent: US 6369209-A 15 09-APR-2002;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 217
LOCUS AR205799 19 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 16 from patent US 6369209.
ACCESSION AR205799
VERSION AR205799.1 GI:21503473
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan, M. and Mohan, V.
TITLE Oligonucleotides having A-DNA form and B-DNA form conformational geometry
JOURNAL Patent: US 6369209-A 16 09-APR-2002;
FEATURES Location/Qualifiers
source 1..19

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/organism="unknown"
/mol_type="unassigned DNA"
Query Match      1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1520 AAAAAAAAAAGTAAAA 1537
Db      19 AAAAAAAAAAAAAAAAAA 2

RESULT 218
LOCUS      AR205800      19 bp      DNA      linear      PAT 20-JUN-2002
DEFINITION Sequence 17 from patent US 6369209.
ACCESSION  AR205800
VERSION     AR205800.1 GI:21503474
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 19)
AUTHORS     Manoharan,M. and Mohan,V.
TITLE       Oligonucleotides having A-DNA form and B-DNA form conformational
            geometry
JOURNAL     Patent: US 6369209-A 17 09-APR-2002;
FEATURES
SOURCE
    Query Match      1.1%; Score 14.8; DB 1; Length 19;
    Best Local Similarity 88.9%; Pred. No. 1.9e+02;
    Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

    Qy      1520 AAAAAAAAAAGTAAAA 1537
    Db      19 AAAAAAAAAAAAAAAAAA 2

RESULT 219
LOCUS      AR205801      19 bp      DNA      linear      PAT 20-JUN-2002
DEFINITION Sequence 18 from patent US 6369209.
ACCESSION  AR205801
VERSION     AR205801.1 GI:21503476
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 19)
AUTHORS     Manoharan,M. and Mohan,V.
TITLE       Oligonucleotides having A-DNA form and B-DNA form conformational
            geometry
JOURNAL     Patent: US 6369209-A 18 09-APR-2002;
FEATURES
SOURCE      1. .19
            Location/Qualifiers
            /organism="unknown"
            /mol_type="unassigned DNA"

    Query Match      1.1%; Score 14.8; DB 1; Length 19;
    Best Local Similarity 88.9%; Pred. No. 1.9e+02;
    Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

    Qy      1520 AAAAAAAAAAGTAAAA 1537
    Db      19 AAAAAAAAAAAAAAAAAA 2

RESULT 220
LOCUS      AR205809      19 bp      DNA      linear      PAT 20-JUN-2002
```

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DEFINITION Sequence 26 from patent US 6369209.
ACCESSION  AR205809
VERSION     AR205809.1 GI:21503486
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 19)
AUTHORS     Manoharan,M. and Mohan,V.
TITLE       Oligonucleotides having A-DNA form and B-DNA form conformational
            geometry
JOURNAL     Patent: US 6369209-A 26 09-APR-2002;
FEATURES
SOURCE      1. .19
            Location/Qualifiers
            /organism="unknown"
            /mol_type="unassigned DNA"

    Query Match      1.1%; Score 14.8; DB 1; Length 19;
    Best Local Similarity 88.9%; Pred. No. 1.9e+02;
    Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

    Qy      1520 AAAAAAAAAAGTAAAA 1537
    Db      19 AAAAAAAAAAAAAAAAAA 2

RESULT 221
LOCUS      AR213490      19 bp      DNA      linear      PAT 25-SEP-2002
DEFINITION Sequence 1 from patent US 6403779.
ACCESSION  AR213490
VERSION     AR213490.1 GI:23310721
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 19)
AUTHORS     Kawasaki,A.M., Frazer,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
TITLE       Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL     Patent: US 6403779-A 1 11-JUN-2002;
FEATURES
SOURCE      1. .19
            Location/Qualifiers
            /organism="unknown"
            /mol_type="genomic DNA"

    Query Match      1.1%; Score 14.8; DB 1; Length 19;
    Best Local Similarity 88.9%; Pred. No. 1.9e+02;
    Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

    Qy      1520 AAAAAAAAAAGTAAAA 1537
    Db      19 AAAAAAAAAAAAAAAAAA 2

RESULT 222
LOCUS      AR213491      19 bp      DNA      linear      PAT 25-SEP-2002
DEFINITION Sequence 2 from patent US 6403779.
ACCESSION  AR213491
VERSION     AR213491.1 GI:23310722
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 19)
AUTHORS     Kawasaki,A.M., Frazer,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
TITLE       Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL     Patent: US 6403779-A 2 11-JUN-2002;
FEATURES
SOURCE      1. .19
            Location/Qualifiers
            /organism="unknown"
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/mol_type="genomic DNA"

Query Match 1.1% Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
DB 19 AAAAAAAAAAAAAAAAAA 2

RESULT 223
AR213492/C
LOCUS AR213492
DEFINITION Sequence 3 from patent US 6403779.
ACCESSION AR213492
VERSION AR213492.1 GI:23310723
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6403779-A 3 11-JUN-2002;
FEATURES
Source Location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1% Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
DB 19 AAAAAAAAAAAAAAAAAA 2

RESULT 224
AR213493/C
LOCUS AR213493
DEFINITION Sequence 4 from patent US 6403779.
ACCESSION AR213493
VERSION AR213493.1 GI:23310724
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6403779-A 4 11-JUN-2002;
FEATURES
Source Location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1% Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
DB 19 AAAAAAAAAAAAAAAAAA 2

RESULT 225
AR213494/C
LOCUS AR213494
DEFINITION Sequence 5 from patent US 6403779.

ACCESSION AR213494
VERSION AR213494.1 GI:23310725
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6403779-A 5 11-JUN-2002;
FEATURES
Source Location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1% Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
DB 19 AAAAAAAAAAAAAAAAAA 2

RESULT 226
AR213495/C
LOCUS AR213495
DEFINITION Sequence 6 from patent US 6403779.
ACCESSION AR213495
VERSION AR213495.1 GI:23310726
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6403779-A 6 11-JUN-2002;
FEATURES
Source Location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1% Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
DB 19 AAAAAAAAAAAAAAAAAA 2

RESULT 227
AR213496/C
LOCUS AR213496
DEFINITION Sequence 7 from patent US 6403779.
ACCESSION AR213496
VERSION AR213496.1 GI:23310727
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6403779-A 7 11-JUN-2002;
FEATURES
Source Location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
DB 19 AAAAAAAAAAAAAAAAAA 2

RESULT 228
AR213497/c 19 bp DNA linear PAT 25-SEP-2002
LOCUS AR213497
DEFINITION Sequence 8 from patent US 6403779.
ACCESSION AR213497
VERSION AR213497.1 GI:23310728
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Frazer,A.S., Manoharan,M., Cook,P.D. and Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6403779-A 8 11-JUN-2002;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
DB 19 AAAAAAAAAAAAAAAAAA 2

RESULT 229
AR213501/c 19 bp DNA linear PAT 25-SEP-2002
LOCUS AR213501
DEFINITION Sequence 12 from patent US 6403779.
ACCESSION AR213501
VERSION AR213501.1 GI:23310732
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Frazer,A.S., Manoharan,M., Cook,P.D. and Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6403779-A 12 11-JUN-2002;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
DB 19 AAAAAAAAAAAAAAAAAA 2

RESULT 230
AR213502/c 19 bp DNA linear PAT 25-SEP-2002
LOCUS AR213502
DEFINITION Sequence 14 from patent US 6403779.
ACCESSION AR213502

VERSION AR213502.1 GI:23310733
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Frazer,A.S., Manoharan,M., Cook,P.D. and Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6403779-A 14 11-JUN-2002;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
DB 19 AAAAAAAAAAAAAAAAAA 2

RESULT 231
AR213503/c 19 bp DNA linear PAT 25-SEP-2002
LOCUS AR213503
DEFINITION Sequence 15 from patent US 6403779.
ACCESSION AR213503
VERSION AR213503.1 GI:23310734
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Frazer,A.S., Manoharan,M., Cook,P.D. and Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6403779-A 15 11-JUN-2002;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
DB 19 AAAAAAAAAAAAAAAAAA 2

RESULT 232
AR213512/c 19 bp DNA linear PAT 25-SEP-2002
LOCUS AR213512
DEFINITION Sequence 25 from patent US 6403779.
ACCESSION AR213512
VERSION AR213512.1 GI:23310743
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Frazer,A.S., Manoharan,M., Cook,P.D. and Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6403779-A 25 11-JUN-2002;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 233
AR222465 19 bp DNA linear PAT 26-SEP-2002
LOCUS AR222465
DEFINITION Sequence 25 from patent US 6429300.
ACCESSION AR222465
VERSION AR222465.1 GI:2332996
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kurz,M., Lohse,P. and Wagner,R.
TITLE Peptide acceptor ligation methods
JOURNAL Patent: US 6429300-A 25 06-AUG-2002;
FEATURES
Source 1. .19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 234
AR237463 19 bp DNA linear PAT 20-DEC-2002
LOCUS AR237463
DEFINITION Sequence 1 from patent US 6465628.
ACCESSION AR237463
VERSION AR237463.1 GI:27282213
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Ravikumar,V.T., Manoharan,M., Capaldi,D.C., Krotz,A., Cole,D.L. and Guzaev,A.
TITLE Process for the synthesis of oligomeric compounds
JOURNAL Patent: US 6465628-A 1 15-OCT-2002;
FEATURES
Source 1. .19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 235
AR295557 19 bp DNA linear PAT 12-JUN-2003
LOCUS AR295557
DEFINITION Sequence 7292 from patent US 6537751.
ACCESSION AR295557
VERSION AR295557.1 GI:31682841
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 7292 25-MAR-2003;
FEATURES
Source 1. .19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1103 TCTACTTCATTTTCC 1120
Db 18 TCTCATTTCCATTTTCC 1

RESULT 236
AR321589 19 bp DNA linear PAT 17-AUG-2003
LOCUS AR321589
DEFINITION Sequence 10 from patent US 6562960.
ACCESSION AR321589
VERSION AR321589.1 GI:33706818
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Baxter,A.D., Collingwood,S.P., Douglas,M.E. and Taylor,R.J.
TITLE Oligonucleotide analogues
JOURNAL Patent: US 6562960-A 10 13-MAY-2003;
FEATURES
Source 1. .19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 237
AR359804 19 bp DNA linear PAT 17-AUG-2003
LOCUS AR359804
DEFINITION Sequence 3 from patent US 6593466.
ACCESSION AR359804
VERSION AR359804.1 GI:33766602
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.D., Prakash,T.P. and Mohan,V.
TITLE Guanine-rich functionalized nucleotides and precursors thereof
JOURNAL Patent: US 6593466-A 3 15-JUN-2003;
FEATURES
Source 1. .19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAAGTAAA 1537
|||||
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 238
LOCUS AR359805/c 19 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 4 from patent US 6593466.
ACCESSION AR359805
VERSION AR359805.1 GI:33766603
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.D., Prakash,T.P. and Mohan,V.
TITLE Guadinium functionalized nucleotides and precursors thereof
JOURNAL Patent: US 6593466-A 4 15-JUL-2003;
FEATURES Location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAAGTAAA 1537
|||||
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 239
LOCUS AR359806/c 19 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 5 from patent US 6593466.
ACCESSION AR359806
VERSION AR359806.1 GI:33766604
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.D., Prakash,T.P. and Mohan,V.
TITLE Guadinium functionalized nucleotides and precursors thereof
JOURNAL Patent: US 6593466-A 5 15-JUL-2003;
FEATURES Location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAAGTAAA 1537
|||||
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 240
LOCUS AR367447/c 19 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 4 from patent US 6328519.
ACCESSION AR367447
VERSION AR367447.1 GI:34600659
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Collingwood,S.P., Moser,H.E., Altmann,K.-H. and Douglas,M.E.

TITLE Intermediates for oligonucleotide synthesis
JOURNAL Patent: US 6328519-A 4 11-DEC-2001;
FEATURES Location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAAGTAAA 1537
|||||
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 241
LOCUS AR399177/c 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 17 from patent US 6617442.
ACCESSION AR399177
VERSION AR399177.1 GI:40137667
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Crooke,S.T., Lima,W.F., Wu,H. and Monoharan,M.
TITLE Human RNase HI and oligonucleotide compositions thereof
JOURNAL Patent: US 6617442-A 17 09-SEP-2003;
FEATURES Location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAAGTAAA 1537
|||||
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 242
LOCUS AR399178/c 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 18 from patent US 6617442.
ACCESSION AR399178
VERSION AR399178.1 GI:40137669
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Crooke,S.T., Lima,W.F., Wu,H. and Monoharan,M.
TITLE Human RNase HI and oligonucleotide compositions thereof
JOURNAL Patent: US 6617442-A 18 09-SEP-2003;
FEATURES Location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAAGTAAA 1537
|||||
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 243

AR403601/c
LOCUS AR403601 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1 from patent US 6624294.
ACCESSION AR403601
VERSION AR403601.1 GI:40151187
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS 1 (bases 1 to 19)
Kawasaki,A.M., Frazer,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 1 23-SEP-2003;
FEATURES
Source Location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
DB 19 AAAAAAAAAAAAAAAAAA 2

RESULT 244
AR403602/c
LOCUS AR403602 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 2 from patent US 6624294.
ACCESSION AR403602
VERSION AR403602.1 GI:40151188
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS 1 (bases 1 to 19)
Kawasaki,A.M., Frazer,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 2 23-SEP-2003;
FEATURES
Source Location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
DB 19 AAAAAAAAAAAAAAAAAA 2

RESULT 245
AR403603/c
LOCUS AR403603 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 3 from patent US 6624294.
ACCESSION AR403603
VERSION AR403603.1 GI:40151189
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS 1 (bases 1 to 19)
Kawasaki,A.M., Frazer,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 3 23-SEP-2003;
FEATURES
Source Location/Qualifiers

source 1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
DB 19 AAAAAAAAAAAAAAAAAA 2

RESULT 246
AR403604/c
LOCUS AR403604 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 4 from patent US 6624294.
ACCESSION AR403604
VERSION AR403604.1 GI:40151190
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS 1 (bases 1 to 19)
Kawasaki,A.M., Frazer,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 4 23-SEP-2003;
FEATURES
Source Location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
DB 19 AAAAAAAAAAAAAAAAAA 2

RESULT 247
AR403605/c
LOCUS AR403605 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 5 from patent US 6624294.
ACCESSION AR403605
VERSION AR403605.1 GI:40151191
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS 1 (bases 1 to 19)
Kawasaki,A.M., Frazer,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 5 23-SEP-2003;
FEATURES
Source Location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
DB 19 AAAAAAAAAAAAAAAAAA 2

RESULT 248
AR403606/c

LOCUS AR403606 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 6 from patent US 6624294.
ACCESSION AR403606
VERSION AR403606.1 GI:40151192
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Frazer,A.S., Manoharan,M., Cook,P.D. and
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 6 23-SEP-2003;
FEATURES
source Location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAA 1537
Db 19 AAAAAAAAAAAAAAAAA 2

RESULT 249
LOCUS AR403607/c 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 7 from patent US 6624294.
ACCESSION AR403607
VERSION AR403607.1 GI:40151193
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Frazer,A.S., Manoharan,M., Cook,P.D. and
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 7 23-SEP-2003;
FEATURES
source Location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAA 1537
Db 19 AAAAAAAAAAAAAAAAA 2

RESULT 250
LOCUS AR403608/c 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 8 from patent US 6624294.
ACCESSION AR403608
VERSION AR403608.1 GI:40151194
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Frazer,A.S., Manoharan,M., Cook,P.D. and
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 8 23-SEP-2003;
FEATURES
source Location/Qualifiers
1..19

/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAA 1537
Db 19 AAAAAAAAAAAAAAAAA 2

RESULT 251
LOCUS AR403612/c 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 12 from patent US 6624294.
ACCESSION AR403612
VERSION AR403612.1 GI:40151198
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Frazer,A.S., Manoharan,M., Cook,P.D. and
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 12 23-SEP-2003;
FEATURES
source Location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAA 1537
Db 19 AAAAAAAAAAAAAAAAA 2

RESULT 252
LOCUS AR403613/c 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 14 from patent US 6624294.
ACCESSION AR403613
VERSION AR403613.1 GI:40151199
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Frazer,A.S., Manoharan,M., Cook,P.D. and
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 14 23-SEP-2003;
FEATURES
source Location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAA 1537
Db 19 AAAAAAAAAAAAAAAAA 2

RESULT 253
LOCUS AR403614/c 19 bp DNA linear PAT 18-DEC-2003

DEFINITION Sequence 15 from patent US 6624294.
ACCESSION AR403614
VERSION AR403614.1 GI:40151200
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 15 23-SEP-2003;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred.No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAAGTAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 254
AR403623/c
LOCUS AR403623 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 25 from patent US 6624294.
ACCESSION AR403623
VERSION AR403623.1 GI:40151209
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 25 23-SEP-2003;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred.No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAAGTAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 255
AR412338/c
LOCUS AR412338 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1 from patent US 6639061.
ACCESSION AR412338
VERSION AR412338.1 GI:40167448
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.D., Manoharan,M., Maier,M. and An,H.
TITLE C3'-methylene hydrogen phosphate oligomers and related compounds
JOURNAL Patent: US 6639061-A 1 28-OCT-2003;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred.No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAAGTAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 256
AR432616/c
LOCUS AR432616 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 6 from patent US 6653458.
ACCESSION AR432616
VERSION AR432616.1 GI:40195149
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.D. and Guinosso,C.J.
TITLE Modified oligonucleotides
JOURNAL Patent: US 6653458-A 6 25-NOV-2003;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred.No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAAGTAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 257
AR432617/c
LOCUS AR432617 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 7 from patent US 6653458.
ACCESSION AR432617
VERSION AR432617.1 GI:40195150
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.D. and Guinosso,C.J.
TITLE Modified oligonucleotides
JOURNAL Patent: US 6653458-A 7 25-NOV-2003;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred.No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAAGTAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 258
AR451262/c
LOCUS AR451262 19 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 5 from patent US 6673912.
ACCESSION AR451262
VERSION AR451262.1 GI:42682240
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M. and Cook,P.D.
TITLE 2'-O-aminethyloxethyl-modified oligonucleotides
JOURNAL Patent: US 6673912-A 5 06-JAN-2004;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 259
LOCUS AR451282 19 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 26 from patent US 6673912.
ACCESSION AR451282
VERSION AR451282.1 GI:42682260
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M. and Cook,P.D.
TITLE 2'-O-aminethyloxethyl-modified oligonucleotides
JOURNAL Patent: US 6673912-A 26 06-JAN-2004;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 260
LOCUS AX059378 19 bp DNA linear PAT 17-JAN-2001
DEFINITION Sequence 111 from Patent WO0055325.
ACCESSION AX059378
VERSION AX059378.1 GI:12311483
KEYWORDS
SOURCE Arabidopsis thaliana (chale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsia.

REFERENCE 1
AUTHORS Preuss,D., Copenhaver,G. and Keith,K.
TITLE Plant chromosome compositions and methods
JOURNAL Patent: WO 0055325-A 11 21-SEP-2000;
FEATURES Location/Qualifiers
source 1..19
/organism="Arabidopsis thaliana"
/mol_type="unassigned DNA"
/db_xref="taxon:3702"

Query Match 1.1%; Score 14.8; DB 1; Length 19;

Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1535 AAGGAGGACGAGATGT 1552
Db 18 AATCGGAGGCGGATGT 1

RESULT 261
LOCUS AX132398 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 3616 from Patent WO0130362.
ACCESSION AX132398
VERSION AX132398.1 GI:14138703
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Robbins,J.M. and Tiltz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases
JOURNAL Patent: WO 0130362-A 3616 03-MAY-2001;
FEATURES IMMUSOL, INC. (US)
Location/Qualifiers
source 1..19
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Cdc25 hs ribozyme binding site"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1305 ATTTTCTTATTTCAGA 1322
Db 18 ATTTCTTATTTCAGA 1

RESULT 262
LOCUS AX226133 19 bp DNA linear PAT 10-SEP-2001
DEFINITION Sequence 52 from Patent WO0160856.
ACCESSION AX226133
VERSION AX226133.1 GI:15555445
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Vlkula,M.
TITLE vnglom gene and its mutations causing disorders with a vascular component
JOURNAL Patent: WO 0160856-A 52 23-AUG-2001;
FEATURES LOCATION/Qualifiers
source 1..19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide"

Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 983 GCGACGCTTCTGTTCTG 1000
Db 2 GCGACGCTTCTGTCGTG 19

RESULT 263
AX349249/c 19 bp DNA linear PAT 06-FEB-2002
LOCUS Sequence 33 from Patent WO0202810.
DEFINITION AX349249
ACCESSION AX349249.1 GI:1615281
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Bickel,R., Ehrlich,R., Ellinger,T., Ermentrout,E., Kaiser,T.,
Schulz,T. and Wagner,G.
TITLE Method for qualitative and/or quantitative detecting of molecular
interactions on probe arrays
JOURNAL Patent: WO 0202810-A 33 10-JAN-2002;
Clondias Chip Technologies GmbH (DE)
FEATURES
source 1..19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide sonde"
Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 1520 AAAAAAAAAAGTAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2
RESULT 264
BD087505/c 19 bp DNA linear PAT 27-AUG-2002
LOCUS Self-assembling microelectronic integration system capable of
DEFINITION designating self address, compartment device, mechanism, method and
operation for molecular biological analysis and diagnosis.
BD087505
ACCESSION BD087505.1 GI:22633115
VERSION JP 2001525193-A/16.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 19)
AUTHORS Sonowaki,R.G., Butler,W.F., Tu,E., Nerenberg,M.I., Heller,M.J. and
Edman,C.F.
TITLE Self-assembling microelectronic integration system capable of
designating self address, compartment device, mechanism, method and
operation for molecular biological analysis and diagnosis
JOURNAL Patent: JP 2001525193-A 16 11-DEC-2001;
NANOGEN INC
COMMENT OS Artificial Sequence
PN JP 2001525193-A/16
PD 11-DEC-2001
PF 01-DEC-1998 JP 2000524303
PR 05-DEC-1997 US 08/986065
PI RONALD G SOSNOMSKI, WILLIAM F BUTLER, EUGENE TU, MICHAEL I PI
NERENBERG,
PI MICHAEL J HELLER, CARL F EDMAN
PC C12Q1/66,C12N15/09,C12N15/00
CC Description of Artificial Sequence: Amino
conjugate to provide
CC with dyes
FH key
FT source 1..19
/organism="Artificial Sequence".
FEATURES
source 1..19
Location/Qualifiers
Location/Qualifiers
1..19
/organism="synthetic construct"
/mol_type="genomic DNA"

/db_xref="taxon:32630"
Query Match 1.1%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 1520 AAAAAAAAAAGTAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2
RESULT 265
AR030917/c 20 bp DNA linear PAT 29-SEP-1999
LOCUS AR030917
DEFINITION Sequence 20 from patent US 5861487.
ACCESSION AR030917
VERSION AR030917.1 GI:5944131
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Holton,T.,Albert., Cornish,E.,Cecily., Kovacic,F., Tanaka,Y. and
Lester,D.,Ruth.
TITLE Genetic sequences encoding flavonoid pathway enzymes and uses
therefor
JOURNAL Patent: US 5861487-A 20 19-JAN-1999;
FEATURES
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 1519 TAAAAAAAAAAGTAAA 1536
Db 18 TAAAAAAAAAAAAAAAAA 1
RESULT 266
AR064875/c 20 bp DNA linear PAT 29-SEP-1999
LOCUS AR064875
DEFINITION Sequence 5 from patent US 5849480.
ACCESSION AR064875
VERSION AR064875.1 GI:5995091
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Gros,P., Kurfurst,R., Battail,N. and Piga,N.
TITLE Process and device for assaying a hapten
JOURNAL Patent: US 5849480-A 5 15-DEC-1998;
FEATURES
source 1..20
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 1520 AAAAAAAAAAGTAAA 1537
Db 20 AAAAAAAAAAAAAAAAAA 3
RESULT 267
AR080000 20 bp DNA linear PAT 31-AUG-2000
LOCUS AR080000
DEFINITION Sequence 83 from patent US 5968524.

ACCESSION AR080000
VERSION AR080000.1 GI:10006735
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 20)
TITLE Watson,J.D. and Tan,P.L.J.
METHODS Methods and compounds for the treatment of immunologically-mediated
JOURNAL Patent: US 5968524-A 83 19-OCT-1999;
FEATURES Location/Qualifiers
Source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 86.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 268
AR085926 20 bp DNA linear PAT 07-SEP-2000
LOCUS
DEFINITION Sequence 83 from patent US 5985287.
ACCESSION AR085926
VERSION AR085926.1 GI:10012692
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Tan,P., Skinner,M. and Prestidge,R.
TITLE Compounds and methods for treatment and diagnosis of mycobacterial
JOURNAL Patent: US 5985287-A 83 16-NOV-1999;
FEATURES Location/Qualifiers
Source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 269
AR087520 20 bp DNA linear PAT 07-SEP-2000
LOCUS
DEFINITION Sequence 1 from patent US 5986084.
ACCESSION AR087520
VERSION AR087520.1 GI:10014283
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Pitsch,S., Weiss,P.A. and Jenny,L.
TITLE Ribonucleoside-derivative and method for preparing the same
JOURNAL Patent: US 5986084-A 1 16-NOV-1999;
FEATURES Location/Qualifiers
Source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAA 1537
Db 20 AAAAAAAAAAAAAAAAAA 3

RESULT 270
AR093312 20 bp DNA linear PAT 08-SEP-2000
LOCUS
DEFINITION Sequence 83 from patent US 6001361.
ACCESSION AR093312
VERSION AR093312.1 GI:10020652
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Tan,P., Hiyama,J., Visser,E., Skinner,M., Scott,L. and Prestidge,R.
TITLE Mycobacterium vaccae antigens
JOURNAL Patent: US 6001361-A 83 14-DEC-1999;
FEATURES Location/Qualifiers
Source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 271
AR118970 20 bp DNA linear PAT 16-MAY-2001
LOCUS
DEFINITION Sequence 96 from patent US 6150092.
ACCESSION AR118970
VERSION AR118970.1 GI:14100880
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Uchida,K., Uchida,T., Tanaka,Y., Matsuda,Y. and Kondo,S.
TITLE Antisense nucleic acid compound targeted to VEGF
JOURNAL Patent: US 6150092-A 96 21-NOV-2000;
FEATURES Location/Qualifiers
Source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAA 1537
Db 20 AAAAAAAAAAAAAAAAAA 3

RESULT 272
AR121540 20 bp DNA linear PAT 16-MAY-2001
LOCUS
DEFINITION Sequence 76 from patent US 6159734.
ACCESSION AR121540
VERSION AR121540.1 GI:14105116
KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS McKay, R., Borchers, A.H. and Baker, B.F.
TITLE Antisense modulation of peroxisome proliferator-activated receptor gamma expression
JOURNAL Patent: US 6159734-A 76 12-DEC-2000;
FEATURES Location/Qualifiers
SOURCE 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 745 GTGACGGATCGCTTCT 762
Db 2 GTGAAGATCGCTTCT 19

RESULT 273
LOCUS AR121692 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 83 from patent US 6160093.
ACCESSION AR121692
VERSION AR121692.1 GI:14105268
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Visser, E.
TITLE Compounds and methods for treatment and diagnosis of mycobacterial infections
JOURNAL Patent: US 6160093-A 83 12-DEC-2000;
FEATURES Location/Qualifiers
SOURCE 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 274
LOCUS AR123335 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1 from patent US 6169176.
ACCESSION AR123335
VERSION AR123335.1 GI:14108301
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bruce, T.C. and Dev, A.P.
TITLE Decynucleic alkyl thiourea compounds and uses thereof
JOURNAL Patent: US 6169176-A 1 02-JAN-2001;
FEATURES Location/Qualifiers
SOURCE 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 275
LOCUS AR139960 20 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 32 from patent US 6207417.
ACCESSION AR139960
VERSION AR139960.1 GI:14482456
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Zeebo, K.M., Bosselman, R.A., Suggs, S.V. and Martin, F.H.
TITLE DNA encoding stem cell factor
JOURNAL Patent: US 6207417-A 32 27-MAR-2001;
FEATURES Location/Qualifiers
SOURCE 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 276
LOCUS AR139962 20 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 34 from patent US 6207417.
ACCESSION AR139962
VERSION AR139962.1 GI:14482458
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Zeebo, K.M., Bosselman, R.A., Suggs, S.V. and Martin, F.H.
TITLE DNA encoding stem cell factor
JOURNAL Patent: US 6207417-A 34 27-MAR-2001;
FEATURES Location/Qualifiers
SOURCE 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 277
LOCUS AR140279 20 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 32 from patent US 6207454.
ACCESSION AR140279
VERSION AR140279.1 GI:14482775
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Zeebo, K.M., Bosselman, R.A., Suggs, S.V. and Martin, F.H.

TITLE Method for enhancing the efficiency of gene transfer with stem cell
JOURNAL factor (SCF) polypeptide
Patent: US 6207454-A 32 27-MAR-2001;
LOCATION/Qualifiers
SOURCE 1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAAGTAAA 1537
DB 18 AAAAAAAAAA 1

RESULT 278
ARI40281/c 20 bp DNA linear PAT 16-JUN-2001
LOCUS ARI40281
DEFINITION Sequence 34 from patent US 6207454.
ACCESSION ARI40281
VERSION ARI40281.1 GI:14482777
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Zeebo, K.M., BosseIman, R.A., Suggs, S.V. and Martin, F.H.
TITLE Method for enhancing the efficiency of gene transfer with stem cell
JOURNAL factor (SCF) polypeptide
Patent: US 6207454-A 34 27-MAR-2001;
LOCATION/Qualifiers
FEATURES
SOURCE 1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAAGTAAA 1537
DB 18 AAAAAAAAAA 1

RESULT 279
ARI40557/c 20 bp DNA linear PAT 16-JUN-2001
LOCUS ARI40557
DEFINITION Sequence 32 from patent US 6207802.
ACCESSION ARI40557
VERSION ARI40557.1 GI:14483053
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Zeebo, K.M., BosseIman, R.A., Suggs, S.V. and Martin, F.H.
TITLE Stem cell factor and compositions
JOURNAL Patent: US 6207802-A 32 27-MAR-2001;
LOCATION/Qualifiers
FEATURES
SOURCE 1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAAGTAAA 1537
DB 18 AAAAAAAAAA 1

RESULT 280
ARI40559/c 20 bp DNA linear PAT 16-JUN-2001
LOCUS ARI40559
DEFINITION Sequence 34 from patent US 6207802.
ACCESSION ARI40559
VERSION ARI40559.1 GI:14483055
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Zeebo, K.M., BosseIman, R.A., Suggs, S.V. and Martin, F.H.
TITLE Stem cell factor and compositions
JOURNAL Patent: US 6207802-A 34 27-MAR-2001;
LOCATION/Qualifiers
FEATURES
SOURCE 1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAAGTAAA 1537
DB 18 AAAAAAAAAA 1

RESULT 281
ARI41070/c 20 bp DNA linear PAT 16-JUN-2001
LOCUS ARI41070
DEFINITION Sequence 1 from patent US 6207819.
ACCESSION ARI41070
VERSION ARI41070.1 GI:14483566
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Manoharan, M. and Maier, M.A.
TITLE Compounds, processes and intermediates for synthesis of mixed
JOURNAL backbone oligomeric compounds
Patent: US 6207819-A 1 27-MAR-2001;
LOCATION/Qualifiers
FEATURES
SOURCE 1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAAGTAAA 1537
DB 20 AAAAAAAAAA 3

RESULT 282
ARI54115/c 20 bp DNA linear PAT 08-AUG-2001
LOCUS ARI54115
DEFINITION Sequence 14 from patent US 6238865.
ACCESSION ARI54115
VERSION ARI54115.1 GI:15122168
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Huang, Z. and Szostak, J.W.
TITLE Simple and efficient method to label and modify 3'-termini of RNA
using DNA polymerase and a synthetic template with defined overhang
nucleotides

JOURNAL Patent: US 6238865-A 14 29-MAY-2001;
FEATURES
source
1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAAGTAAAA 1537
Db 20 AAAAAAAAAAAGTAAAA 3

RESULT 283
LOCUS AR164658 20 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 13 from patent US 6274321.
ACCESSION AR164658
VERSION AR164658.1 GI:16237754
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
1 (bases 1 to 20)
REFERENCE
AUTHORS Blumberg, B.
TITLE High throughput functional screening of cDNAs
JOURNAL Patent: US 6274321-A 13 14-AUG-2001;
FEATURES
source
1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAAGTAAAA 1537
Db 1 AAAAAAAAAAAGTAAAA 18

RESULT 284
LOCUS BD218101 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Compositions derived from mycobacterium vaccae and methods for their use.
ACCESSION BD218101
VERSION BD218101.1 GI:33027871
KEYWORDS JP 2002514385-A/26.
SOURCE
ORGANISM
synthetic construct
artificial sequence.
1 (bases 1 to 20)
REFERENCE
AUTHORS Tan, P., Watson, J., Visser, E.S., Skinner, M.A. and Prestid, R.L.
TITLE Compositions derived from mycobacterium vaccae and methods for their use.
JOURNAL Patent: JP 2002514385-A 26 21-MAY-2002;
GENESIS RESEARCH AND DEVELOPMENT CORP LTD
OS Artificial Sequence
PN JP 2002514385-A/26
PD 21-MAY-2002
PF 23-DEC-1998 JP 2000525553
PR 23-DEC-1997 US 08/997362, 23-DEC-1997 US 08/997080 PR
23-DEC-1997 US 08/996624, 11-JUN-1998 US 09/095855 PR
17-SEP-1998 US 09/156181, 04-DEC-1998 US 09/205426 PI PAUL
TAN, JAMES MARSON, ELIZABETH S VISSER, MARGOT A SKINNER, ROSS
PI L PRESTIDGE
PC C12N15/09, A61K31/711, A61K39/04, A61K48/00, A61P11/00, A61P11/06,
PC A61P17/00,
PC A61P17/06, A61P31/00, A61P31/06, A61P37/04, C07K14/35, C07K16/12,
PC C07K19/00,

PC C12N1/19, C12N1/21, C12N5/10, C12P21/08, C12Q1/02, G01N33/569, PC
G01N33/68//
PC (C12N15/09, C12R1:32), C12N15/00, C12N5/00, (C12N15/00, C12R1:32)
CC Made in a lab
FH Key
FT source
1. .20
/organism="Artificial Sequence".
Location/Qualifiers
1. .20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAAGTAAAA 1537
Db 1 AAAAAAAAAAAGTAAAA 18

RESULT 285
LOCUS BD234126 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Protein skeleton of antibody mimetics and other binding proteins.
ACCESSION BD234126
VERSION BD234126.1 GI:33043896
KEYWORDS JP 2002532072-A/14.
SOURCE
ORGANISM
synthetic construct
artificial sequence.
1 (bases 1 to 20)
REFERENCE
AUTHORS Lipovsek, D.
TITLE Protein skeleton of antibody mimetics and other binding proteins
JOURNAL Patent: JP 2002532072-A 14 02-OCT-2002;
PHYLOS INC
OS Artificial Sequence
PN JP 2002532072-A/14
PD 02-OCT-2002
PF 09-DEC-1999 JP 2000587187
PR 10-DEC-1998 US 60/111737
PI DASA LIPOVSEK
PC C12N15/09, C07K14/04, C07K14/78, C07K16/46, C07K17/00, C07K19/00, PC
C12P21/02,
PC C12N15/00
CC Puromycin linker oligonucleotide
FH Key
FT source
1. .20
/organism="Artificial Sequence".
Location/Qualifiers
1. .20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAAGTAAAA 1537
Db 1 AAAAAAAAAAAGTAAAA 18

RESULT 286
LOCUS CQ759610 20 bp DNA linear PAT 01-MAR-2004
DEFINITION Sequence 40 from Patent WO2003106672.
ACCESSION CQ759610
VERSION CQ759610.1 GI:44849560
KEYWORDS
SOURCE
synthetic construct

ORGANISM eynthetic construct
REFERENCE 1
AUTHORS Hayashizaki,Y., Carinci,P. and Harbers,M.T.
TITLE Method of utilizing the 5' end of transcribed nucleic acid regions
JOURNAL Patent: WO 200310672-A 40 24-DEC-2003;
 Riken (JP) ; Kabushiki Kaisha Dnaform (JP)
FEATURES
 source 1..20
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="tag8"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 545 TGTGGTGCCTGTGCGCTG 562
 |||||
 2 TGTGTGTGTGTGCGCTG 19

Db

RESULT 287
E12676/c E12676 20 bp DNA linear PAT 27-APR-1998
LOCUS Anti-HTLV-1 antisense oligonucleotide.
DEFINITION E12676
ACCESSION E12676
VERSION E12676.1 GI:3251508
KEYWORDS JP 1997052898-A/10.
SOURCE unidentified
ORGANISM unidentified
 unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS M1nuguchi,M., Kuroaki,N., Makino,K., Koyanagi,Y. and Yamamoto,N.
TITLE ANTI-HTLV-1 ANTI-SENSE OLIGONUCLEOTIDE
JOURNAL Patent: JP 1997052898-A 10 25-FEB-1997;
 SOYAKU GIUTSU KENKYUSHO:KK
COMMENT OS None
 OC Artificial sequences.
 PN JP 1997052898-A/10
 PD 25-FEB-1997
 PF 09-AUG-1995 JP 1995224606
 PI MIZUGUCHI MASATSUGU, KUROSAKI NAKO, MAKINO KEISUKE, PI
 KOYANAGI YOSHIO,
 PI YAMAMOTO NAKO
 PC C07H21/04//A61K31/70;
 CC strandedness: Single;
 CC topology: linear;
 CC hypothetical: No;
 CC anti-sense: Yes;
 FH key Location/Qualifiers
 FT source 1..20
 /organism="Artificial sequences".
 Location/Qualifiers
 1..20
 /organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"

FEATURES
 source 1..20
 Location/Qualifiers
 1..20
 /organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAAGTAAA 1537
 |||||
 20 AAAAAAAAAAAAAAAAAA 3

Db

RESULT 288
128309/c

LOCUS 128309 20 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 20 from patent US 5569832.
ACCESSION 128309
VERSION 128309.1 GI:1819085
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Holton,T.A., Cornish,E.C., Kovacic,F., Tanaka,Y. and Lester,D.R.
TITLE Genetic sequences encoding flavonoid pathway enzymes and uses
 therefor
JOURNAL Patent: US 5569832-A 20 29-OCT-1996;
 Location/Qualifiers
FEATURES
 source 1..20
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1519 TAAATAAAAAAAAAAGTAAA 1536
 |||||
 18 TAAATAAAAAAAAAAAAAA 1

Db

RESULT 289
136180/c 136180 20 bp DNA linear PAT 13-MAY-1997
LOCUS Sequence 16 from patent US 5605662.
DEFINITION 136180
ACCESSION 136180
VERSION 136180.1 GI:2086693
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Heller,M.J. and Tu,E.
TITLE Active programmable electronic devices for molecular biological
 analysis and diagnostics
JOURNAL Patent: US 5605662-A 16 25-FEB-1997;
 Location/Qualifiers
FEATURES
 source 1..20
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAAGTAAA 1537
 |||||
 20 AAAAAAAAAAAAAAAAAA 3

Db

RESULT 290
147310/c 147310 20 bp DNA linear PAT 07-OCT-1997
LOCUS Sequence 11 from patent US 5639870.
DEFINITION 147310
ACCESSION 147310
VERSION 147310.1 GI:2471275
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Holton,T.Albert., Cornish,E.Cecily. and Tanaka,Y.
TITLE Genetic sequences encoding flavonoid pathway enzymes and uses
 therefor
JOURNAL Patent: US 5639870-A 11 17-JUN-1997;
 Location/Qualifiers
FEATURES
 source 1..20
 Location/Qualifiers
 1..20

/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1519 TAAAAAAGTAAAG 1536
Db 18 TAAAAAAGTAAAG 1

RESULT 291
LOCUS AR213738 20 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 83 from patent US 6406704.
ACCESSION AR213738
VERSION AR213738.1 GI:2311025
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Tan, P., Vlasier, E., Prestidge, R. and Watson, J.D.
TITLE Compounds and methods for treatment and diagnosis of mycobacterial infections
JOURNAL Patent: US 6406704-A 83 18-JUN-2002;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAGTAAAG 1537
Db 1 AAAAAAAGTAAAG 18

RESULT 292
LOCUS AR222466 20 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 26 from patent US 6429300.
ACCESSION AR222466
VERSION AR222466.1 GI:2323997
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kurz, M., Lohse, P. and Wagner, R.
TITLE Peptide acceptor ligation methods
JOURNAL Patent: US 6429300-A 26 06-AUG-2002;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAGTAAAG 1537
Db 1 AAAAAAAGTAAAG 18

RESULT 293
LOCUS AR213112 20 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 49 from patent US 6451968.

ACCESSION AR231312
VERSION AR231312.1 GI:27272243
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Egholm, M., Nielsen, P., Buchardt, O., Dueholm, K.L., Christensen, L., Coll, J.M., Kieley, J. and Griffith, M.
TITLE Peptide nucleic acids
JOURNAL Patent: US 6451968-A 49 17-SEP-2002;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1521 AAAAAAAGTAAAG 1539
Db 19 AAAAAAAGTAAAG 1

RESULT 294
LOCUS AR236083 20 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 1 from patent US 6462184.
ACCESSION AR236083
VERSION AR236083.1 GI:27279782
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Manoharan, M. and Maier, M.A.
TITLE Compounds, processes and intermediates for synthesis of mixed backbone oligomeric compounds
JOURNAL Patent: US 6462184-A 1 08-OCT-2002;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAGTAAAG 1537
Db 20 AAAAAAAGTAAAG 3

RESULT 295
LOCUS AR274394 20 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 55 from patent US 6506564.
ACCESSION AR274394
VERSION AR274394.1 GI:29706840
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Mirkin, C.A., Letsinger, R.L., Mucic, R.C., Storchoff, J.J., Elghanian, R. and Taton, T.A.
TITLE Nanoparticles having oligonucleotides attached thereto and uses therefor
JOURNAL Patent: US 6506564-A 55 14-JAN-2003;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"

/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
DB 1 AAAAAAAAAAAAAAAAAA 18

RESULT 296
AR343047/c AR343047 20 bp DNA linear PAT 17-AUG-2003
LOCUS Sequence 10 from patent US 6576752.
ACCESSION AR343047
VERSION AR343047.1 GI:33738375
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Manoharan, M., Iomberg, H., Salo, H. and Vitra, P.
TITLE Aminooxy functionalized oligomers
JOURNAL Patent: US 6576752-A 10 10-JUN-2003;
FEATURES Location/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
DB 20 AAAAAAAAAAAAAAAAAA 3

RESULT 297
AR344936 AR344936 20 bp DNA linear PAT 17-AUG-2003
LOCUS Sequence 55 from patent US 6582921.
ACCESSION AR344936
VERSION AR344936.1 GI:33741017
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Mirkin, C.A., Letsinger, R.L., Mucic, R.C., Storchoff, J.J., Elghanian, R. and Taton, T.A.
TITLE Nanoparticles having oligonucleotides attached thereto and uses thereof
JOURNAL Patent: US 6582921-A 55 24-JUN-2003;
FEATURES Location/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
DB 1 AAAAAAAAAAAAAAAAAA 18

RESULT 298
AR365970 AR365970 20 bp DNA linear PAT 12-SEP-2003
LOCUS Sequence 83 from patent US 6328978.
DEFINITION

ACCESSION AR365970
VERSION AR365970.1 GI:34598223
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Watson, J.D., Tan, P.L.J. and Prestidge, R.
TITLE Methods for the treatment of immunologically-mediated skin disorders
JOURNAL Patent: US 6328978-A 83 11-DEC-2001;
FEATURES Location/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
DB 1 AAAAAAAAAAAAAAAAAA 18

RESULT 299
AR382312 AR382312 20 bp DNA linear PAT 18-DEC-2003
LOCUS Sequence 55 from patent US 6610491.
ACCESSION AR382312
VERSION AR382312.1 GI:40090724
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Mirkin, C.A., Letsinger, R.L., Mucic, R.C., Storchoff, J.J., Elghanian, R. and Taton, T.A.
TITLE Nanoparticles having oligonucleotides attached thereto and uses thereof
JOURNAL Patent: US 6610491-A 55 26-AUG-2003;
FEATURES Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
DB 1 AAAAAAAAAAAAAAAAAA 18

RESULT 300
AR429653 AR429653 20 bp DNA linear PAT 18-DEC-2003
LOCUS Sequence 55 from patent US 6645721.
ACCESSION AR429653
VERSION AR429653.1 GI:40189949
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Mirkin, C.A., Letsinger, R.L., Mucic, R.C., Storchoff, J.J., Elghanian, R. and Taton, T.A.
TITLE Nanoparticles having oligonucleotides attached thereto and uses thereof
JOURNAL Patent: US 6645721-A 55 11-NOV-2003;
FEATURES Location/Qualifiers
1..20

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/organism="unknown"
/mol_type="genomic DNA"

Query Match      1.1% Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1520 AAAAAAAAAAGTAAA 1537
      1 AAAAAAAAAAAAAAAAAA 18

Db

RESULT 301
AR447441
LOCUS      AR447441      20 bp      DNA      linear      PAT 20-FEB-2004
DEFINITION Sequence 55 from patent US 6673548.
ACCESSION AR447441
VERSION    AR447441.1 GI:42675765
KEYWORDS
SOURCE
ORGANISM   unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storchoff,J.J.,
            Elghanian,R. and Taton,T.A.
TITLE      Nanoparticles having oligonucleotides attached thereto and uses
            therefor
JOURNAL    Patent: US 6673548-A 55 06-JAN-2004;
FEATURES
SOURCE
/mol_type="genomic DNA"

Query Match      1.1% Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1520 AAAAAAAAAAGTAAA 1537
      1 AAAAAAAAAAAAAAAAAA 18

Db

RESULT 302
AR451990
LOCUS      AR451990      20 bp      DNA      linear      PAT 20-FEB-2004
DEFINITION Sequence 55 from patent US 6677122.
ACCESSION AR451990
VERSION    AR451990.1 GI:42683297
KEYWORDS
SOURCE
ORGANISM   unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storchoff,J.J.,
            Elghanian,R. and Taton,T.A.
TITLE      Nanoparticles having oligonucleotides attached thereto and uses
            therefor
JOURNAL    Patent: US 6677122-A 55 13-JAN-2004;
FEATURES
SOURCE
/mol_type="genomic DNA"

Query Match      1.1% Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1520 AAAAAAAAAAGTAAA 1537
      1 AAAAAAAAAAAAAAAAAA 18

Db

RESULT 303
AR451990
LOCUS      AR451990      20 bp      DNA      linear      PAT 20-FEB-2004
DEFINITION Sequence 55 from patent US 6677122.
ACCESSION AR451990
VERSION    AR451990.1 GI:42683297
KEYWORDS
SOURCE
ORGANISM   unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storchoff,J.J.,
            Elghanian,R. and Taton,T.A.
TITLE      Nanoparticles having oligonucleotides attached thereto and uses
            therefor
JOURNAL    Patent: US 6677122-A 55 13-JAN-2004;
FEATURES
SOURCE
/mol_type="genomic DNA"
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AR454776
LOCUS      AR454776      20 bp      DNA      linear      PAT 20-FEB-2004
DEFINITION Sequence 55 from patent US 6682895.
ACCESSION AR454776
VERSION    AR454776.1 GI:42688297
KEYWORDS
SOURCE
ORGANISM   unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storchoff,J.J.,
            Elghanian,R. and Taton,T.A.
TITLE      Nanoparticles having oligonucleotides attached thereto and uses
            therefor
JOURNAL    Patent: US 6682895-A 55 27-JAN-2004;
FEATURES
SOURCE
/mol_type="genomic DNA"

Query Match      1.1% Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1520 AAAAAAAAAAGTAAA 1537
      1 AAAAAAAAAAAAAAAAAA 18

Db

RESULT 304
AR488890/c
LOCUS      AR488890/c      20 bp      DNA      linear      PAT 15-MAY-2004
DEFINITION Sequence 7 from patent US 6709818.
ACCESSION AR488890
VERSION    AR488890.1 GI:47255117
KEYWORDS
SOURCE
ORGANISM   unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Nelson,W.G., Lin,X., Tchou,J.C. and Bakker,J.
TITLE      Methods of diagnosing and treating hepatic cell proliferative
            disorders
JOURNAL    Patent: US 6709818-A 7 23-MAR-2004;
FEATURES
SOURCE
/mol_type="genomic DNA"

Query Match      1.1% Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1518 TTAATAAAAAAAAAAGTAA 1535
      19 TTAATAAAAAAAAAAATTA 2

Db

RESULT 305
AR489044
LOCUS      AR489044      20 bp      DNA      linear      PAT 15-MAY-2004
DEFINITION Sequence 55 from patent US 6709825..
ACCESSION AR489044
VERSION    AR489044.1 GI:47255475
KEYWORDS
SOURCE
ORGANISM   unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storchoff,J.J.,
            Elghanian,R. and Taton,T.A.
TITLE      Nanoparticles having oligonucleotides attached thereto and uses
            therefor
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JOURNAL Patent: US 6709825-A 55 23-MAR-2004;
FEATURES
source
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAA 1537
DB 1 AAAAAAAAAAAAAAAAAA 18

RESULT 306
LOCUS AR494116 20 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 55 from patent US 6720147.
ACCESSION AR494116
VERSION AR494116.1 GI:47266895
KEYWORDS
SOURCE
ORGANISM
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storchoff,J.J., Elghanian,R. and Taton,T.A.
TITLE Nanoparticles having oligonucleotides attached thereto and uses thereof
JOURNAL Patent: US 6720147-A 55 13-APR-2004;
FEATURES
source
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAA 1537
DB 1 AAAAAAAAAAAAAAAAAA 18

RESULT 307
LOCUS AR494728 20 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 55 from patent US 6720411.
ACCESSION AR494728
VERSION AR494728.1 GI:47269581
KEYWORDS
SOURCE
ORGANISM
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storchoff,J.J., Elghanian,R. and Taton,T.A.
TITLE Nanoparticles having oligonucleotides attached thereto and uses thereof
JOURNAL Patent: US 6720411-A 55 13-APR-2004;
FEATURES
source
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAA 1537
DB 1 AAAAAAAAAAAAAAAAAA 18

RESULT 308
LOCUS AX004876/c 20 bp DNA linear PAT 24-AUG-2000
DEFINITION Sequence 5 from Patent WO9910527.
ACCESSION AX004876
VERSION AX004876.1 GI:9928276
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Bayer,E. and Schewitz,J.
TITLE Method for isolating anionic organic substances from aqueous systems using cationic polymer nanoparticles
JOURNAL Patent: WO 9910527-A 5 04-MAR-1999;
FEATURES
source
Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="phosphorothioate oligonucleotide"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAA 1537
DB 20 AAAAAAAAAAAAAAAAAA 3

RESULT 309
LOCUS AX045779/c 20 bp DNA linear PAT 24-NOV-2000
DEFINITION Sequence 9 from Patent WO0067023.
ACCESSION AX045779
VERSION AX045779.1 GI:11344146
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Noll,B.O., Schetter,C. and Krieg,A.M.
TITLE Screening for immunostimulatory dna functional modifiers
JOURNAL Patent: WO 0067023-A 9 09-NOV-2000;
FEATURES
source
Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"
/note="modified with digoxigenin"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAA 1537
DB 20 AAAAAAAAAAAAAAAAAA 3

RESULT 310
LOCUS AX045787/c 20 bp DNA linear PAT 24-NOV-2000
DEFINITION Sequence 17 from Patent WO0067023.
ACCESSION AX045787

VERSION AX045787.1 GI:11344154
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Noll,B.O., Schetter,C. and Krieg,A.M.
TITLE Screening for immunostimulatory dna functional modifiers
JOURNAL Patent: WO 0067023-A 17 09-NOV-2000;
CPG Immunopharmaceuticals GmbH (DE) ; UNIVERSITY OF IOWA RESEARCH
FOUNDATION (US)
FEATURES
source Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"
1..20
/note="phosphorothioate backbone"
misc_feature
1
/note="modified with digoxigenin"
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1520 AAAAAAAAAAGTAAA 1537
Db 20 AAAAAAAAAAAAAAAAAA 3
RESULT 311
AX045790/c AX045790 20 bp DNA linear PAT 24-NOV-2000
LOCUS Sequence 20 from Patent WO0067023.
DEFINITION AX045790
ACCESSION AX045790
VERSION AX045790.1 GI:11344157
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Noll,B.O., Schetter,C. and Krieg,A.M.
TITLE Screening for immunostimulatory dna functional modifiers
JOURNAL Patent: WO 0067023-A 20 09-NOV-2000;
CPG Immunopharmaceuticals GmbH (DE) ; UNIVERSITY OF IOWA RESEARCH
FOUNDATION (US)
FEATURES
source Location/Qualifiers
1..20
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1520 AAAAAAAAAAGTAAA 1537
Db 20 AAAAAAAAAAAAAAAAAA 3
RESULT 312
AX056597/c AX056597 20 bp DNA linear PAT 13-JAN-2001
LOCUS Sequence 241 from Patent WO0073469.
DEFINITION AX056597
ACCESSION AX056597
VERSION AX056597.1 GI:12229186
KEYWORDS
SOURCE Murinae gen. sp.
ORGANISM Murinae gen. sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae.
REFERENCE 1
AUTHORS Ploewman,G.D., Martinez,R., Whyte,D. and Sudersanam,S.
TITLE Protein Kinases
JOURNAL Patent: WO 0073469-A 241 07-DEC-2000;
Sugen, Inc. (US)
FEATURES
source Location/Qualifiers
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/organism="Murinae gen. sp."
/mol_type="unassigned DNA"
/db_xref="taxon:39108"
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 698 CTGCTGAATGAGTCGCG 715
Db 20 CTGCTCAATGCTGTCGCG 3
RESULT 313
AX104034/c AX104034 20 bp DNA linear PAT 30-APR-2001
LOCUS Sequence 226 from Patent WO0122972.
DEFINITION AX104034
ACCESSION AX104034
VERSION AX104034.1 GI:13920231
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 226 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
source Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1520 AAAAAAAAAAGTAAA 1537
Db 20 AAAAAAAAAAAAAAAAAA 3
RESULT 314
AX104364/c AX104364 20 bp DNA linear PAT 30-APR-2001
LOCUS Sequence 556 from Patent WO0122972.
DEFINITION AX104364
ACCESSION AX104364
VERSION AX104364.1 GI:13920561
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 556 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
source Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAA 1537
|||||
Db 20 AAAAAAAAAAAAAA 3

RESULT 315
AX104368 20 bp DNA linear PAT 30-APR-2001
LOCUS
DEFINITION Sequence 560 from Patent WO0122972.
ACCESSION AX104368
VERSION AX104368.1 GI:13920565
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Krieg, A.M., Schetter, C. and Vollmer, J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 560 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
source 1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAA 1537
|||||
Db 1 AAAAAAAAAAAAAA 18

RESULT 316
AX196224 20 bp DNA linear PAT 28-AUG-2001
LOCUS
DEFINITION Sequence 55 from Patent WO0151665.
ACCESSION AX196224
VERSION AX196224.1 GI:15386427
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Mitkin, C.A., Leisinger, R.L., Mucic, R.C., Storchoff, J.J.,
TITLE Elghanian, R., Taton, T.A. and Li, Z.
JOURNAL Nanoparticles having oligonucleotides attached thereto and uses
therefor
Patent: WO 0151665-A 55 19-JUL-2001;
Nanosphere, Inc. (US)
FEATURES
source 1. .20
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="random synthetic sequence"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAA 1537
|||||
Db 1 AAAAAAAAAAAAAA 18

RESULT 317
AX196239 20 bp DNA linear PAT 28-AUG-2001
LOCUS
DEFINITION Sequence 70 from Patent WO0151665.
ACCESSION AX196239
VERSION AX196239.1 GI:15386442
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Mitkin, C.A., Leisinger, R.L., Mucic, R.C., Storchoff, J.J.,
TITLE Elghanian, R., Taton, T.A. and Li, Z.
JOURNAL Nanoparticles having oligonucleotides attached thereto and uses
therefor
Patent: WO 0151665-A 70 19-JUL-2001;
Nanosphere, Inc. (US)
FEATURES
source 1. .20
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="random synthetic sequence"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAA 1537
|||||
Db 1 AAAAAAAAAAAAAA 18

RESULT 318
AX354974 20 bp DNA linear PAT 06-FEB-2002
LOCUS
DEFINITION Sequence 2 from Patent WO0197843.
ACCESSION AX354974
VERSION AX354974.1 GI:18619641
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Weiner, G. and Hartmann, G.
TITLE Methods for enhancing antibody-induced cell lysis and treating
cancer
JOURNAL Patent: WO 0197843-A 2 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES
source 1. .20
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide-phosphodiester backbone"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAA 1537
|||||
Db 1 AAAAAAAAAAAAAA 18

RESULT 319
AX355810/c 20 bp DNA linear PAT 06-FEB-2002
LOCUS
DEFINITION Sequence 838 from Patent WO0197843.
ACCESSION AX355810
VERSION AX355810.1 GI:18620478
KEYWORDS

SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Weiner G. and Hartmann, G.
TITLE Methods for enhancing antibody-induced cell lysis and creating cancer
JOURNAL Patent: WO 0197843-A 838 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)

FEATURES
source
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide-phosphorothioate backbone"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1520 AAAAAAAAAAAGTAAA 1537
Db 20 AAAAAAAAAAAAAAAAAA 3

RESULT 320
AX355811/C
LOCUS AX355811 20 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 839 from Patent WO0197843.
ACCESSION AX355811
VERSION AX355811.1 GI:18620479
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Weiner, G. and Hartmann, G.
TITLE Method for enhancing antibody-induced cell lysis and creating cancer
JOURNAL Patent: WO 0197843-A 839 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)

FEATURES
source
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide-phosphodiester backbone"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1520 AAAAAAAAAAAGTAAA 1537
Db 20 AAAAAAAAAAAAAAAAAA 3

RESULT 321
AX440125
LOCUS AX440125 20 bp DNA linear PAT 28-JUN-2002
DEFINITION Sequence 55 from Patent WO0173123.
ACCESSION AX440125
VERSION AX440125.1 GI:21664936
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Mirkin, C.A., Letsinger, R.L., Mucic, R.C., Storchoff, J.J., Elghanian, R., Taton, T.A., Park, S.J. and Li, Z.
TITLE Nanoparticles having oligonucleotides attached thereto and uses therefor

JOURNAL Patent: WO 0173123-A 55 04-OCT-2001;
Nanosphere, Inc. (US)

FEATURES
source
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="random synthetic sequence"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1520 AAAAAAAAAAAGTAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 322
AX440140
LOCUS AX440140 20 bp DNA linear PAT 28-JUN-2002
DEFINITION Sequence 70 from Patent WO0173123.
ACCESSION AX440140
VERSION AX440140.1 GI:21664951
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Mirkin, C.A., Letsinger, R.L., Mucic, R.C., Storchoff, J.J., Elghanian, R., Taton, T.A., Park, S.J. and Li, Z.
TITLE Nanoparticles having oligonucleotides attached thereto and uses therefor
JOURNAL Patent: WO 0173123-A 70 04-OCT-2001;
Nanosphere, Inc. (US)

FEATURES
source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="random synthetic sequence"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1520 AAAAAAAAAAAGTAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 323
AX465311
LOCUS AX465311 20 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 55 from Patent WO0218643.
ACCESSION AX465311
VERSION AX465311.1 GI:21899674
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Mirkin, C.A., Letsinger, R.L., Mucic, R.C., Storchoff, J.J., Elghanian, R., Taton, T.A., Garmeli, V., Li, Z. and Park, S.J.
TITLE Nanoparticles having oligonucleotides attached thereto and uses therefor
JOURNAL Patent: WO 0218643-A 55 07-MAR-2002;
Nanosphere, Inc. (US)

FEATURES
source
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

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Query Match      1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      1520 AAAAAAAAAAGTAAAA 1537
      1 AAAAAAAAAAAAAAAAAAAAA 18
Db
RESULT 324
AX465326      20 bp      DNA      linear      PAT 16-JUL-2002
LOCUS      Sequence 70 from Patent WO0218643.
AX465326
ACCESSION      AX465326.1 GI:21899689
KEYWORDS
SOURCE      .
ORGANISM      synthetic construct
      synthetic construct
      artificial sequences.
REFERENCE      1
AUTHORS      Matkin,C.A., Letsinger,R.L., Mucic,R.C., Strohoff,J.J.,
      Eghannian,R., Jaton,T.A., Garimella,V., Li,Z. and Park,S.J.
      Nanoparticles having oligonucleotides attached thereto and uses
      thereof
      Patent: WO 0218643-A 70 07-MAR-2002;
      Nanosphere, Inc. (US)
JOURNAL      Location/Qualifiers
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      /note="random synthetic sequence"
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Best Local Similarity 88.9%; Pred. No. 1.8e+02;
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QY      1520 AAAAAAAAAAGTAAAA 1537
      1 AAAAAAAAAAAAAAAAAAAAA 18
Db
RESULT 325
AX524879/c      20 bp      DNA      linear      PAT 21-NOV-2002
LOCUS      AX524879
DEFINITION      Sequence 8 from Patent EP1236806.
ACCESSION      AX524879
VERSION      AX524879.1 GI:25169966
KEYWORDS
SOURCE      .
ORGANISM      synthetic construct
      synthetic construct
      artificial sequences.
REFERENCE      1
AUTHORS      Maruyama,T., Ishiguro,T. and Taya,T.
      Oligonucleotide and method for detecting verotoxin
      Patent: EP 1236806-A 8 04-SEP-2002;
      Tosoh Corporation (JP)
JOURNAL      Location/Qualifiers
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      /db_xref="taxon:32630"
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Query Match      1.1%; Score 14.8; DB 1; Length 20;
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QY      831 ATCAGCGCGTGTGAC 848
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Db      20 ATCAGCGCGTGTGAC 3
RESULT 326
AX547087/c      20 bp      DNA      linear      PAT 01-MAR-2003
LOCUS      AX547087
DEFINITION      Sequence 226 from Patent WO02053141.
ACCESSION      AX547087
VERSION      AX547087.1 GI:25812231
KEYWORDS
SOURCE      .
ORGANISM      synthetic construct
      synthetic construct
      artificial sequences.
REFERENCE      1
AUTHORS      Bratzler,R.L.
      Inhibition of angiogenesis by nucleic acids
      Patent: WO 02053141-A 226 11-JUL-2002;
      Coley Pharmaceutical Group, Inc. (US)
JOURNAL      Location/Qualifiers
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Query Match      1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      1520 AAAAAAAAAAGTAAAA 1537
      20 AAAAAAAAAAAAAAAAAAAAA 3
Db
RESULT 327
AX547417/c      20 bp      DNA      linear      PAT 01-MAR-2003
LOCUS      AX547417
DEFINITION      Sequence 556 from Patent WO02053141.
ACCESSION      AX547417
VERSION      AX547417.1 GI:25812561
KEYWORDS
SOURCE      .
ORGANISM      synthetic construct
      synthetic construct
      artificial sequences.
REFERENCE      1
AUTHORS      Bratzler,R.L.
      Inhibition of angiogenesis by nucleic acids
      Patent: WO 02053141-A 556 11-JUL-2002;
      Coley Pharmaceutical Group, Inc. (US)
JOURNAL      Location/Qualifiers
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      /note="Synthetic Sequence"
Query Match      1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      1520 AAAAAAAAAAGTAAAA 1537
      20 AAAAAAAAAAAAAAAAAAAAA 3
Db
RESULT 328
AX547421      20 bp      DNA      linear      PAT 01-MAR-2003
LOCUS      AX547421
DEFINITION      Sequence 560 from Patent WO02053141.
ACCESSION      AX547421
VERSION      AX547421.1 GI:25812565
KEYWORDS
SOURCE      .
      synthetic construct
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ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Bratzler, R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 560 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)

FEATURES
source Location/Qualifiers
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/note="Synthetic Sequence"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
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Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAAGTAAA 1537
|||||
1 AAAAAAAAAAAAAAAAAA 18

RESULT 329
AX556124 20 bp DNA linear PAT 27-NOV-2002
LOCUS AX556124
DEFINITION Sequence 55 from Patent WO0246472.
ACCESSION AX556124
VERSION AX556124.1 GI:25899506
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Minkin, C.A., Letsinger, R.L., Mucic, R.C., Storchoff, J.J.,
Elghanian, R., Taton, T.A., Garimella, V., Li, Z. and Park, S.J.
TITLE Nanoparticles having oligonucleotides attached thereto and uses
JOURNAL Patent: WO 0246472-A 55 13-JUN-2002;
Nanosphere, Inc. (US)

FEATURES
source Location/Qualifiers
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/organism="synthetic construct"
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/note="random synthetic sequence"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
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Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAAGTAAA 1537
|||||
1 AAAAAAAAAAAAAAAAAA 18

RESULT 330
AX556139 20 bp DNA linear PAT 27-NOV-2002
LOCUS AX556139
DEFINITION Sequence 70 from Patent WO0246472.
ACCESSION AX556139
VERSION AX556139.1 GI:25899521
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Minkin, C.A., Letsinger, R.L., Mucic, R.C., Storchoff, J.J.,
Elghanian, R., Taton, T.A., Garimella, V., Li, Z. and Park, S.J.
TITLE Nanoparticles having oligonucleotides attached thereto and uses
JOURNAL Patent: WO 0246472-A 70 13-JUN-2002;
Nanosphere, Inc. (US)

FEATURES
source Location/Qualifiers
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/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="random synthetic sequence"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
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Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1520 AAAAAAAAAAAGTAAA 1537
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1 AAAAAAAAAAAAAAAAAA 18

RESULT 331
AX664307 20 bp DNA linear PAT 22-MAR-2003
LOCUS AX664307
DEFINITION Sequence 5 from Patent WO0246398.
ACCESSION AX664307
VERSION AX664307.1 GI:29164237
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Willson, R.C. and Murphy, J.C.
TITLE Nucleic acid separation using immobilized metal affinity
JOURNAL Chromatography
Patent: WO 0246398-A 5 13-JUN-2002;
The University of Houston System (US)

FEATURES
source Location/Qualifiers
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/db_xref="taxon:32630"
/note="Synthetic Oligonucleotide Sequence"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
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Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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|||||
1 AAAAAAAAAAAAAAAAAA 18

RESULT 332
AX664308 20 bp DNA linear PAT 22-MAR-2003
LOCUS AX664308
DEFINITION Sequence 6 from Patent WO0246398.
ACCESSION AX664308
VERSION AX664308.1 GI:29164238
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Willson, R.C. and Murphy, J.C.
TITLE Nucleic acid separation using immobilized metal affinity
JOURNAL Chromatography
Patent: WO 0246398-A 6 13-JUN-2002;
The University of Houston System (US)

FEATURES
source Location/Qualifiers
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Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
|||||
Db 20 AAAAAAAAAAAAAAAAAA 3

RESULT 333
AX708893 20 bp DNA linear PAT 04-APR-2003
LOCUS AX708893
DEFINITION Sequence 75 from Patent WO02101045.
ACCESSION AX708893
VERSION AX708893.1 GI:29564623
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
Novartis AG (CH) ; IRM LLC (BM)
Location/Qualifiers
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide primer"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 722 GTTTGCTGCTGCTG 739
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Db 3 GTTTGCTGCTGCTG 20

RESULT 334
AX741040/c 20 bp DNA linear PAT 10-MAY-2003
LOCUS AX741040
DEFINITION Sequence 14 from Patent WO03027328.
ACCESSION AX741040
VERSION AX741040.1 GI:30523901
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
Patent: WO 03027328-A 14 03-APR-2003;
Boston Probes, Inc. (US) ; DakoCytomation Denmark A/S (DK)
Location/Qualifiers
1. .20
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/db_xref="taxon:32630"
/note="Description of Combined DNA/RNA Molecule:Synthetic
Oligomer Sequence-Synthetic Probe Sequence"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
|||||
Db 20 AAAAAAAAAAAAAAAAAA 3

RESULT 335
AX741052 20 bp DNA linear PAT 10-MAY-2003
LOCUS AX741052
DEFINITION Sequence 26 from Patent WO03027328.
ACCESSION AX741052
VERSION AX741052.1 GI:30523913
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
Kitsen, N.V., Hyldig-Nielsen, J.J. and Williams, B.F.
Methods, kits and compositions pertaining to the suppression of
detectable probe binding to randomly distributed repeat sequences
in genomic nucleic acid
Patent: WO 03027328-A 26 03-APR-2003;
Boston Probes, Inc. (US) ; DakoCytomation Denmark A/S (DK)
Location/Qualifiers
1. .20
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/db_xref="taxon:32630"
/note="Description of Combined DNA/RNA Molecule:Synthetic
Oligomer Sequence-Synthetic Probe Sequence"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
|||||
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 336
BD008523 20 bp DNA linear PAT 31-JAN-2002
LOCUS BD008523
DEFINITION Compounds and methods for treatment and diagnosis of Mycobacterial
infections.
ACCESSION BD008523
VERSION BD008523.1 GI:18636896
KEYWORDS JP 2001503969-A/26.
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
Patent: JP 2001503969-A 26 27-MAR-2001;
GENESIS RESEARCH & DEVELOPMENT CO LTD
OS Unidentified
PN JP 2001503969-A/26
PD 27-MAR-2001
PF 28-AUG-1997 JP 1998511516
PR
PI PAUL TAN, JUN HIYAMA, ELIZABETH S VISSER, MARGOT A SKINNER, PI
LINDA M SCOTT,
PI ROSS L PRESTIDGE
PC A61K39/04,A61K35/74,C07K14/35,C12N15/63
CC Strandedness: Single;
CC Topology: Linear;
FH Key
FT Location/Qualifiers
FT source 1. .20
/organism="Unidentified".

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
|||||
Db 1 AAAAAAAAAAAAAAAAAA 18

Query Match 1.1%; Score 14.8; DB 1; Length 20;

Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAA 1537
DB 1 AAAAAAAAAAAAAAAAAA 18

RESULT 337
BD080522/c 20 bp RNA linear PAT 27-AUG-2002
LOCUS Ribonucleoside-derivative and method for preparing the same.
DEFINITION BD080522
ACCESSION BD080522.1 GI:22626125
VERSION JP 2001515087-A/1.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 20)
Pitsch, S., Weiss, P. A. and Jenny, L.
Ribonucleoside-derivative and method for preparing the same
Patent: JP 2001515087-A 1 18-SEP-2001;
STEFAN PITTSCH, PATRICK A WEISS, LUZI JENNY
OS Artificial Sequence
PN JP 2001515087-A/1
PD 18-SEP-2001
PF 17-AUG-1998 JP 2000509723
PR 18-AUG-1997 CH 1931/97
PI STEFAN PITTSCH, PATRICK A WEISS, LUZI JENNY
PC C07H19/06, C07F7/18, C07H19/16, C07H21/02, C07H23/00 CC
Description of Artificial Sequence: synthetic polynucleotide FH
Key
FT source Location/Qualifiers
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/organism="Artificial Sequence".
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/mol_type="genomic RNA"
/db_xref="taxon:32630"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAA 1537
DB 20 AAAAAAAAAAAAAAAAAA 3

RESULT 338
BD107450/c 20 bp DNA linear PAT 18-SEP-2002
LOCUS Method of detecting single base polymorphism.
DEFINITION BD107450
ACCESSION BD107450.1 GI:23202268
VERSION UP 2002034599-A/9.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 20)
Segawa, M., Takarada, H., Aono, T. and Yoshiga, S.
Method of detecting single base polymorphism
Patent: JP 2002034599-A 9 05-FEB-2002;
TOYOBO CO LTD
OS Artificial Sequence
PN JP 2002034599-A/9
PD 05-FEB-2002
PF 26-JUL-2000 JP 2000225354
PI MASAYA SEGAWA, HIROSHI TAKARADA, TOSHIYA AONO, SATOKO YOSHIGA PC
C12Q1/68, C12M15/09, C12M15/00
CC Description of Artificial Sequence: primer
FH Key Location/Qualifiers
1..20
FT source Location/Qualifiers
1..20
/organism="unknown"

FT Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAA 1537
DB 20 AAAAAAAAAAAAAAAAAA 3

RESULT 339
BD174543/c 20 bp DNA linear PAT 18-MAR-2003
LOCUS Oligonucleotide for detecting Vero toxin and detection method.
DEFINITION BD174543
ACCESSION BD174543.1 GI:29120233
VERSION JP 2002253257-A/8.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 20)
Maruyama, T., Ishiguro, T. and Taya, T.
Oligonucleotide for detecting Vero toxin and detection method
Patent: JP 2002253257-A 8 10-SEP-2002;
TOSOH CORP
OS Artificial Sequence
PN JP 2002253257-A/8
PD 10-SEP-2002
PF 02-MAR-2001 JP 2001058143
PI TAKAHIRO MARUYAMA, TAKAHIRO ISHIGURO, TOSHITAKA TAYA PC
C12N15/09, C12Q1/68, G01N33/53, G01N33/566, C12N15/00 CC
Oligonucleotide capable of binding specifically to VT2 RNA FH Key
FT source Location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 831 ATCAGCGCGGTGTGACG 848
DB 20 ATCAGCGCGGTGTGACG 3

RESULT 340
AR080294 21 bp DNA linear PAT 31-AUG-2000
LOCUS Sequence 13 from patent US 5968754.
DEFINITION AR080294
ACCESSION AR080294
VERSION AR080294.1 GI:10007029
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
Watson, M. A. and Fleming, T. P.
Mammaglobin, a mammary-specific breast cancer protein
Patent: US 5968754-A 13 19-OCT-1999;
FH Key Location/Qualifiers
1..21
/organism="unknown"

/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
Db 21 AAAAAAAAAAAAAAAAAA 4

RESULT 341
AR084521 21 bp DNA linear PAT 01-SEP-2000
LOCUS AR084521
DEFINITION Sequence 10 from patent US 5981185.
ACCESSION AR084521
VERSION AR084521.1 GI:10011292
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Watson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 10 09-NOV-1999;
FEATURES
Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 342
AR084524/c 21 bp DNA linear PAT 01-SEP-2000
LOCUS AR084524
DEFINITION Sequence 13 from patent US 5981185.
ACCESSION AR084524
VERSION AR084524.1 GI:10011295
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Watson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 13 09-NOV-1999;
FEATURES
Location/Qualifiers
1..21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
Db 21 AAAAAAAAAAAAAAAAAA 4

RESULT 343
AR093143 21 bp DNA linear PAT 08-SEP-2000
LOCUS AR093143
DEFINITION Sequence 12 from patent US 5998596.
ACCESSION AR093143
VERSION AR093143.1 GI:10019895

KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Bergan,R. and Neckers,L.
TITLE Inhibition of protein kinase activity by aptameric action of oligonucleotides
JOURNAL Patent: US 5998596-A 12 07-DEC-1999;
FEATURES
Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
Db 21 AAAAAAAAAAAAAAAAAA 4

RESULT 344
AR095412/c 21 bp DNA linear PAT 08-SEP-2000
LOCUS AR095412
DEFINITION Sequence 13 from patent US 6004756.
ACCESSION AR095412
VERSION AR095412.1 GI:10023262
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Watson,M.A. and Fleming,T.P.
TITLE Method for detecting the presence of breast cancer by detecting an increase in mammaglobin mRNA expression
JOURNAL Patent: US 6004756-A 13 21-DEC-1999;
FEATURES
Location/Qualifiers
1..21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAA 1537
Db 21 AAAAAAAAAAAAAAAAAA 4

RESULT 345
AR103542 21 bp DNA linear PAT 14-FEB-2001
LOCUS AR103542
DEFINITION Sequence 66 from patent US 6087485.
ACCESSION AR103542
VERSION AR103542.1 GI:12815130
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Brookes-Wilson,A.R., Buckler,A., Cardon,L., Carey,A.H., Galvin,M., Miller,A. and North,M.
TITLE Asthma related genes
JOURNAL Patent: US 6087485-A 66 11-JUL-2000;
FEATURES
Location/Qualifiers
1..21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 21;

Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1225 CTCTAGCTCTAGCTCTCTC 1244
Db 1 CTTCTTCTCTYGTCTCTC 20

RESULT 346
LOCUS AR118155 21 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 23 from patent US 6140489.
ACCESSION AR118155
VERSION AR118155.1 GI:14099061
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Brenner, S.
TITLE Compositions for sorting polynucleotides
JOURNAL Patent: US 6140489-A 23 31-OCT-2000;
FEATURES
Source Location/Qualifiers
1..21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAA 1537
Db 21 AAAAAAAAAAAAAAAAAA 4

RESULT 347
LOCUS AR153849 21 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 2 from patent US 6238624.
ACCESSION AR153849
VERSION AR153849.1 GI:15121902
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Heller, M.J., Tu, B., Evans, G.A. and Sosnowski, R.G.
TITLE Methods for transport in molecular biological analysis and
diagnostics
JOURNAL Patent: US 6238624-A 2 29-MAY-2001;
FEATURES
Source Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAA 1537
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 348
LOCUS BD224108 21 bp DNA linear PAT 17-JUL-2003
DEFINITION Mammaglobin, breast cancer secretory protein specific to mamma.
ACCESSION BD224108
VERSION BD224108.1 GI:33033878
KEYWORDS
SOURCE synthetic construct

ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 21)
AUTHORS Watson, M.A. and Fleming, T.P.
TITLE Mammaglobin, breast cancer secretory protein specific to mamma
JOURNAL Patent: JP 2002525098-A 10 13-AUG-2002;
WASHINGTON UNIVERSITY
OS Artificial Sequence
COMMENT PN JP 2002525098-A/10
PD 13-AUG-2002
PF 29-SEP-1999 JP 2000572241
PR 29-SEP-1998 US 09/162622
PI MARK A WATSON, TIMOTHY P FLEMING
PC C12N15/09, C12Q1/68, G01N33/53, G01N33/566, G01N33/577//G01N33/574, PC
C12N15/00
CC Description of Artificial Sequence: Synthetic
FH Key Location/Qualifiers
FT source 1..21
FT Location/Qualifiers
1..21
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAA 1537
Db 21 AAAAAAAAAAAAAAAAAA 4

RESULT 349
LOCUS C0846797 21 bp RNA linear PAT 02-AUG-2004
DEFINITION Sequence 46 from Patent WO2004036221.
ACCESSION C0846797
VERSION C0846797.1 GI:50895947
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS O'Toole, M.M. and Liu, W.
TITLE Compositions and methods for diagnosing and treating autoimmune
disease
JOURNAL Patent: WO 2004036221-A 46 29-APR-2004;
Wyleth (US); O'Toole, Margot Mary (US); Liu, Wei (US)
FEATURES
Source Location/Qualifiers
1..21
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 981 CGCGGACGCTTCTGTC 998
Db 3 CGCGTGAAGTCATGTC 20

RESULT 350
LOCUS I36166 21 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 2 from patent US 5605662.
ACCESSION I36166
VERSION I36166.1 GI:2086679

KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Heller, M.J. and Tu, B.
TITLE Active programmable electronic devices for molecular biological analysis and diagnostics
JOURNAL Patent: US 5605662-A 2 25-FEB-1997;
FEATURES Location/Qualifiers
1. .21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAA 1537
Db 1 AAAAAAAAAAAAAAAAA 18

RESULT 351
165744/c 165744 21 bp DNA linear PAT 07-OCT-1997
LOCUS Sequence 13 from patent US 5668267.
165744
ACCESSION 165744
VERSION 165744.1 GI:2482314
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Watson, M.A. and Fleming, T.P.
TITLE Polynucleotides encoding mammaglobin, a mammary-specific breast cancer protein
JOURNAL Patent: US 5668267-A 13 16-SEP-1997;
FEATURES Location/Qualifiers
1. .21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAA 1537
Db 21 AAAAAAAAAAAAAAAAA 4

RESULT 352
164433/c 164433 21 bp DNA linear PAT 04-APR-1998
LOCUS Sequence 23 from patent US 5695934.
164433
ACCESSION 164433
VERSION 164433.1 GI:3021953
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Brenner, S.
TITLE Massively parallel sequencing of sorted polynucleotides
JOURNAL Patent: US 5695934-A 23 09-DEC-1997;
FEATURES Location/Qualifiers
1. .21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAA 1537
Db 21 AAAAAAAAAAAAAAAAA 4

RESULT 353
AR322245/c AR322245 21 bp DNA linear PAT 17-AUG-2003
LOCUS Sequence 13 from patent US 6566072.
DEFINITION AR322245
ACCESSION AR322245
VERSION AR322245.1 GI:33707814
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Watson, M.A. and Fleming, T.P.
TITLE Mammaglobin, a secreted mammary-specific breast cancer protein
JOURNAL Patent: US 6566072-A 13 20-MAY-2003;
FEATURES Location/Qualifiers
1. .21
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAA 1537
Db 21 AAAAAAAAAAAAAAAAA 4

RESULT 354
AR452591/c AR452591 21 bp mRNA linear PAT 20-FEB-2004
LOCUS Sequence 13 from patent US 6677428.
DEFINITION AR452591
ACCESSION AR452591
VERSION AR452591.1 GI:42684381
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Watson, M.A. and Fleming, T.P.
TITLE Mammaglobin, a secreted mammary-specific breast cancer protein
JOURNAL Patent: US 6677428-A 13 13-JAN-2004;
FEATURES Location/Qualifiers
1. .21
/organism="unknown"
/mol_type="mRNA"

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAA 1537
Db 21 AAAAAAAAAAAAAAAAA 4

RESULT 355
AX104720/c AX104720 21 bp DNA linear PAT 30-APR-2001
LOCUS Sequence 912 from Patent WO0122972.
DEFINITION AX104720
ACCESSION AX104720
VERSION AX104720.1 GI:13920917
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Kriegl, A.M., Schetter, C. and Vollmer, J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 912 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
SOURCE 1. .21
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1520 AAAAAAAAAAGTAAAA 1537
Db 21 AAAAAAAAAAAAAAAAAAAAA 4

RESULT 356
LOCUS AX355812 21 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 840 from Patent WO0197843.
ACCESSION AX355812
VERSION AX355812.1 GI:18620480
KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Weiner, G. and Hartmann, G.
TITLE Method for enhancing antibody-induced cell lysis and treating
Cancer
JOURNAL Patent: WO 0197843-A 840 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES
SOURCE 1. .21
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide-phosphorothioate
backbone"

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1520 AAAAAAAAAAGTAAAA 1537
Db 21 AAAAAAAAAAAAAAAAAAAAA 4

RESULT 357
LOCUS AX547773 21 bp DNA linear PAT 01-MAR-2003
DEFINITION Sequence 912 from Patent WO02053141.
ACCESSION AX547773
VERSION AX547773.1 GI:25812917
KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Bratzler, R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 912 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
FEATURES
SOURCE 1. .21
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"

/db_xref="taxon:32630"
/note="Synthetic Sequence"

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1520 AAAAAAAAAAGTAAAA 1537
Db 21 AAAAAAAAAAAAAAAAAAAAA 4

RESULT 358
LOCUS AX825123 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 21 from Patent WO03072818.
ACCESSION AX825123
VERSION AX825123.1 GI:39750852
KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 21 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
SOURCE 1. .21
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"

misc_binding 1
/bound_moiety="Biotin"

modified_base 3
/note="TNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

modified_base 6
/note="TNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

modified_base 9
/note="TNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

modified_base 12
/note="TNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

modified_base 15
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/mod_base=OTHER

modified_base 18
/note="TNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1520 AAAAAAAAAAGTAAAA 1537
Db 18 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 359
LOCUS AX825124 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 22 from Patent WO03072818.
ACCESSION AX825124
VERSION AX825124.1 GI:39750853
KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequences

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REFERENCE
1      artificial sequences.
AUTHORS
1      Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE
1      Method for sorting single-stranded nucleic acids
JOURNAL
1      Patent: WO 03072818-A 22 04-SEP-2003;
FEATURES
source
1      .
21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
misc_binding
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/bound_moiety="Biotin"
modified_base
3
/note="LNA-T (Locked Nucleic Acid)"
modified_base
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/note="LNA-T (Locked Nucleic Acid)"
modified_base
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/note="LNA-T (Locked Nucleic Acid)"
modified_base
12
/note="LNA-T (Locked Nucleic Acid)"
modified_base
15
/note="LNA-T (Locked Nucleic Acid)"
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modified_base
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/note="LNA-T (Locked Nucleic Acid)"
Query Match
1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy
1520 AAAAAAAAAAGTAAAA 1537
Db
18 AAAAAAAAAAAAAAAAAA 1
RESULT 360
AX825125/c 21 bp DNA linear PAT 11-DEC-2003
LOCUS
DEFINITION
Sequence 23 from Patent WO03072818.
ACCESSION
AX825125
VERSION
AX825125.1 GI:39750854
KEYWORDS
.
SOURCE
synthetic construct
ORGANISM
artificial sequences.
REFERENCE
1
Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
AUTHORS
Method for sorting single-stranded nucleic acids
TITLE
Patent: WO 03072818-A 23 04-SEP-2003;
JOURNAL
Degussa Bioactives GmbH (DE)
FEATURES
source
1
21
/location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
misc_binding
1
/bound_moiety="Biotin"
modified_base
3
/note="LNA-T (Locked Nucleic Acid)"
modified_base
6
/note="LNA-T (Locked Nucleic Acid)"
modified_base
9
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modified_base
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/note="LNA-T (Locked Nucleic Acid)"
modified_base
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modified_base
18
/note="LNA-T (Locked Nucleic Acid)"
Query Match
1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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modified_base
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modified_base
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/note="LNA-T (Locked Nucleic Acid)"
modified_base
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/note="LNA-T (Locked Nucleic Acid)"
modified_base
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/note="LNA-T (Locked Nucleic Acid)"
Query Match
1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy
1520 AAAAAAAAAAGTAAAA 1537
Db
18 AAAAAAAAAAAAAAAAAA 1
RESULT 361
AX825126/c 21 bp DNA linear PAT 11-DEC-2003
LOCUS
DEFINITION
Sequence 24 from Patent WO03072818.
ACCESSION
AX825126
VERSION
AX825126.1 GI:39750855
KEYWORDS
.
SOURCE
synthetic construct
ORGANISM
artificial sequences.
REFERENCE
1
Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
AUTHORS
Method for sorting single-stranded nucleic acids
TITLE
Patent: WO 03072818-A 24 04-SEP-2003;
JOURNAL
Degussa Bioactives GmbH (DE)
FEATURES
source
1
21
/location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
misc_binding
1
/bound_moiety="Biotin"
modified_base
3
/note="LNA-T (Locked Nucleic Acid)"
modified_base
6
/note="LNA-T (Locked Nucleic Acid)"
modified_base
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/note="LNA-T (Locked Nucleic Acid)"
modified_base
12
/note="LNA-T (Locked Nucleic Acid)"
modified_base
15
/note="LNA-T (Locked Nucleic Acid)"
modified_base
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modified_base
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/note="LNA-T (Locked Nucleic Acid)"
Query Match
1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy
1520 AAAAAAAAAAGTAAAA 1537
Db
18 AAAAAAAAAAAAAAAAAA 1
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LOCUS	AX825127/c	21 bp	DNA	linear	PAT 11-DEC-2003
DEFINITION	Sequence 25 from Patent WO03072818.				
ACCESSION	AX825127				
VERSION	AX825127.1				
KEYWORDS	GI:39750856				
SOURCE					
ORGANISM	synthetic construct artificial sequences.				
REFERENCE	1				
AUTHORS	Boekenkamp, D., Dieck, T. H. and Hoppe, H. U.				
TITLE	Method for sorting single-stranded nucleic acids				
JOURNAL	Patent: WO 03072818-A 25 04-SBP-2003;				
DEGUS	Degussa Bioactives GmbH (DE)				
FEATURES	Location/Qualifiers				
Source	1..21				
	/organism="synthetic construct"				
	/mol_type="unassigned DNA"				
	/db_xref="taxon:32630"				
	/note="Beschreibung der kuenstlichen Sequenz: Capture-Oligonukleotid"				
	1				
	/bound_molecly="Biotin"				
	3				
	/note="LNA-T (Locked Nucleic Acid)"				
	/mod_base=OTHER				
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	/note="LNA-T (Locked Nucleic Acid)"				
	/mod_base=OTHER				
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	15				
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	18				
	/note="LNA-T (Locked Nucleic Acid)"				
	/mod_base=OTHER				
	18				
	/note="LNA-T (Locked Nucleic Acid)"				
	/mod_base=OTHER				
Query Match	1.1%; Score 14.8; DB 1; Length 21;				
Best Local Similarity	88.9%; Pred. No. 1.7e+02;				
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;					
QY	1520 AAAAAAAAAAAGTAAA 1537				
Db	18 AAAAAAAAAAAAAAAAAA 1				
RESULT 363					
LOCUS	AX825128/c	21 bp	DNA	linear	PAT 11-DEC-2003
DEFINITION	Sequence 26 from Patent WO03072818.				
ACCESSION	AX825128				
VERSION	AX825128.1				
KEYWORDS	GI:39750857				
SOURCE					
ORGANISM	synthetic construct artificial sequences.				
REFERENCE	1				
AUTHORS	Boekenkamp, D., Dieck, T. H. and Hoppe, H. U.				
TITLE	Method for sorting single-stranded nucleic acids				
JOURNAL	Patent: WO 03072818-A 26 04-SBP-2003;				
DEGUS	Degussa Bioactives GmbH (DE)				
FEATURES	Location/Qualifiers				
Source	1..21				
	/organism="synthetic construct"				
	/mol_type="unassigned DNA"				
	/db_xref="taxon:32630"				

	/note="Beschreibung der kuenstlichen Sequenz:Capture-Oligonukleotid"			
misc_binding	1	/bound_moiety="Biotin"		
modified_base	3	/note="LNA-T (Locked Nucleic Acid)"		
	6	/mod_base=OTHER		
modified_base	6	/note="LNA-T (Locked Nucleic Acid)"		
	9	/mod_base=OTHER		
modified_base	9	/note="LNA-T (Locked Nucleic Acid)"		
	12	/mod_base=OTHER		
modified_base	12	/note="LNA-T (Locked Nucleic Acid)"		
	15	/mod_base=OTHER		
modified_base	15	/note="LNA-T (Locked Nucleic Acid)"		
	18	/mod_base=OTHER		
modified_base	18	/note="LNA-T (Locked Nucleic Acid)"		
		/mod_base=OTHER		
Query Match	1.1k	Score 14.8	DB 1	Length 21;
Best Local Similarity	88.9k	Pred. No. 1.7e+02		
Matches	16	Conservative	0	Mismatches 2; Indels 0; Gaps 0;
Qy	1520	AAAAAAAAAAAGTAAA	1537	
Db	18	AAAAAAAAAAAAAAAAAAAA	1	
RESULT 364				
AX825129/c				
LOCUS	AX825129	21 bp	DNA	linear
DEFINITION	Sequence 27 from Patent WO03072818.			PAT 11-DEC-2003
ACCESSION	AX825129			
VERSION	AX825129.1	GI:39750858		
KEYWORDS				
SOURCE				
ORGANISM				
		synthetic construct		
		synthetic construct		
		artificial sequences.		
REFERENCE	1			
AUTHORS	Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.			
TITLE	Method for sorting single-stranded nucleic acids			
JOURNAL	Patent: WO 03072818-A 27 04-SEP-2003;			
	Degussa Bioactives GmbH (DE)			
FEATURES		Location/Qualifiers		
Source		1..21		
		/organism="synthetic construct"		
		/mol_type="unassigned DNA"		
		/db_xref="taxon:32630"		
		/note="Beschreibung der kuenstlichen Sequenz:Capture-Oligonukleotid"		
		1		
		/bound_moiety="Biotin"		
		3		
		/note="LNA-T (Locked Nucleic Acid)"		
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		6		
		/note="LNA-T (Locked Nucleic Acid)"		
		/mod_base=OTHER		
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		/note="LNA-T (Locked Nucleic Acid)"		
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Query Match                      1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      1520 AAAAAAAAAAGTAAA 1537
Db      18 AAAAAAAAAAAAAAAAAA 1

RESULT 365
AX825130/c      AX825130      21 bp      DNA      linear      PAT 11-DEC-2003
DEFINITION      Sequence 28 from Patent WO03072818.
ACCESSION       AX825130
VERSION         AX825130.1 GI:39750859
KEYWORDS
SOURCE          . synthetic construct
ORGANISM        synthetic construct
                artificial sequences.
REFERENCE
1
AUTHORS         Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
JOURNAL         Method for sorting single-stranded nucleic acids
                Patent: WO 03072818-A 28 04-SEP-2003;
                Degussa Bioactives GmbH (DE)
                Location/Qualifiers
FEATURES
source          1..21
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Beschreibung der kuenstlichen
                Sequenz:Capture-Oligonukleotid"
misc_binding    1
                /bound_moiety="Biotin"
modified_base   3
                /note="LNA-T (Locked Nucleic Acid)"
modified_base   6
                /mod_base=OTHER
modified_base   9
                /note="LNA-T (Locked Nucleic Acid)"
modified_base   12
                /mod_base=OTHER
modified_base   15
                /note="LNA-T (Locked Nucleic Acid)"
modified_base   18
                /note="LNA-T (Locked Nucleic Acid)"
modified_base   18
                /mod_base=OTHER
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Query Match                      1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      1520 AAAAAAAAAAGTAAA 1537
Db      18 AAAAAAAAAAAAAAAAAA 1

RESULT 366
AX825131/c      AX825131      21 bp      DNA      linear      PAT 11-DEC-2003
DEFINITION      Sequence 29 from Patent WO03072818.
ACCESSION       AX825131
VERSION         AX825131.1 GI:39750860
KEYWORDS
SOURCE          . synthetic construct
ORGANISM        synthetic construct
                artificial sequences.
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REFERENCE
1
AUTHORS         Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
JOURNAL         Method for sorting single-stranded nucleic acids
                Patent: WO 03072818-A 29 04-SEP-2003;
                Degussa Bioactives GmbH (DE)
                Location/Qualifiers
FEATURES
source          1..21
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Beschreibung der kuenstlichen
                Sequenz:Capture-Oligonukleotid"
misc_binding    1
                /bound_moiety="Biotin"
modified_base   3
                /note="LNA-T (Locked Nucleic Acid)"
modified_base   6
                /mod_base=OTHER
modified_base   9
                /note="LNA-T (Locked Nucleic Acid)"
modified_base   12
                /mod_base=OTHER
modified_base   15
                /note="LNA-T (Locked Nucleic Acid)"
modified_base   18
                /note="LNA-T (Locked Nucleic Acid)"
modified_base   18
                /mod_base=OTHER

Query Match                      1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      1520 AAAAAAAAAAGTAAA 1537
Db      18 AAAAAAAAAAAAAAAAAA 1

RESULT 367
AX825132/c      AX825132      21 bp      DNA      linear      PAT 11-DEC-2003
DEFINITION      Sequence 30 from Patent WO03072818.
ACCESSION       AX825132
VERSION         AX825132.1 GI:39750861
KEYWORDS
SOURCE          . synthetic construct
ORGANISM        synthetic construct
                artificial sequences.
REFERENCE
1
AUTHORS         Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
JOURNAL         Method for sorting single-stranded nucleic acids
                Patent: WO 03072818-A 30 04-SEP-2003;
                Degussa Bioactives GmbH (DE)
                Location/Qualifiers
FEATURES
source          1..21
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Beschreibung der kuenstlichen
                Sequenz:Capture-Oligonukleotid"
misc_binding    1
                /bound_moiety="Biotin"
modified_base   3
                /note="LNA-T (Locked Nucleic Acid)"
modified_base   6
                /mod_base=OTHER
modified_base   9
                /note="LNA-T (Locked Nucleic Acid)"
modified_base   12
                /mod_base=OTHER
modified_base   15
                /note="LNA-T (Locked Nucleic Acid)"
modified_base   18
                /note="LNA-T (Locked Nucleic Acid)"
modified_base   18
                /mod_base=OTHER
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/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
12 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
15 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
18 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1520 AAAAAAAAAAGTAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 368
AX825133/c AX825133 21 bp DNA linear PAT 11-DEC-2003
LOCUS DEFINITION Sequence 31 from Patent WO03072818.
ACCESSION AX825133
VERSION AX825133.1 GI:39750862
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 31 04-SEP-2003;
Degussa Bioactives GmbH (DE)

FEATURES
source location/Qualifiers

1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
misc_binding
1 /bound_moiety="Biotin"
3 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
6 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
9 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
12 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
15 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
18 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1520 AAAAAAAAAAGTAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 369
AX825134/c AX825134 21 bp DNA linear PAT 11-DEC-2003
LOCUS DEFINITION Sequence 32 from Patent WO03072818.
ACCESSION AX825134
VERSION AX825134.1 GI:39750863
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 32 04-SEP-2003;
Degussa Bioactives GmbH (DE)

FEATURES
source location/Qualifiers

1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
misc_binding
1 /bound_moiety="Biotin"
3 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
6 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
9 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
12 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
15 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
18 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1520 AAAAAAAAAAGTAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 370
AX825139/c AX825139 21 bp DNA linear PAT 11-DEC-2003
LOCUS DEFINITION Sequence 37 from Patent WO03072818.
ACCESSION AX825139
VERSION AX825139.1 GI:39750868
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 37 04-SEP-2003;
Degussa Bioactives GmbH (DE)

FEATURES
source location/Qualifiers
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen

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misc_binding      Sequenz: Capture-Oligonukleotid"
modified_base     1 /bound moiety="Biotin"
modified_base     3 /note="LNA-T (Locked Nucleic Acid) "
modified_base     /mod_base=OTHER
modified_base     6 /note="LNA-T (Locked Nucleic Acid) "
modified_base     /mod_base=OTHER
modified_base     9 /note="LNA-T (Locked Nucleic Acid) "
modified_base     12 /mod_base=OTHER
modified_base     15 /note="LNA-T (Locked Nucleic Acid) "
modified_base     /mod_base=OTHER
modified_base     18 /note="LNA-T (Locked Nucleic Acid) "
modified_base     /mod_base=OTHER
modified_base     /note="LNA-T (Locked Nucleic Acid) "
modified_base     /mod_base=OTHER

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Query Match	1.1%	Score 14.8	DB 1	Length 21
Best Local Similarity	88.9%	Pred. No. 1.7e+02		
Matches 16	Conservative 0	Mismatches 2	Indels 0	Gaps 0

QY	1520	AAAAAAAAAAGTAAA	1537
Db	18	AAAAAAAAAAAAAAA	1

RESULT 371					
AX825140/c					
LOCUS					
AX825140	21 bp	DNA	linear	PAT 11-DEC-2003	
Sequence	38 from Patent WO03072818.				
DEFINITION					

SOURCE	synthetic construct
ORGANISM	synthetic construct
REFERENCE	artificial sequences.
AUTHORS	1
TITLE	Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
JOURNAL	Method for sorting single-stranded nucleic acids.
	Patent: WO 03072818-A 38 04-SEP-2003;

FEATURES	Location/Qualifiers
source	1. .21

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misc_binding      1
modified_base     3 /bound_molety="Biotin"
modified_base     /note="LNA-T (Locked Nucleic Acid) "
modified_base     /mod_base=OTHER
modified_base     6 /note="LNA-T (Locked Nucleic Acid) "
modified_base     /mod_base=OTHER
modified_base     9 /note="LNA-T (Locked Nucleic Acid) "
modified_base     12 /mod_base=OTHER
modified_base     15 /note="LNA-T (Locked Nucleic Acid) "
modified_base     /mod_base=OTHER
modified_base     18 /note="LNA-T (Locked Nucleic Acid) "
modified_base     /mod_base=OTHER

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Query Match      1.1%   Score 14.6; DB 1; Length 21;
Best Local Similarity 88.9%; Prod. No. 1.7+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0.
```

RESULT	372					
AX825141/c						
LOCUS	AX825141	21 bp	DNA	linear	PAT 11-DEC-2003	
DEFINITION	Sequence 39 from Patent WO03072818.					
ACCESSION	AX825141					
VERSION	AX825141.1	GI:39750870				

REFERENCE	1
AUTHORS	Boekenkamp, D., Dieck, T. H. and Hoppe, H. U.
TITLE	Method for sorting single-stranded nucleic acids
JOURNAL	Patent: WO 03072818-A 39 04-SEP-2003;
DEGUSA	Degussa Bioactives GmbH (DE)
FEATURES	Location/Qualifiers

FEATURES	Location/Qualifiers
source	1. .21

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misc_binding      /note="Beschreibung der kuenstlichen  
Sequenz:capture-Oligonukleotid"  
modified_base    1  
                  /bound_moiety="Biotin"  
modified_base    3  
                  /note="LNA-T (locked Nucleic Acid) "  
modified_base    6  
                  /mod_base=OTHER  
modified_base    9  
                  /note="LNA-T (locked Nucleic Acid) "  
modified_base   12  
                  /mod_base=OTHER  
modified_base   15  
                  /note="LNA-T (locked Nucleic Acid) "  
modified_base   18  
                  /mod_base=OTHER  
modified_base   18  
                  /note="LNA-T (locked Nucleic Acid) "  
modified_base   /mod_base=OTHER
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Query Match	1.1%;	Score 14.8;	DB 1;	Length 21;
Best Local Similarity	88.9%;	Pred. No. 1.7e+02;		
Matches 16;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;

```
QY      1520 AAAAAAAAAAAGTAAA 1537
          |||||
Db      18 AAAAAAAAAAAAAAA 1
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RESULT	373				
LOCUS	AX825142/c				
DEFINITION	AX825142	21 bp	DNA	linear	PAT 11-DEC-2003
ACCESSION	Sequence 40 from Patent MO03072818.				
VERSION	AX825142				
KEYWORDS	AX825142.1	GI:39750871			
SOURCE	.				
ORGANISM	synthetic construct				
	synthetic construct				
REFERENCE	synthetic sequences.				
	1				

AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 40 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
misc_binding
1
/bound_moiety="Biotin"
modified_base
3
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
6
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
9
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
12
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
15
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
18
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred.No.1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAGTAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1
RESULT 374
AX825143/C 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 41 from Patent WO03072818.
ACCESSION AX825143
VERSION AX825143.1 GI:39750872
KEYWORDS
SOURCE .
synthetic construct
synthetic construct
artificial sequences.
ORGANISM 1
Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 41 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
misc_binding
1
/bound_moiety="Biotin"
modified_base
3
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
6
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
9
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
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/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
15
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
18
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

/mod_base=OTHER
modified_base
12
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
15
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
18
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred.No.1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAGTAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1
RESULT 376
AX825144/C 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 42 from Patent WO03072818.
ACCESSION AX825144
VERSION AX825144.1 GI:39750873
KEYWORDS
SOURCE .
synthetic construct
synthetic construct
artificial sequences.
ORGANISM 1
Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 42 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
misc_binding
1
/bound_moiety="Biotin"
modified_base
3
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
6
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
9
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
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/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
15
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
18
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred.No.1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAGTAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1
RESULT 376

AX825145/c
LOCUS AX825145 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 43 from Patent WO03072818.
ACCESSION AX825145
VERSION AX825145.1 GI:39750874
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.
1
REFERENCE
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 43 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
1
misc_binding
1 /bound_moiety="Biotin"
3 /note="LNA-T (Locked Nucleic Acid) "
6 /mod_base=OTHER
modified_base
9 /note="LNA-T (Locked Nucleic Acid) "
12 /mod_base=OTHER
modified_base
15 /note="LNA-T (Locked Nucleic Acid) "
18 /mod_base=OTHER
modified_base
18 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 1520 AAAAAAAAAAGTAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1
RESULT 377
AX825146/c
LOCUS AX825146 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 44 from Patent WO03072818.
ACCESSION AX825146
VERSION AX825146.1 GI:39750875
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.
1
REFERENCE
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 44 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"

misc_binding
1 /bound_moiety="Biotin"
3 /note="LNA-T (Locked Nucleic Acid) "
6 /mod_base=OTHER
modified_base
9 /note="LNA-T (Locked Nucleic Acid) "
12 /mod_base=OTHER
modified_base
15 /note="LNA-T (Locked Nucleic Acid) "
18 /mod_base=OTHER
modified_base
18 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 1520 AAAAAAAAAAGTAAA 1537
Db 18 AAAAAAAAAAAAAAAAAA 1
RESULT 378
AX825147/c
LOCUS AX825147 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 45 from Patent WO03072818.
ACCESSION AX825147
VERSION AX825147.1 GI:39750876
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.
1
REFERENCE
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 45 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
1
misc_binding
1 /bound_moiety="Biotin"
3 /note="LNA-T (Locked Nucleic Acid) "
6 /mod_base=OTHER
modified_base
9 /note="LNA-T (Locked Nucleic Acid) "
12 /mod_base=OTHER
modified_base
15 /note="LNA-T (Locked Nucleic Acid) "
18 /mod_base=OTHER
modified_base
18 /note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER


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modified_base 12 /note="LNA-T (Locked Nucleic Acid)"
modified_base 15 /mod_base=OTHER
modified_base 18 /note="LNA-T (Locked Nucleic Acid)"
modified_base 18 /mod_base=OTHER
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
|||||
18 AAAAAAAAAAAAAAAAAA 1

RESULT 382
AX825156 21 bp DNA linear PAT 11-DEC-2003
LOCUS AX825156/c
DEFINITION Sequence 54 from Patent WO03072818.
ACCESSION AX825156
VERSION AX825156.1 GI:39750885
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
AUTHORS Method for sorting single-stranded nucleic acids
TITLE Patent: WO 03072818-A 54 04-SEP-2003;
JOURNAL Degussa Bioactives GmbH (DE)
FEATURES
source
1. 21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
misc_binding 1 /bound_moiety="Biotin"
modified_base 3 /note="LNA-T (Locked Nucleic Acid)"
modified_base 6 /mod_base=OTHER
modified_base 9 /note="LNA-T (Locked Nucleic Acid)"
modified_base 9 /mod_base=OTHER
modified_base 12 /note="LNA-T (Locked Nucleic Acid)"
modified_base 12 /mod_base=OTHER
modified_base 15 /note="LNA-T (Locked Nucleic Acid)"
modified_base 15 /mod_base=OTHER
modified_base 18 /note="LNA-T (Locked Nucleic Acid)"
modified_base 18 /mod_base=OTHER

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
|||||
19 AAAAAAAAAAAAAAAAAA 2

RESULT 383
AX825157/c
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LOCUS AX825157 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 55 from Patent WO03072818.
ACCESSION AX825157
VERSION AX825157.1 GI:39750886
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
AUTHORS Method for sorting single-stranded nucleic acids
TITLE Patent: WO 03072818-A 55 04-SEP-2003;
JOURNAL Degussa Bioactives GmbH (DE)
FEATURES
source
1. 21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
misc_binding 1 /bound_moiety="Biotin"
modified_base 3 /note="LNA-T (Locked Nucleic Acid)"
modified_base 6 /mod_base=OTHER
modified_base 9 /note="LNA-T (Locked Nucleic Acid)"
modified_base 9 /mod_base=OTHER
modified_base 12 /note="LNA-T (Locked Nucleic Acid)"
modified_base 12 /mod_base=OTHER
modified_base 15 /note="LNA-T (Locked Nucleic Acid)"
modified_base 15 /mod_base=OTHER
modified_base 18 /note="LNA-T (Locked Nucleic Acid)"
modified_base 18 /mod_base=OTHER

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAAA 1537
|||||
19 AAAAAAAAAAAAAAAAAA 2

RESULT 384
AX825158 21 bp DNA linear PAT 11-DEC-2003
LOCUS AX825158/c
DEFINITION Sequence 56 from Patent WO03072818.
ACCESSION AX825158
VERSION AX825158.1 GI:39750887
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
AUTHORS Method for sorting single-stranded nucleic acids
TITLE Patent: WO 03072818-A 56 04-SEP-2003;
JOURNAL Degussa Bioactives GmbH (DE)
FEATURES
source
1. 21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
misc_binding 1
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/bound_molecly="Biotin"
modified_base 3 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 6 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 9 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 12 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 15 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 18 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 385
AX825160/c 21 bp DNA linear PAT 11-DEC-2003
LOCUS DEFINITION Sequence 58 from Patent WO03072818.
ACCESSION AX825160
VERSION AX825160.1 GI:39750889
KEYWORDS
SOURCE . synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
JOURNAL Method for sorting single-stranded nucleic acids
Degussa Bioactives GmbH (DE)
FEATURES
SOURCE location/Qualifiers
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuensentlichen
Sequenz: Capture-Oligonukleotid"
misc_binding 1 /bound_molecly="Biotin"
modified_base 3 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 6 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 9 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 12 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 15 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 18 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 386
AX825161/c 21 bp DNA linear PAT 11-DEC-2003
LOCUS DEFINITION Sequence 59 from Patent WO03072818.
ACCESSION AX825161
VERSION AX825161.1 GI:39750890
KEYWORDS
SOURCE . synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
JOURNAL Method for sorting single-stranded nucleic acids
Degussa Bioactives GmbH (DE)
FEATURES
SOURCE location/Qualifiers
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuensentlichen
Sequenz: Capture-Oligonukleotid"
misc_binding 1 /bound_molecly="Biotin"
modified_base 3 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 6 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 9 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 12 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 15 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 18 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAA 1537
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 387
AX825162/c 21 bp DNA linear PAT 11-DEC-2003
LOCUS DEFINITION Sequence 60 from Patent WO03072818.
ACCESSION AX825162
VERSION AX825162.1 GI:39750891
KEYWORDS
SOURCE . synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
JOURNAL Method for sorting single-stranded nucleic acids
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JOURNAL Patent: WO 03072818-A 60 04-SEP-2003;
Degussa Bioactives GmbH (DE)
location/Qualifiers

FEATURES
source
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"

misc_binding
1
/bound_moiety="Biotin"

modified_base
3
/note="LNA-T (Locked Nucleic Acid) "

modified_base
6
/mod_base=OTHER

modified_base
9
/note="LNA-T (Locked Nucleic Acid) "

modified_base
12
/mod_base=OTHER

modified_base
15
/note="LNA-T (Locked Nucleic Acid) "

modified_base
18
/mod_base=OTHER

modified_base
18
/note="LNA-T (Locked Nucleic Acid) "

modified_base
/mod_base=OTHER

Query Match
1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAA 1537
DB 19 AAAAAAAAAAAAAAAAAA 2

RESULT 388
AX825164/c
LOCUS AX825164 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 62 from Patent WO03072818.
ACCESSION AX825164
VERSION AX825164.1 GI:39750893
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
1 Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
AUTHORS Method for sorting single-stranded nucleic acids
TITLE Patent: WO 03072818-A 62 04-SEP-2003;
JOURNAL Degussa Bioactives GmbH (DE)
location/Qualifiers

FEATURES
source
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"

misc_binding
1
/bound_moiety="Biotin"

modified_base
3
/note="LNA-T (Locked Nucleic Acid) "

modified_base
6
/mod_base=OTHER

modified_base
9
/note="LNA-T (Locked Nucleic Acid) "

modified_base
12
/mod_base=OTHER

modified_base
15
/note="LNA-T (Locked Nucleic Acid) "

modified_base
18
/mod_base=OTHER

modified_base
18
/note="LNA-T (Locked Nucleic Acid) "

modified_base
/mod_base=OTHER

Query Match
1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAA 1537
DB 20 AAAAAAAAAAAAAAAAAA 3

RESULT 389
AX825165/c
LOCUS AX825165 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 63 from Patent WO03072818.
ACCESSION AX825165
VERSION AX825165.1 GI:39750894
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
1 Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
AUTHORS Method for sorting single-stranded nucleic acids
TITLE Patent: WO 03072818-A 63 04-SEP-2003;
JOURNAL Degussa Bioactives GmbH (DE)
location/Qualifiers

FEATURES
source
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"

misc_binding
1
/bound_moiety="Biotin"

modified_base
3
/note="LNA-T (Locked Nucleic Acid) "

modified_base
6
/mod_base=OTHER

modified_base
9
/note="LNA-T (Locked Nucleic Acid) "

modified_base
12
/mod_base=OTHER

modified_base
15
/note="LNA-T (Locked Nucleic Acid) "

modified_base
18
/mod_base=OTHER

modified_base
18
/note="LNA-T (Locked Nucleic Acid) "

modified_base
/mod_base=OTHER

Query Match
1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAGTAAA 1537
DB 20 AAAAAAAAAAAAAAAAAA 3

RESULT 390
AX825166/c
LOCUS AX825166 21 bp DNA linear PAT 11-DEC-2003

DEFINITION Sequence 64 from Patent WO03072818.
ACCESSION AX825166
VERSION AX825166.1 GI:39750895
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
 artificial sequences.
REFERENCE
1 Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
AUTHORS Method for sorting single-stranded nucleic acids
TITLE Patent: WO 03072818-A 64 04-SEP-2003;
JOURNAL Degussa Bioactives GmbH (DE)
FEATURES
source
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
misc_binding
1 /bound_moiety="Biotin"
modified_base
3 /note="LNA-T (locked Nucleic Acid) "
/mod_base=OTHER
modified_base
6 /note="LNA-T (locked Nucleic Acid) "
/mod_base=OTHER
modified_base
9 /note="LNA-T (locked Nucleic Acid) "
/mod_base=OTHER
modified_base
12 /note="LNA-T (locked Nucleic Acid) "
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modified_base
15 /note="LNA-T (locked Nucleic Acid) "
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modified_base
18 /note="LNA-T (locked Nucleic Acid) "
/mod_base=OTHER
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAAGTAAA 1537
DB 21 AAAAAAAAAAAAAAAAAA 4
RESULT 391
BD080832/c 21 bp DNA linear PAT 27-AUG-2002
LOCUS Mammaglobin, a secreted mammary specific breast cancer protein.
DEFINITION BD080832
ACCESSION BD080832
VERSION BD080832.1 GI:22626435
KEYWORDS JP 2001516569-A/10.
SOURCE unidentified
ORGANISM unidentified
 unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Watson,M.A. and Fleming,T.P.
TITLE Mammaglobin, a secreted mammary specific breast cancer protein
JOURNAL Patent: JP 2001516569-A 10 02-OCT-2001;
WASHINGTON UNIVERSITY
COMMENT OS Unidentified
PN JP 2001516569-A/10
PD 02-OCT-2001
PF 18-SEP-1998 JP 2000511779
PR 18-SEP-1997 US 08/933149
PI MARK A WATSON,TIMOTHY P FLEMING
PC C12N15/09,A61K35/26,A61K39/00,A61K39/395,A61K39/395,
A61P35/00,
PC C07K14/47,C12N15/00

CC Strandedness: Single;
CC Topology: Linear;
CC Mammaglobin, a secreted mammary specific breast cancer protein
FH Key Location/Qualifiers
FT source 1. .21
 /organism='Unidentified'.
FEATURES
source
1. .21
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAAGTAAA 1537
DB 21 AAAAAAAAAAAAAAAAAA 4
RESULT 392
BD087491 21 bp DNA linear PAT 27-AUG-2002
LOCUS Self-assembling microelectronic integration system capable of
DEFINITION designating self address, compartment device, mechanism, method and
 operation for molecular biological analysis and diagnosis.
ACCESSION BD087491 GI:22631101
VERSION BD087491.1 GI:22631101
KEYWORDS JP 2001525193-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
 artificial sequences.
REFERENCE 1 (bases 1 to 21)
AUTHORS Sosnowski,R.G., Butler,W.F., Tu,E., Nerenberg,M.I., Heller,M.J. and
 Edman,C.F.
TITLE Self-assembling microelectronic integration system capable of
 designating self address, compartment device, mechanism, method and
 operation for molecular biological analysis and diagnosis
JOURNAL Patent: JP 2001525193-A 2 11-DEC-2001;
NANOGEN INC
COMMENT OS Artificial Sequence
PN JP 2001525193-A/2
PD 11-DEC-2001
PF 01-DEC-1998 JP 2000524303
PR 05-DEC-1997 US 08/986065
PI RONALD G SOSNOWSKI,WILLIAM F BUTLER,EUGENE TU,MICHAEL I PI
NERENBERG,
PI MICHAEL J HELLER,CARL F EDMAN
PC C12Q1/68,C12N15/09,C12N15/00
CC Description of Artificial Sequence: Synthesized with u at 3'
CC terminus to
CC provide ribonucleic acid base for reactivity; Poly A sequence
CC for reduced
CC secondary structure
FH key Location/Qualifiers
FT source 1. .21
 /organism='Artificial Sequence'.
FEATURES
source
1. .21
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 AAAAAAAAAAAGTAAA 1537
DB 1 AAAAAAAAAAAAAAAAAA 18

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RESULT 393
LOCUS BD129772 21 bp DNA linear PAT 18-SEP-2002
DEFINITION Asclhma-associated gene.
ACCESSION BD129772
VERSION BD129772.1 GI:23224717
KEYWORDS JP 2002500895-A/62.
SOURCE unclassified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Wilson,A.R.B., Buckler,A., Cardon,L., Carey,A.H., Galvin,M.,
Miller,A. and North,M.
TITLE Asclhma-associated gene
JOURNAL Patent: JP 2002500895-A 62 15-JAN-2002;
AXYS PHARMACEUTICALS INC
COMMENT OS Unclassified
PN JP 2002500895-A/62
PD 15-JAN-2002
PF 21-JAN-1998 JP 2000528715
PI ANGELA R BROOKS WILSON,ALAN BUCKLER,ION
CARDON,ALISOUN H CAREY,
PI MARGARET GALVIN,ANDREW MILLER,MICHAEL NORTH
PC C1201/66,A01K67/027,C07K14/47,C12N15/09,C12N15/00 CC
Strandedness: Single;
CC Topology: Linear;
CC Asclhma-associated gene
FH Key Location/Qualifiers
FT source 1..21
FT Location/Qualifiers
1..21
/mol_type="unclassified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 1.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 1225 CTCTAGCTTAGCTTCTCCTC 1244
Db 1 CTCTTTCTCTTGTCTTCTC 20

RESULT 394
LOCUS A79657 19 bp DNA linear PAT 20-OCT-1999
DEFINITION Sequence 6 from Patent WO9720069.
ACCESSION A79657
VERSION A79657.1 GI:6092611
KEYWORDS
SOURCE unclassified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Emrich,T. and Leying,H.
TITLE METHOD OF DETECTING TELOMERASE ACTIVITY
JOURNAL Patent: WO 9720069-A 6 05-JUN-1997;
BOEHRINGER MANNHEIM GMBH (DE); EMRICH THOMAS (DE)
FEATURES
Source 1..19
/organism="unclassified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 1.0%; Score 14.6; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 2.2e+02;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 1518 TTAATAAAAAAAAAAGTAA 1536
Db 19 DKAAAAAAAAAAAAAAAAA 1
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RESULT 395
LOCUS ARI47331 19 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 6 from patent US 6221584.
ACCESSION ARI47331
VERSION ARI47331.1 GI:15111134
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Emrich,T., Leying,H., Hinzpeter,M. and Karl,G.
TITLE Method of detecting telomerase activity
JOURNAL Patent: US 6221584-A 6 24-APR-2001;
FEATURES
Source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 14.6; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 2.2e+02;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 1518 TTAATAAAAAAAAAAGTAA 1536
Db 19 DKAAAAAAAAAAAAAAAAA 1

RESULT 396
LOCUS AX825107 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 5 from Patent WO03072818.
ACCESSION AX825107
VERSION AX825107.1 GI:39750836
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 5 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
Source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
1
/bound_moiety="Biotin"
3/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
6/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
9/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
12/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
15/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
18/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
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modified_base
modified_base
modified_base
modified_base
modified_base
modified_base
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Query Match 1.0%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1302 TCTATTGTTTATTTTACAGA 1332
DB 1 TTTTATTTTTTTTTTTTGA 21

RESULT 397
AX825117
LOCUS AX825117 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 15 from Patent WO03072818.
ACCESSION AX825117
VERSION AX825117.1 GI:39750846
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Boekenkamp, D., Dieck, T. H. and Hoppe, H. U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 15 04-SBP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
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/bound_moiety="Bioclin"
misc_binding
3
/note="LNA-T (Locked Nucleic Acid) "
modified_base
6
/mod_base=OTHER
/note="LNA-T (Locked Nucleic Acid) "
modified_base
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/mod_base=OTHER
/note="LNA-T (Locked Nucleic Acid) "
modified_base
15
/mod_base=OTHER
/note="LNA-T (Locked Nucleic Acid) "
modified_base
18
/note="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER

Query Match 1.0%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1246 TCTTGTGTTTGTGTTTATC 1266
DB 1 TTTTATTTTTTTTTTTATC 21

RESULT 398
BD085544/c
LOCUS BD085544 22 bp RNA linear PAT 27-AUG-2002
DEFINITION Method of comparison and detection of RNA amount and DNA amount.
ACCESSION BD085544
VERSION BD085544.1 GI:22631154
KEYWORDS JP 2001333800-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 22)

AUTHORS Shimada, K.
TITLE Method of comparison and detection of RNA amount and DNA amount
JOURNAL Patent: JP 2001333800-A 1 04-DEC-2001;
UNITBECH CO LTD
COMMENT OS Homo sapiens (human)
PN JP 200133800-A/1
PD 04-DEC-2001
PF 30-MAY-2000 JP 2000160324
PI KAORI SHIMADA
PC C1201/68, C12N15/09, G01N33/50, C12N15/00
CC Method of comparison and detection of RNA amount and DNA CC
amount

FEATURES
FH Key Location/Qualifiers
FT source 1..22
/organism="Homo sapiens (human)".
source 1..22
/organism="Homo sapiens"
/mol_type="genomic RNA"
/db_xref="taxon:9606"

Query Match 1.0%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1246 TCTTGTGTTTGTGTTTATC 1266
DB 21 TTTTATTTTTTTTTTTATC 1

RESULT 399
AX692829/c
LOCUS AX692829 25 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5561 from Patent EP1261758.
ACCESSION AX692829
VERSION AX692829.1 GI:29415792
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1
AUTHORS Shannon, M., Gu, Y. and Nguyen, C. T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
JOURNAL Patent: EP 1261758-A 5561 05-FEB-2003;
Aecomica, Inc. (US)
FEATURES
source 1..25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.0%; Score 14.6; DB 1; Length 25;
Best Local Similarity 81.0%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1512 TGTTAATTAAAAAAAAG 1532
DB 21 TCTCAAAAAAAAAAAAAAG 1

RESULT 400
AR089217/c
LOCUS AR089217 17 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 13 from patent US 5994061.
ACCESSION AR089217
VERSION AR089217.1 GI:10015974
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 17)

AUTHORS Tam, S.-P. and Zhang, X.
TITLE DNA constructs and methods for screening for increased expression
JOURNAL of human apo A1 gene
Patent: US 5994061-A 13 30-NOV-1999;
FEATURES
source
1. 17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 345 CTGCCGCGCGCCGCGAG 360
Db 16 CTGCCGCGCGCCGCGAG 1

RESULT 401
BD201511/c 17 bp RNA linear PAT 17-JUL-2003
LOCUS Method and reagent for treating diseases or conditions concerning
DEFINITION molecule participating in vasculogenic response.
ACCESSION BD201511.1 GI:33011281
VERSION JP 2002509721-A/4537.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco, P.A., Roberts, E., Jarvis, T., Coeshott, C. and Mcswiggen, J.A.
TITLE Method and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response
JOURNAL Patent: JP 2002509721-A 4537 02-APR-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Homo sapiens (human)
PN JP 2002509721-A/4537
PD 02-APR-2002
PF 24-MAR-1999 JP 2000541291
PR 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,
PI JAMES A MCSWIGGEN
PC C12N15/09, A61K31/7088, A61K31/7125, A61K48/00, A61P3/10, A61P17/06, PC
A61P29/00,
PC A61P35/00, A61P43/00, C12N5/10, C12N9/00//A61K35/76, C12N15/00, PC
C12N5/00
CC Method and reagent for treating diseases or conditions CC
concerning molecule
CC participating in vasculogenic response
FH Key Location/Qualifiers
FT source 1. 17
FT /organism="Homo sapiens (human)".
FEATURES
source
1. 17
/organism="Homo sapiens"
/mol_type="genomic RNA"
/db_xref="taxon:9606"

Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1512 TGTATATTAATAAAAA 1527
Db 17 TGTATATTAATAAAAA 2

RESULT 402
BD201512/c 17 bp RNA linear PAT 17-JUL-2003
LOCUS Method and reagent for treating diseases or conditions concerning
DEFINITION

ACCESSION BD201512
VERSION BD201512.1 GI:33011282
KEYWORDS JP 2002509721-A/4538.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco, P.A., Roberts, E., Jarvis, T., Coeshott, C. and Mcswiggen, J.A.
TITLE Method and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response
JOURNAL Patent: JP 2002509721-A 4538 02-APR-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Homo sapiens (human)
PN JP 2002509721-A/4538
PD 02-APR-2002
PF 24-MAR-1999 JP 2000541291
PR 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,
PI JAMES A MCSWIGGEN
PC C12N15/09, A61K31/7088, A61K31/7125, A61K48/00, A61P3/10, A61P17/06, PC
A61P29/00,
PC A61P35/00, A61P43/00, C12N5/10, C12N9/00//A61K35/76, C12N15/00, PC
C12N5/00
CC Method and reagent for treating diseases or conditions CC
concerning molecule
CC participating in vasculogenic response
FH Key Location/Qualifiers
FT source 1. 17
FT /organism="Homo sapiens (human)".
FEATURES
source
1. 17
/organism="Homo sapiens"
/mol_type="genomic RNA"
/db_xref="taxon:9606"

Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1512 TGTATATTAATAAAAA 1527
Db 16 TGTATATTAATAAAAA 1

RESULT 403
BD258338 17 bp DNA linear PAT 17-JUL-2003
LOCUS Regulation of repressor gene using nucleic acid molecules.
DEFINITION BD258338
ACCESSION BD258338.1 GI:33068108
VERSION JP 2002541795-A/6131.
KEYWORDS JP 2002541795-A/6131.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
TITLE Regulation of repressor gene using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 6131 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Eukaryote
PN JP 2002541795-A/6131
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/128390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN
PI C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC
C12P21/02,
PC C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1.91), (C12P21/02, PC
C12R1.91),

PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
PC A61K37/02,
PC (C12N5/00,C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key Location/Qualifiers
FT source 1..17
/organism='Eukaryote'.
Location/Qualifiers
1..17
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1247 CTTTGTGTTGTTT 1262
|||||
Db 2 CTTGTTTGTGTTT 17

RESULT 404
LOCUS BD258339 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD258339
VERSION BD258339.1 GI:33068109
KEYWORDS JP 2002541795-A/6132.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt,L., Zwick,M., Pavco,P. and Mcswigen,J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 6132 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
OS Eukaryote
PN JP 2002541795-A/6132
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PI 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGEN PC
C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
C12P21/02,
PC
C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
C12R1:91),
PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
PC A61K37/02,
PC (C12N5/00,C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key Location/Qualifiers
FT source 1..17
/organism='Eukaryote'.
Location/Qualifiers
1..17
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1247 CTTTGTGTTGTTT 1262
|||||
Db 1 CTTGTTTGTGTTT 16

RESULT 405
LOCUS CQ616719/C 17 bp DNA linear PAT 02-FEB-2004

DEFINITION Sequence 1459 from Patent WO0192524.
ACCESSION CQ616719
VERSION CQ616719.1 GI:41666937
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 1459 06-DEC-2001;
Aecomica, Inc. (US)
KEYWORDS Location/Qualifiers
1..17
/organism='Homo sapiens'
/mol_type='unassigned DNA'
/db_xref='taxon:9606'

Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 332 TTCCGAGAGCTCTG 347
|||||
Db 16 TTCCGAGAGCTGCTG 1

RESULT 407
LOCUS CQ617530/C 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 2270 from Patent WO0192524.
ACCESSION CQ617530
VERSION CQ617530.1 GI:41667748
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1

AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
 TITLE Myosin-like gene expressed in human heart and muscle
 JOURNAL Patent: WO 0192524-A 2270 06-DEC-2001;
 Aecomica, Inc. (US)
 FEATURES Location/Qualifiers
 source 1..17
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 1.0%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2.7e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 396 GCCGAGGCCCGCAGG 411
 Db 17 GCCGAGGCCCGCAGG 2

RESULT 408
 LOCUS C0617531/c 17 bp DNA linear PAT 02-FEB-2004
 DEFINITION Sequence 2271 from Patent WO0192524.
 ACCESSION C0617531
 VERSION C0617531.1 GI:41667749
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1
 AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
 TITLE Myosin-like gene expressed in human heart and muscle
 JOURNAL Patent: WO 0192524-A 2271 06-DEC-2001;
 Aecomica, Inc. (US)
 FEATURES Location/Qualifiers
 source 1..17
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 1.0%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2.7e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 396 GCCGAGGCCCGCAGG 411
 Db 16 GCCGAGGCCCGCAGG 1

RESULT 409
 LOCUS AR187057/c 17 bp DNA linear PAT 20-APR-2002
 DEFINITION Sequence 2545 from patent US 6346398.
 ACCESSION AR187057
 VERSION AR187057.1 GI:20233022
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
 TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
 JOURNAL Patent: US 6346398-A 2545 12-FEB-2002;
 FEATURES Location/Qualifiers
 source 1..17
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 1.0%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2.7e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 396 GCCGAGGCCCGCAGG 411
 Db 16 GCCGAGGCCCGCAGG 1

Best Local Similarity 93.8%; Pred. No. 2.7e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1521 AAAAAAAAAAGTAAA 1536
 Db 17 AAAAAAAAAAGTAAA 2

RESULT 410
 LOCUS AR285940/c 17 bp RNA linear PAT 10-APR-2003
 DEFINITION Sequence 312 from patent US 6528640.
 ACCESSION AR285940
 VERSION AR285940.1 GI:29723536
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Beigelman,L., Burgin,A., Beaudry,A., Karpelisky,A., Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
 TITLE Synthetic ribonucleic acids with RNase activity
 JOURNAL Patent: US 6528640-A 312 04-MAR-2003;
 FEATURES Location/Qualifiers
 source 1..17
 /organism="unknown"
 /mol_type="unassigned RNA"

Query Match 1.0%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2.7e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 469 GGGGCGCGCGCTGAC 484
 Db 17 GGGGCGCGCGCTGCC 2

RESULT 411
 LOCUS AR323667/c 17 bp RNA linear PAT 17-AUG-2003
 DEFINITION Sequence 1069 from patent US 6566127.
 ACCESSION AR323667
 VERSION AR323667.1 GI:33709475
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
 TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
 JOURNAL Patent: US 6566127-A 1069 20-MAY-2003;
 FEATURES Location/Qualifiers
 source 1..17
 /organism="unknown"
 /mol_type="unassigned RNA"

Query Match 1.0%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2.7e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1521 AAAAAAAAAAGTAAA 1536
 Db 17 AAAAAAAAAAGTAGA 2

RESULT 412
 LOCUS AR397930/c 17 bp RNA linear PAT 18-DEC-2003
 DEFINITION Sequence 311 from patent US 6617438.
 ACCESSION AR397930
 VERSION AR397930.1 GI:40135323
 KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 17)
TITLE Beigelman, L., Burgin, A. B., Beaudry, A., Karpelsky, A.,
Matulic-Adamic, J., Sweedler, D. and Zinnen, S.
JOURNAL Oligonucleotides with enzymatic activity
FEATURES Patent: US 6617438-A 311 09-SEP-2003;
Location/Qualifiers
1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 469 GGGGGCGCGCTGAC 484
DB 17 GGGGGCGCGCTGCC 2

RESULT 413
LOCUS AR457782/c 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 1459 from patent US 6686188.
ACCESSION AR457782
VERSION AR457782.1 GI:42692839
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 17)
TITLE Gu, Y., Ji, Y., Penn, S. G., Hanzel, D. K., Rank, D. R., Chen, W. and
Shannon, M. E.
JOURNAL Polynucleotide encoding a human myosin-like polypeptide expressed
FEATURES predominantly in heart and muscle
Patent: US 6686188-A 1459 03-FEB-2004;
Location/Qualifiers
1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 332 TTCCGAGAGCTCTG 347
DB 17 TTCCGAGAGCTGCTG 2

RESULT 414
LOCUS AR457783/c 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 1460 from patent US 6686188.
ACCESSION AR457783
VERSION AR457783.1 GI:42692840
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 17)
TITLE Gu, Y., Ji, Y., Penn, S. G., Hanzel, D. K., Rank, D. R., Chen, W. and
Shannon, M. E.
JOURNAL Polynucleotide encoding a human myosin-like polypeptide expressed
FEATURES predominantly in heart and muscle
Patent: US 6686188-A 1460 03-FEB-2004;
Location/Qualifiers
1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 332 TTCCGAGAGCTCTG 347
DB 16 TTCCGAGAGCTGCTG 1

RESULT 415
LOCUS AR458593/c 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 2270 from patent US 6686188.
ACCESSION AR458593
VERSION AR458593.1 GI:42693650
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 17)
TITLE Gu, Y., Ji, Y., Penn, S. G., Hanzel, D. K., Rank, D. R., Chen, W. and
Shannon, M. E.
JOURNAL Polynucleotide encoding a human myosin-like polypeptide expressed
FEATURES predominantly in heart and muscle
Patent: US 6686188-A 2270 03-FEB-2004;
Location/Qualifiers
1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 396 GCCGAGGCCCGCAGG 411
DB 17 GCCGAGGCCCGCAGG 2

RESULT 416
LOCUS AR458594/c 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 2271 from patent US 6686188.
ACCESSION AR458594
VERSION AR458594.1 GI:42693651
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 17)
TITLE Gu, Y., Ji, Y., Penn, S. G., Hanzel, D. K., Rank, D. R., Chen, W. and
Shannon, M. E.
JOURNAL Polynucleotide encoding a human myosin-like polypeptide expressed
FEATURES predominantly in heart and muscle
Patent: US 6686188-A 2271 03-FEB-2004;
Location/Qualifiers
1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 396 GCCGAGGCCCGCAGG 411
DB 16 GCCGAGGCCCGCAGG 1

RESULT 417
LOCUS AX674744 17 bp DNA linear PAT 27-MAR-2003
DEFINITION Sequence 3189 from Patent WO03004526.

ACCESSION AX674744
VERSION AX674744.1 GI:29333092
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS 1
TITLE Telerman, A., Amson, R. and Tuijinder, M.
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and their use as
medicines
JOURNAL Patent: WO 03004526-A 3189 16-JAN-2003;
Molecular Engines Laboratories (FR)
FEATURES
source 1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1348 ATTTTATTTCCCTT 1363
DB 2 ATCTTATTTCCCTT 17

RESULT 418
AX729555 17 bp DNA linear PAT 08-MAY-2003
LOCUS AX729555
DEFINITION Sequence 1189 from Patent WO03025175.
ACCESSION AX729555
VERSION AX729555.1 GI:30508898
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS 1
TITLE Telerman, A., Amson, R. and Tuijinder, M.
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 1189 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source 1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1348 ATTTTATTTCCCTT 1363
DB 2 ATCTTATTTCCCTT 17

RESULT 419
AX730083 17 bp DNA linear PAT 08-MAY-2003
LOCUS AX730083
DEFINITION Sequence 1717 from Patent WO03025175.
ACCESSION AX730083
VERSION AX730083.1 GI:30509426
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS 1
TITLE Telerman, A., Amson, R. and Tuijinder, M.
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 1717 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source 1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1315 TTTTCAGACAGATC 1330
DB 16 TTTTCAGACAGATC 1

RESULT 420
AX761696 17 bp DNA linear PAT 25-JUN-2003
LOCUS AX761696
DEFINITION Sequence 5017 from Patent WO03040369.
ACCESSION AX761696
VERSION AX761696.1 GI:32256312
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS 1
TITLE Telerman, A., Amson, R. and Tuijinder, M.
Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 5017 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES
source 1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1348 ATTTTATTTCCCTT 1363
DB 2 ATCTTATTTCCCTT 17

RESULT 421
A89378 18 bp DNA linear PAT 22-JAN-2000
LOCUS A89378
DEFINITION Sequence 1526 from Patent WO9833904.
ACCESSION A89378
VERSION A89378.1 GI:6737948
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.

REFERENCE
AUTHORS 1 (bases 1 to 18)
TITLE Brysch, W. and Schlingensiepen, K.
AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 1526 06-AUG-1998;
BIOLOGISTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
source 1. .18
/organism="unidentified"

/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 1.0%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1312 TTATTTTCAGACAG 1327
Db 16 TTATTTTCAGACAG 1

RESULT 422
LOCUS AR106885 18 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 46 from patent US 6107092.
ACCESSION AR106885
VERSION AR106885.1 GI:12821415
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 18)
AUTHORS Cowser, L.M., Bennett, C., Frank, and O'Malley, B.W.
TITLE Antisense modulation of SRA expression
JOURNAL Patent: US 6107092-A 46 22-AUG-2000;
FEATURES
Location/Qualifiers
1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1491 ACATTATTCAGAAA 1506
Db 18 AGATTATTCAGAAA 3

RESULT 423
LOCUS AX662307 18 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 46 from Patent WO02059293.
ACCESSION AX662307
VERSION AX662307.1 GI:29163190
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Forster, A.C. and Blacklow, S.C.
TITLE Process and compositions for peptide, protein and peptidomimetic synthesis
JOURNAL Patent: WO 02059293-A 46 01-AUG-2002;
FEATURES
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="FROM SYNTHETIC DNA"

Query Match 1.0%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1514 TTAATTAATAAAAAA 1529
Db 16 TGAATTAATAAAAAA 1

RESULT 424

BD066891/c 18 bp DNA linear PAT 27-AUG-2002
LOCUS BD066891
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD066891
VERSION BD066891.1 GI:22612494
KEYWORDS JP 2001511000-A/1526.
SOURCE unidentified
ORGANISM unidentified
REFERENCE
1 (bases 1 to 18)
AUTHORS Schlingensiepen, K.H. and Brysch, W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 1526 07-AUG-2001;
COMMENT BIOLOGISCHES INSTITUT FÜR BIOMOLEKULARE DIAGNOSTIK MBH
OS Unknown
PN JP 2001511000-A/1526
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN, WOLFGANG BRYSCH
PC C12N15/11, C07H21/04, A61K31/70
CC An antisense oligonucleotide preparation method FH key
FEATURES
Location/Qualifiers
FT source 1..18
/organism="Unknown".
source 1..18
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 1.0%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1312 TTATTTTCAGACAG 1327
Db 16 TTATTTTCAGACAG 1

RESULT 425
LOCUS BD096088 18 bp DNA linear PAT 27-AUG-2002
DEFINITION Rice peroxidase having various characteristics.
ACCESSION BD096088
VERSION BD096088.1 GI:22641676
KEYWORDS WO 0142475-A/27.
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 18)
AUTHORS Oryza sativa
TITLE Rice peroxidase having various characteristics
JOURNAL Patent: WO 0142475-A 27 14-JUN-2001;
COMMENT JAPAN AS REPRESENTED BY DIRECTOR GENERAL OF MINISTRY OF AGRICULTURE FORESTRY AND FISHERIES NATIONAL INSTITUTE OF AGROBIOLOGICAL RESOURCES, KENICHI NOGUCHI YUKO OHASHI ICHIRO MITSUHASHI, TAKUJI SASAKI, YOSHIKI NAGAMURA, HIROYUKI ITO, TAKAYOSHI IMAI, SUSUNU HIRAGA
OS Oryza sativa (rice)
PN WO 0142475-A/27
PD 14-JUN-2001
PF 08-DEC-2000 WO 2000JP008728
PR 10-DEC-1999 JP 99P 352472
PI YUKO OHASHI, ICHIRO MITSUHASHI, TAKUJI SASAKI, YOSHIKI NAGAMURA, HIROYUKI ITO, TAKAYOSHI IMAI, SUSUNU HIRAGA
PC C12N15/53, C12N9/08, C12Q1/68
CC R1420FPI
FH key Location/Qualifiers

FT source 1.18
/organism='Oryza sativa (rice)'.
FEATURES
source 1.18
/organism="Oryza sativa"
/mol_type="genomic DNA"
/db_xref="taxon:4530"

Query Match 1.0%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 669 TCACCTCTGACGCCGC 684
|||||
2 TCACCTCTGACGCCGC 17

RESULT 426
A40129/c A40129 20 bp DNA linear PAT 05-MAR-1997
LOCUS Sequence 5 from Patent WO9423026.
DEFINITION A40129
ACCESSION A40129
VERSION A40129.1 GI:2296287
KEYWORDS
SOURCE unidentified
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Vasseer,M., Blumenfeld,M., Megueni,S. and Poddevin,B.
TITLE STABLE AND SEMI-STABLE OLIGONUCLEOTIDES, METHOD OF PREPARATION AND APPLICATIONS
JOURNAL Patent: WO 9423026-A 5 13-OCT-1994;
COMMENT Other publication AU 6432094 941024
Other publication FR 2703053 940930.
FEATURES
source 1.20
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1302 TCTATTTTATTTATTT 1317
|||||
16 TCTATTTTATTTT 1

Db 16 TCTATTTTATTTT 1

RESULT 427
BD244919 20 bp DNA linear PAT 17-JUL-2003
LOCUS BD244919
DEFINITION Modulation of gene expression by combination therapy.
ACCESSION BD244919
VERSION BD244919.1 GI:33054689
KEYWORDS JP 2002528391-A/47.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Besterman,J.M., Macleod,A.R. and Sidors,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: JP 2002528391-A 47 03-SEP-2002;
METHYGENE INC
COMMENT OS Artificial Sequence
PN JP 2002528391-A/47
PD 03-SEP-2002
PF 19-OCT-1999 JP 2000576885
PR 19-OCT-1998 US 60/104804
PI JEFFREY M BESTERMAN,ALAN ROBERT MACLEOD, WILLIAM M SIDERS PC
A61K48/00,A61K31/165,A61K31/19,A61K31/513,A61K31/517,A61K31/PC
706.

PC A61K31/7068,A61K31/7088,A61K31/7125,A61K45/00,A61P35/00,C12N15/PC
09//
PC C12N5/10,C12N15/00,C12N5/00
CC antisense
FH Key Location/Qualifiers
FT source 1.20
/organism='Artificial Sequence'.

FEATURES
source 1.20
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 726 TGCTGTGCTGCTGCC 741
|||||
4 TGCTGTGCTGCTGCC 19

Db 4 TGCTGTGCTGCTGCC 19

RESULT 428
AR298254 20 bp DNA linear PAT 12-JUN-2003
LOCUS AR298254
DEFINITION Sequence 9989 from patent US 6537751.
ACCESSION AR298254
VERSION AR298254.1 GI:3168538
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 9989 25-MAR-2003;
FEATURES
source 1.20
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1348 ATTTTATTTTCCCTT 1363
|||||
1 ATTTTATTTTCCCTT 16

Db 1 ATTTTATTTTCCCTT 16

RESULT 429
AR315939 20 bp DNA linear PAT 12-JUN-2003
LOCUS AR315939
DEFINITION Sequence 6476 from patent US 6559294.
ACCESSION AR315939
VERSION AR315939.1 GI:31709365
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffiths,R., Hoiseh,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
Sankaran,B. and Fletcher,L.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 6476 06-MAY-2003;
FEATURES
source 1.20
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.0%; Score 14.4; DB 1; Length 20;

Best Local Similarity 93.8%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 725 TTGCTGTTGCTGCTGCC 740
|||||
2 TTGCTGTTGCTGCTGCC 17

Db

RESULT 430

AR491020 20 bp DNA linear PAT 15-MAY-2004

LOCUS AR491020 Sequence 114 from patent US 6713300.

ACCESSION AR491020

VERSION AR491020.1 GI:47258553

KEYWORDS

SOURCE

ORGANISM

Unclassified.

1 (bases 1 to 20)

REFERENCE Allikmets, R., Anderson, K.L., Dean, M., Leppert, M., Lewis, R.A.,

AUTHORS Li, Y., Lupski, J.R., Nathans, J., Ratner, A., Shroyer, N.F., Singh, N.,

Smalwood, P. and Sun, H.

Nucleic acid and amino acid sequences for ATP-binding cassette

transporter and methods of screening for agents that modify

ATP-binding cassette transporter

PATENT: US 6713300-A 114 30-MAR-2004;

LOCATION/Qualifiers

1. .20

/mol_type="genomic DNA"

SOURCE

Query Match 1.0%; Score 14.4; DB 1; Length 20;

Best Local Similarity 93.8%; Pred. No. 2.3e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1191 TTGCTGTTGCTGCTTT 1206
|||||
5 TTGCTGTTGCTGCTTT 20

Db

RESULT 431

AX048436 20 bp DNA linear PAT 12-JAN-2001

LOCUS AX048436 Sequence 35 from Patent WO0071747.

ACCESSION AX048436

VERSION AX048436.1 GI:12225600

KEYWORDS

SOURCE

synthetic construct

artificial sequences.

REFERENCE

1 Boekenkamp, D., Hoppe, H.U. and Burgstaller, P.

Detection system for separating constituents of a sample and

production and use of the same

PATENT: WO 0071747-A 35 30-NOV-2000;

LOCATION/Qualifiers

1. .20

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="Beschreibung der künstlichen

Sequenz:Erkennungssystem"

SOURCE

Query Match 1.0%; Score 14.4; DB 1; Length 20;

Best Local Similarity 93.8%; Pred. No. 2.3e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1516 AATTAAAAA 1531
|||||
17 ACTTAAAAA 2

Db

RESULT 432
AX053082 20 bp DNA linear PAT 12-JAN-2001

LOCUS AX053082 Sequence 6 from Patent WO0071703.

ACCESSION AX053082

VERSION AX053082.1 GI:12227139

KEYWORDS

SOURCE

synthetic construct

artificial sequences.

REFERENCE

1 Macleod, A.R., Li, Z. and Besterman, J.M.

Inhibition of histone deacetylase

PATENT: WO 0071703-A 6 30-NOV-2000;

LOCATION/Qualifiers

1. .20

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="synthetic oligonucleotide"

SOURCE

Query Match 1.0%; Score 14.4; DB 1; Length 20;

Best Local Similarity 93.8%; Pred. No. 2.3e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 726 TGCTGTTGCTGCTGCC 741
|||||
4 TGCTGTTGCTGCTGCC 19

Db

RESULT 433

AX053091 20 bp DNA linear PAT 12-JAN-2001

LOCUS AX053091 Sequence 15 from Patent WO0071703.

ACCESSION AX053091

VERSION AX053091.1 GI:12227148

KEYWORDS

SOURCE

synthetic construct

artificial sequences.

REFERENCE

1 Macleod, A.R., Li, Z. and Besterman, J.M.

Inhibition of histone deacetylase

PATENT: WO 0071703-A 15 30-NOV-2000;

LOCATION/Qualifiers

1. .20

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="Description of Combined DNA/RNA Molecule: Positions

1-4 and 17-20 are 2'-methoxyribose substituted

nucleotides; positions 5-16 are deoxyribonucleotides"

SOURCE

Query Match 1.0%; Score 14.4; DB 1; Length 20;

Best Local Similarity 93.8%; Pred. No. 2.3e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 726 TGCTGTTGCTGCTGCC 741
|||||
4 TGCTGTTGCTGCTGCC 19

Db

RESULT 434

AX184293 20 bp DNA linear PAT 06-AUG-2001

LOCUS AX184293 Sequence 2046 from Patent WO0142511.

ACCESSION AX184293

VERSION AX184293.1 GI:15135639

KEYWORDS

SOURCE

Homo sapiens

ORGANISM

Homo sapiens (human)

REFERENCE
AUTHORS 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE Daly M., Hudson T.J., Lander E.S., Rioux J. and Simionovitch K.
JOURNAL Jbtd-related polymorphisms
Patent: WO 0142511-A 2546 14-JUN-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Ellipse
Biotherapeutics Corporation (CA)
Location/Qualifiers

FEATURES
source

1..20
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 88.2%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1311 TTATTTTTCAGACAG 1327
|||||
20 TTATTTTNGACAG 4

RESULT 435
AX546302 20 bp DNA linear PAT 26-NOV-2002
LOCUS
DEFINITION Sequence 51 from Patent EPI243290.
ACCESSION AX546302
VERSION AX546302.1 GI:25811493
KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequences.

REFERENCE
AUTHORS 1 Besterman J.M., Macleod A.R. and Siders W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: EP 1243290-A 51 25-SEP-2002;
Methylgene, Inc. (CA)
Location/Qualifiers

FEATURES
source

1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide"

Query Match 1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 726 TGCTGTGCTGCTGCC 741
|||||
4 TGCTGCTGCTGCTGCC 19

RESULT 436
AX546392 20 bp DNA linear PAT 26-NOV-2002
LOCUS
DEFINITION Sequence 51 from Patent EPI243289.
ACCESSION AX546392
VERSION AX546392.1 GI:25811583
KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequences.

REFERENCE
AUTHORS 1 Besterman J.M., Macleod A.R. and Siders W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: EP 1243289-A 51 25-SEP-2002;
Methylgene, Inc. (CA)
Location/Qualifiers

FEATURES
source
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"

/db_xref="taxon:32630"
/note="Oligonucleotide"

Query Match 1.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 726 TGCTGTGCTGCTGCC 741
|||||
4 TGCTGCTGCTGCTGCC 19

RESULT 437
A88414/c 19 bp DNA linear PAT 22-JAN-2000
LOCUS
DEFINITION Sequence 562 from Patent WO9833904.
ACCESSION A88414
VERSION A88414.1 GI:6736984
KEYWORDS
SOURCE
ORGANISM
unidentified
unclassified.

REFERENCE
AUTHORS 1 (bases 1 to 19)
TITLE Brysch W. and Schlingensiepen K.
JOURNAL AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
Patent: WO 9833904-A 562 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
Location/Qualifiers

1..19
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 1.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1298 TTAATCTATTTTATT 1316
|||||
19 TTGATTTCTTTTATT 1

RESULT 438
A90381/c 19 bp DNA linear PAT 22-JAN-2000
LOCUS
DEFINITION Sequence 562 from Patent EP0856579.
ACCESSION A90381
VERSION A90381.1 GI:6738895
KEYWORDS
SOURCE
ORGANISM
unidentified
unclassified.

REFERENCE
AUTHORS 1 (bases 1 to 19)
TITLE Brysch W.D. and Schlingensiepen K.D.
JOURNAL An antisense oligonucleotide preparation method
Patent: EP 0856579-A 562 05-AUG-1998;
BIOGNOSTIK GES (DE)
Location/Qualifiers

1..19
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 1.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1298 TTAATCTATTTTATT 1316
|||||
19 TTGATTTCTTTTATT 1

RESULT 439

BD184608/c
LOCUS BD184608 19 bp DNA linear PAT 17-JUN-2003
DEFINITION Method and detector for identifying subtypes of human papilloma virus98.
ACCESSION BD184608.1 GI:31876808
VERSION JP 2002360271-A/587.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 19)
AUTHORS Ling,C., Lin,R., Yoo,Z., Huang,X., Lee,B., Lee,S., Lin,Y., Huang,C., Hsu,H., Shi,C., Yeh,C., Cao,Y. and Pan,C.
TITLE Method and detector for identifying subtypes of human papilloma
JOURNAL Patent: JP 2002360271-A 587 17-Dec-2002;
KING CAR FOOD INDUSTRIAL CO LTD
COMMENT OS Artificial Sequence
PN JP 2002360271-A/587
PD 17-DEC-2002
PF 28-NOV-2001 JP 2001362595
PR 04-MAY-2001 TW 90110785
PI CHING-YEE LING, RUEY-WEN LIN, ZHOU-MENG YOO, XIN-HSIUAN HUANG, BOW-PI HAENG LEE,
PI SHENG-HSIUNG LEE, YI-JU LIN, CI-CHUNG HUANG, HAN-CHANG HSU, CHA-PI WEN SHI,
PI CHIH-XIN YEH, YI-FENG CAO, CHIH-LONG PAN
PC C12N15/09, C12N15/09, C12M1/34, C12Q1/04, C12Q1/42, C12Q1/68 PC
, C12Q1/70, G01N21/64,
PC G01N33/53, G01N33/574, G01N33/58, G01N37/00// (C12M1/34, C12R1.93),
PC (C12Q1/70, C12R1.93), C12N15/00, C12N15/00
CC Oligonucleotide M806108 for identifying HPV CP8061. FH Key
Location/Qualifiers
FT source 1..19 /organism='Artificial Sequence'.
FEATURES
source 1..19
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 1.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 847 GCCCTTAGTATGACCA 865
DB 19 GTCCTCCAGTATGACCA 1
RESULT 440
LOCUS AR294423 19 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 6158 from patent US 6537751.
ACCESSION AR294423
VERSION AR294423.1 GI:31681707
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density
JOURNAL diSeguilbrium map of the human genome
PATENT: US 6537751-A 6158 25-MAR-2003;
LOCATION/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1105 TAACCTCCATTTTCCCC 1123
DB 1 TACTTTCATTTTCCCC 19
RESULT 441
LOCUS AX132831 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 4049 from Patent WO0130362.
ACCESSION AX132831
VERSION AX132831.1 GI:14139141
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Robbins,J.M. and Tritz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases
JOURNAL Patent: WO 0130362-A 4049 03-MAY-2001;
IMMUSOL, INC. (US)
LOCATION/Qualifiers
source 1..19
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="PCNA HH ribozyme binding site"
Query Match 1.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1299 TAATCTATTTTATT 1317
DB 1 TAACCTATTTTCTCT 19
RESULT 442
LOCUS AX352893 19 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 99 from Patent EP1174518.
ACCESSION AX352893
VERSION AX352893.1 GI:18617975
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Loukachov,V.V., van Gemen,B. and Goudsmilt,J.
TITLE Collection of binding molecules
JOURNAL Patent: EP 1174518-A 99 23-JAN-2002;
Amsterdam Support Diagnostics B.V. (NL)
LOCATION/Qualifiers
1..19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="position 65"
Query Match 1.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1303 CTATTTTCTTTATTCAG 1321
DB 19 CTATTTTCTTTATAG 1
RESULT 443
LOCUS AX362738 19 bp DNA linear PAT 15-FEB-2002
DEFINITION Sequence 99 from Patent WO0208463.

ACCESSION AX362738
VERSION AX362738.1 GI:18694878
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Loukachov,V.V., Goudsmilt,V. and van Gemen,B.
TITLE Collection of binding molecules
JOURNAL Patent: WO 0208463-A 99 31-JAN-2002;
Amsterdam Support Diagnostics B.V. (NL)
FEATURES
source
1..19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="position 65"

Query Match 1.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1303 CTATTTTATTTTCAG 1321
DB 19 CTATTTTCTTTATAG 1

RESULT 444
LOCUS AX742755 19 bp DNA linear PAT 12-MAY-2003
DEFINITION Sequence 558 from Patent EP1302550.
ACCESSION AX742755
VERSION AX742755.1 GI:30576744
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Lin,C.Y., Lin,R.W., You,C.M., Huang,H.H., Lee,B.H., Lee,H.H.,
Lin,Y.J., Fan,C.C., Hsu,H.C., Shih,C.W., Yeh,C.H., Kao,Y.F.,
Pan,C.L. and Chan,P.
TITLE Method and detector for identifying subtypes of human papilloma
JOURNAL Patent: EP 1302550-A 558 16-APR-2003;
King Car Food Industrial Co., Ltd. (TW)
FEATURES
source
1..19
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide for identifying HPV CP8061"

Query Match 1.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 847 GCCCTTAGTAGTACGA 865
DB 19 GTCTCCAGTATGTACGA 1

RESULT 445
LOCUS BD065927 19 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD065927
VERSION BD065927.1 GI:22611530
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 19)
AUTHORS Schlingensiefen,K.H. and Brysch,W.

TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 562 07-AUG-2001;
BIOGENOSITIK GESELLSCHAFT FÜR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT
OS Unknown
PN JP 2001511000-A/562
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEFEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
FEATURES
FT source 1..19
Location/Qualifier
FT
1..19
/organism="Unknown"
source
1..19
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 1.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1298 TTATCTATTTTATT 1316
DB 19 TTGATTTCTTTTATT 1

RESULT 446
LOCUS A40129 20 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 5 from Patent WO9423026.
ACCESSION A40129
VERSION A40129.1 GI:2296287
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Vaasseur,M., Blumentfeld,M., Meguenni,S. and Poddevin,B.
TITLE STABLE AND SEMI-STABLE OLIGONUCLEOTIDES, METHOD OF PREPARATION AND
JOURNAL Patent: WO 9423026-A 5 13-OCT-1994;
GENSET (FR)
COMMENT Other publication AU 6432094 941024
Other publication FR 2703053 940930.
FEATURES
source
1..20
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAAGTAAAG 1538
DB 1 AAAAAAAAAAATGAAG 19

RESULT 447
LOCUS A70736 20 bp DNA linear PAT 07-MAY-1999
DEFINITION Sequence 57 from Patent WO9813490.
ACCESSION A70736
VERSION A70736.1 GI:4774739
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 20)
AUTHORS

AUTHORS Ophoff,R.A., Terwindt,G.M., Ferrari,M.D. and Frants,R.R.
TITLE A gene related to migraine in man
JOURNAL Patent: WO 9813490-A 57 02-APR-1998;
ORHOFF ROEL ANDRE (NL)
FEATURES
source Location/Qualifiers
1..20
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1634 TCCTACCCCTTTGAAAT 1652
Db 1 TCCTTCCTTCCTTTGTAGAT 19

RESULT 448
A79220 A79220 20 bp DNA linear PAT 20-OCT-1999
LOCUS
DEFINITION Sequence 57 from Patent EP0834561.
ACCESSION A79220
VERSION A79220.1 GI:6092265
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 20)
AUTHORS A GENE RELATED TO MIGRAINE IN MAN
TITLE Patent: EP 0834561-A 57 08-APR-1998;
JOURNAL UNIV LEIDEN (NL)
FEATURES
source Location/Qualifiers
1..20
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1634 TCCTACCCCTTTGAAAT 1652
Db 1 TCCTTCCTTCCTTTGTAGAT 19

RESULT 449
AR086304 AR086304 20 bp DNA linear PAT 07-SEP-2000
LOCUS
DEFINITION Sequence 125 from patent US 5985558.
ACCESSION AR086304
VERSION AR086304.1 GI:10013070
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dean,N.M., McKay,R., Miraglia,L. and Baker,B.
TITLE Antisense oligonucleotide compositions and methods for the
inhibition of c-Jun and c-Fos
JOURNAL Patent: US 5985558-A 125 16-NOV-1999;
FEATURES
source Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1290 TTGTGTGTTAATCTATT 1308
Db 19 TTGTGTTTAAATTATT 1

RESULT 450
AR086311 AR086311 20 bp DNA linear PAT 07-SEP-2000
LOCUS
DEFINITION Sequence 132 from patent US 5985558.
ACCESSION AR086311
VERSION AR086311.1 GI:10013077
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dean,N.M., McKay,R., Miraglia,L. and Baker,B.
TITLE Antisense oligonucleotide compositions and methods for the
inhibition of c-Jun and c-Fos
JOURNAL Patent: US 5985558-A 132 16-NOV-1999;
FEATURES
source Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1290 TTGTGTGTTAATCTATT 1308
Db 19 TTGTGTTTAAATTATT 1

RESULT 451
AR129739 AR129739 20 bp DNA linear PAT 16-MAY-2001
LOCUS
DEFINITION Sequence 143 from patent US 6187545.
ACCESSION AR129739
VERSION AR129739.1 GI:14117636
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS McKay,R., Butler,M.M., Wyatt,J. and Cowsett,L.M.
TITLE Antisense modulation of peptid-cytosolic expression
JOURNAL Patent: US 6187545-A 143 13-FEB-2001;
FEATURES
source Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1563 GCCAGCCCAACAGTGTAT 1581
Db 2 GCCAGCCCAACAGTGTAT 20

RESULT 452
AR142677 AR142677 20 bp DNA linear PAT 08-AUG-2001
LOCUS
DEFINITION Sequence 7 from patent US 6203988.
ACCESSION AR142677
VERSION AR142677.1 GI:15103963
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)

AUTHORS Kambara,H. and Uematsu,C.
TITLE DNA fragment preparation method for gene expression profiling
JOURNAL Patent: US 6203988-A 7 20-MAR-2001;
FEATURES Location/Qualifiers
SOURCE 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1306 TTTTATTATTTCAGACA 1324
|||||
19 TTTTATTATTTCAGACA 1

RESULT 453
AR158717 20 bp DNA linear PAT 17-OCT-2001
LOCUS Sequence 339 from patent US 6251588.
DEFINITION AR158717
ACCESSION AR158717
VERSION AR158717.1 GI:16220917
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Shannon,K.W., Wolber,P.K., Delenettarr,G.C., Webb,P.G. and Kincaid,R.H.
TITLE Method for evaluating oligonucleotide probe sequences
JOURNAL Patent: US 6251588-A 339 26-JUN-2001;
FEATURES Location/Qualifiers
SOURCE 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1246 TCTTGTGTTGTTTAA 1264
|||||
2 TCTGTGATTTGTTTAA 20

RESULT 454
AR158718 20 bp DNA linear PAT 17-OCT-2001
LOCUS Sequence 340 from patent US 6251588.
DEFINITION AR158718
ACCESSION AR158718
VERSION AR158718.1 GI:16220919
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Shannon,K.W., Wolber,P.K., Delenettarr,G.C., Webb,P.G. and Kincaid,R.H.
TITLE Method for evaluating oligonucleotide probe sequences
JOURNAL Patent: US 6251588-A 340 26-JUN-2001;
FEATURES Location/Qualifiers
SOURCE 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1246 TCTTGTGTTGTTTAA 1264
|||||
1 TCTGTGATTTGTTTAA 19

RESULT 455
AR163731 20 bp DNA linear PAT 17-OCT-2001
LOCUS Sequence 18 from patent US 6271029.
DEFINITION AR163731
ACCESSION AR163731
VERSION AR163731.1 GI:16234426
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,C.Frank, and Cowseert,L.M.
TITLE Antisense inhibition of cytohesin-2 expression
JOURNAL Patent: US 6271029-A 18 07-AUG-2001;
FEATURES Location/Qualifiers
SOURCE 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 352 GCCCGCAGAGGGCCTCG 370
|||||
1 GTCCCGCAGTCGGGCTCG 19

RESULT 456
AR169510 20 bp DNA linear PAT 17-DEC-2001
LOCUS Sequence 6 from patent US 6291173.
DEFINITION AR169510
ACCESSION AR169510
VERSION AR169510.1 GI:17907377
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bartel,P.L. and Tavtigian,S.V.
TITLE WMS2--an MMAC1 interacting protein
JOURNAL Patent: US 6291173-A 6 18-SEP-2001;
FEATURES Location/Qualifiers
SOURCE 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1238 CTTCTCATCTTTGTTTG 1256
|||||
1 CTTCTCTCTTTGTATAG 19

RESULT 457
AR176870 20 bp DNA linear PAT 17-DEC-2001
LOCUS Sequence 125 from patent US 6312900.
DEFINITION AR176870
ACCESSION AR176870
VERSION AR176870.1 GI:17919225
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dean,N.M., McKay,R., Miraglia,L. and Baker,B.
TITLE Antisense oligonucleotide compositions and methods for the modulation of activating protein 1
JOURNAL Patent: US 6312900-A 125 06-NOV-2001;

FEATURES
source
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1290 TTGTGTGTTAATCTATT 1308
Db 19 TTGTGTGTTAATCTATT 1

RESULT 458
AR176877/c AR176877 20 bp DNA linear PAT 17-DEC-2001
LOCUS Sequence 132 from patent US 6312900.
DEFINITION AR176877
ACCESSION AR176877
VERSION AR176877.1 GI:17919232
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 20)
AUTHORS Dean,N.M., McKay,R., Miraglia,L. and Baker,B.
TITLE Antisense oligonucleotide compositions and methods for the
modulation of activating protein 1
JOURNAL Patent: US 6312900-A 132 06-NOV-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1290 TTGTGTGTTAATCTATT 1308
Db 19 TTGTGTGTTAATCTATT 1

RESULT 459
E05497 20 bp DNA linear PAT 29-SEP-1997
LOCUS PCR primer for detecting polymorphism of Oryza sativa and Zea
maize.
DEFINITION E05497
ACCESSION E05497.1 GI:2173685
VERSION E05497.1 GI:2173685
KEYWORDS JP 1993244995-A/7.
SOURCE Synthetic construct
ORGANISM Synthetic construct
REFERENCE 1 (bases 1 to 20)
AUTHORS Komatsu,Y. and Kikuchi,Y.
TITLE NEW PRIMER
JOURNAL Patent: JP 1993244995-A 7 24-SEP-1993;
COMMENT KYOMA HAKKO KOGYO CO LTD
OS Artificial gene
OC Artificial sequence; Genes.
OS Zea maize
PN JP 1993244995-A/7
PD 24-SEP-1993
PI 24-SEP-1991 JP 1991244122
PI KOMATSU YUKI, KIKUCHI YASUHIRO
PC C1201/68,C12N15/11;
CC C1201/68,C12N15/11;
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No.
FEATURES Location/Qualifiers
source 1..20

/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 545 TTGTGTGTCGTCGTCGTC 563
Db 1 TTGTGTGTCGTCGTCGTC 19

RESULT 460
E28096/c E28096 20 bp DNA linear PAT 18-JUN-2001
LOCUS Method for analyzing DNA fragment.
DEFINITION E28096
ACCESSION E28096
VERSION E28096.1 GI:13018321
KEYWORDS JP 1999196874-A/7.
SOURCE unidentified
ORGANISM unidentified
REFERENCE Unclassified.
1 (bases 1 to 20)
AUTHORS Hideki,K. and Senshu,U.
TITLE Method for analyzing DNA fragment
JOURNAL Patent: JP 1999196874-A 7 27-JUL-1999;
COMMENT HITACHI LTD
OS Unidentified
PN JP 1999196874-A/7
PD 27-JUL-1999
PF 14-JAN-1998 JP 1998005399
PR HIDEKI KAMIBARA,SENSHU UEMATSU
PI C12N15/09,C12Q1/68,GOIN27/447,C12N15/00,GOIN27/26 CC
PC C12N15/09,C12Q1/68,GOIN27/447,C12N15/00,GOIN27/26 CC
Strandedness: Single;
CC Topology: Linear;
FH Key
FT source 1..20
/organism="Unidentified".
FEATURES Location/Qualifiers
source 1..20
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1306 TTTTGTGTTTTCAGAGA 1324
Db 19 TTTTGTGTTTTCAGAGA 1

RESULT 461
E44159/c E44159 20 bp DNA linear PAT 27-AUG-2002
LOCUS Methods of identification and specific detection of slow-growing
DEFINITION E44159 mycobacteria by using characteristic base sequence occurring in DNA
gyrase gene.
ACCESSION E44159
VERSION E44159.1 GI:22553300
KEYWORDS JP 2001128679-A/2.
SOURCE Synthetic construct
ORGANISM Synthetic construct
REFERENCE 1 (bases 1 to 20)
AUTHORS Kasai,H., Ezaki,T. and Harayama,S.
TITLE Methods of identification and specific detection of slow-growing
mycobacteria by using characteristic base sequence occurring in DNA
gyrase gene
JOURNAL Patent: JP 2001128679-A 2 15-MAY-2001;

COMMENT MARINE BIOTECHNOLOGY INST CO LTD
OS Artificial Sequence
PN JP 2001128679-A/2
PD 15-MAY-2001
PF 02-NOV-1999 JP 1999312525
PI HIROAKI KASAI, TAKAYUKI EZAKI, SHIGEAKI HARAYAMA PC
C12N15/09, C12Q1/04, C12Q1/68, C12N15/00
CC

FEATURES
source Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 348 CGCGCGCGCGCAGAGGCGC 366
Db 19 CGCGCGCGCGCAGAGGTC 1

RESULT 462
LOCUS E59328 20 bp DNA linear PAT 31-JAN-2002
DEFINITION Method for purifying oligonucleotide.
ACCESSION E59328
VERSION E59328.1 GI:18622505
KEYWORDS JP 2000342265-A/9.
synthetic construct
synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Hirose K. and Yoshida, T.
TITLE Method for purifying oligonucleotide
JOURNAL Patent: JP 2000342265-A 9 12-DEC-2000;
TOGOSEI CHEM IND CO LTD
OS Artificial Sequence
PN JP 2000342265-A/9
PD 12-DEC-2000
PF 02-JUN-1999 JP 1999154974
PR KUNIHICO HIROSE, TADAO YOSHIDA
PI C12N15/09, B01D15/08, C12N15/00
PC
CC
FH Key Location/Qualifiers
FT source 1..20
/organism="Artificial Sequence".
1..20
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

FEATURES
source Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1519 TAAAAAAGAAAGTAAAA 1537
Db 1 TAAAAAAGAAAGTAAAA 19

RESULT 463
LOCUS I17092 20 bp DNA linear PAT 03-APR-1996
DEFINITION Sequence 7 from patent US 5484703.
ACCESSION I17092
VERSION I17092.1 GI:1252000
KEYWORDS
SOURCE Unknown.

ORGANISM Unknown:
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Raben, N.; Nichols, R., Plotz, P. and Jeff, R.
TITLE Assay using recombinant histidyl-tRNA synthetase
JOURNAL Patent: US 5484703-A 7 16-JAN-1996;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1032 GCAGAGTGGCGGCGGTGG 1050
Db 1 GCAGAGCGTGGCGGCGTGG 19

RESULT 464
LOCUS I63487 20 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 7 from patent US 5663066.
ACCESSION I63487
VERSION I63487.1 GI:2481060
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown:
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Raben, N.; Nichols, R., Plotz, P. and Jeff, R.
TITLE Assay using recombinant histidyl-tRNA synthetase
JOURNAL Patent: US 5663066-A 7 02-SEP-1997;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1032 GCAGAGTGGCGGCGGTGG 1050
Db 1 GCAGAGCGTGGCGGCGTGG 19

RESULT 465
LOCUS AR200176/c 20 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 51 from patent US 6355782.
ACCESSION AR200176
VERSION AR200176.1 GI:20250250
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown:
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Zonana, J., Ferguson, B.M., Heaton, D. and Overbeek, P.
TITLE Hypohidrotic ectodermal dysplasia genes and proteins
JOURNAL Patent: US 6355782-A 51 12-MAR-2002;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1018 ACCTGAGATTGACGCAGA 1036
||| ||||| ||||| |||

Db 19 ACATGAGAAATGACGCTGA 1

RESULT 466

LOCUS AR224778 20 bp DNA linear PAT 26-SEP-2002

DEFINITION Sequence 83 from patent US 6440739.

ACCESSION AR224778

VERSION AR224778.1 GI:23333618

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)

Unclassified.

AUTHORS Bennett,C.F. and Freier,S.M.

TITLE Antisense modulation of glioma-associated oncogene-2 expression

JOURNAL Patent: US 6440739-A 83 27-AUG-2002;

FEATURES

source 1..20

/organism="unknown"

/mol_type="genomic DNA"

Query Match 1.0%; Score 14.2; DB 1; Length 20;

Best Local Similarity 84.2%; Pred.No.2.5e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1627 CAATCTCTCCCTACCTTT 1645

Db 2 CAATGCTCCCTACCTCT 20

RESULT 467

LOCUS AR307902 20 bp DNA linear PAT 12-JUN-2003

DEFINITION Sequence 113 from patent US 6551826.

ACCESSION AR307902

VERSION AR307902.1 GI:31698658

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)

Unclassified.

AUTHORS Watt,A.T.

TITLE Antisense modulation of raiid expression

JOURNAL Patent: US 6551826-A 113 22-APR-2003;

FEATURES

source 1..20

/organism="unknown"

/mol_type="genomic DNA"

Query Match 1.0%; Score 14.2; DB 1; Length 20;

Best Local Similarity 84.2%; Pred.No.2.5e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1540 GAAGGCAAGATGCACCA 1558

Db 1 GAAGGCAAGATGCACCA 19

RESULT 468

LOCUS AR313596/c 20 bp DNA linear PAT 12-JUN-2003

DEFINITION Sequence 4133 from patent US 6559294.

ACCESSION AR313596

VERSION AR313596.1 GI:31707022

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)

Unclassified.

AUTHORS Griffais,R., Holseeth,S.K., Zagureky,R.J., Metcalf,B.J., Peek,J.A.,

Sankaran,B. and Fletcher,L.D.

TITLE Chlamydia pneumoniae polynucleotides and uses thereof

JOURNAL Patent: US 6559294-A 4133 06-MAY-2003;

FEATURES

Location/Qualifiers

source 1..20

/organism="unknown"

/mol_type="genomic DNA"

Query Match 1.0%; Score 14.2; DB 1; Length 20;

Best Local Similarity 84.2%; Pred.No.2.5e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 985 GGACCTTCTGTTCTGTGG 1003

Db 20 GGACCTACTTTTCTGTGG 2

RESULT 469

LOCUS AR314906 20 bp DNA linear PAT 12-JUN-2003

DEFINITION Sequence 5443 from patent US 6559294.

ACCESSION AR314906

VERSION AR314906.1 GI:31708332

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)

Unclassified.

AUTHORS Griffais,R., Holseeth,S.K., Zagureky,R.J., Metcalf,B.J., Peek,J.A.,

Sankaran,B. and Fletcher,L.D.

TITLE Chlamydia pneumoniae polynucleotides and uses thereof

JOURNAL Patent: US 6559294-A 5443 06-MAY-2003;

FEATURES

source 1..20

/organism="unknown"

/mol_type="genomic DNA"

Query Match 1.0%; Score 14.2; DB 1; Length 20;

Best Local Similarity 84.2%; Pred.No.2.5e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 706 TGGAGTCGCGTTCCTCTT 724

Db 20 TGGAGTCGCTGTTCTCTT 2

RESULT 470

LOCUS AR371268 20 bp DNA linear PAT 12-SEP-2003

DEFINITION Sequence 4 from patent US 6395474.

ACCESSION AR371268

VERSION AR371268.1 GI:34608200

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)

Unclassified.

AUTHORS Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.

TITLE Peptide nucleic acids

JOURNAL Patent: US 6395474-A 4 28-MAY-2002;

FEATURES

Location/Qualifiers

source 1..20

/organism="unknown"

/mol_type="genomic DNA"

Query Match 1.0%; Score 14.2; DB 1; Length 20;

Best Local Similarity 84.2%; Pred.No.2.5e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1520 AAAAAAAAAAGTAAAG 1538

Db 2 AAAAAAAAAAAAAAAAAAG 20

RESULT 471

AR428075/c
LOCUS AR428075 20 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 5 from patent US 6641818.
ACCESSION AR428075
VERSION AR428075.1 GI:40187443
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
SOURCE

Query Match
Best Local Similarity 1.0%; Score 14.2; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 726 TGCTGTGCTGCTGCTTT 744
DB 19 TGCTGTGCTGCTGCTTT 1

RESULT 472
AR489489 20 bp DNA linear PAT 15-MAY-2004
LOCUS AR489489
DEFINITION Sequence 4 from patent US 6710163.
ACCESSION AR489489
VERSION AR489489.1 GI:47256514
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
SOURCE

Query Match
Best Local Similarity 1.0%; Score 14.2; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAG 1538
DB 2 AAAAAAAAAAAAAAAAAAG 20

RESULT 473
AR491100 20 bp DNA linear PAT 15-MAY-2004
LOCUS AR491100
DEFINITION Sequence 4 from patent US 6713602.
ACCESSION AR491100
VERSION AR491100.1 GI:47258960
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
SOURCE

Query Match
Best Local Similarity 1.0%; Score 14.2; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAG 1538
DB 2 AAAAAAAAAAAAAAAAAAG 20

RESULT 473
AR491100 20 bp DNA linear PAT 15-MAY-2004
LOCUS AR491100
DEFINITION Sequence 4 from patent US 6713602.
ACCESSION AR491100
VERSION AR491100.1 GI:47258960
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
SOURCE

/organism="unknown"
/mol_type="genomic DNA"
Query Match
Best Local Similarity 1.0%; Score 14.2; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1520 AAAAAAAAAAGTAAAG 1538
DB 2 AAAAAAAAAAAAAAAAAAG 20

RESULT 474
AX078001 20 bp DNA linear PAT 22-FEB-2001
LOCUS AX078001
DEFINITION Sequence 15 from patent WO0105435.
ACCESSION AX078001
VERSION AX078001.1 GI:13157746
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
SOURCE

Query Match
Best Local Similarity 1.0%; Score 14.2; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1304 TATTTTATTTTATTTTCA 1322
DB 2 TTTTATTTTATTTTCAAA 20

RESULT 475
AX078001/c 20 bp DNA linear PAT 22-FEB-2001
LOCUS AX078001/c
DEFINITION Sequence 15 from patent WO0105435.
ACCESSION AX078001
VERSION AX078001.1 GI:13157746
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
SOURCE

Query Match
Best Local Similarity 1.0%; Score 14.2; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1518 TTAATAAAAAAAAAAGTAA 1536
DB 19 TTGAAAAAAAAAAAAAAAAA 1

RESULT 476
LOCUS AX137428/c 20 bp DNA linear PAT 30-MAY-2001
DEFINITION Sequence 3 from Patent EP1098003.
ACCESSION AX137428
VERSION AX137428.1 GI:14273633
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Kasai, H., Harayama, S. and Ezaki, T.
TITLE Identification method and specific detection method of slow growing
JOURNAL mycobacteria utilizing dna gyrase gene
MARINE BIOTECHNOLOGY INSTITUTE CO., LTD. (JP)
LOCATION/Qualifiers
FEATURES
source
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic DNA"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 348 CGCCGCCCGCAGAGCGGC 366
Db 19 CGCCGCCCGCAGAGGTC 1

RESULT 477
LOCUS AX293619/c 20 bp DNA linear PAT 21-NOV-2001
DEFINITION Sequence 5381 from Patent WO0179548.
ACCESSION AX293619
VERSION AX293619.1 GI:17055302
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Barany, F., Zivvi, M., Gerry, N.P., Favis, R. and Kloman, R.
TITLE Method of designing addressable array for detection of nucleic acid
JOURNAL Sequence differences using ligase detection reaction
Patent: WO 0179548-A 5381 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
LOCATION/Qualifiers
FEATURES
source
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1184 ACGCGATTCTGTGTGTGT 1202
Db 19 ACGCGATTCTGTGTGTGT 1

RESULT 478
LOCUS AX298452 20 bp DNA linear PAT 26-NOV-2001
DEFINITION Sequence 86 from Patent WO0183749.
ACCESSION AX298452
VERSION AX298452.1 GI:17128442
KEYWORDS
SOURCE
Mue sp.

ORGANISM Mue sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1
AUTHORS Bachmannov, A.A., Beauchamp, G.K., Chatterjee, A., de Jong, P.J., Li, S.,
Li, X., Ohmen, J.D., Reed, D.R., Ross, D. and Tordoff, M.G.
TITLE Gene and sequence variation associated with sensing carbohydrate
JOURNAL compounds and other sweeteners
Patent: WO 0183749-A 86 08-NOV-2001;
WARNER-LAMBERT COMPANY (US); The Monell Chemical Senses Center
(US)
LOCATION/Qualifiers
FEATURES
source
1..20
/organism="Mus sp."
/mol_type="unassigned DNA"
/db_xref="taxon:10095"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1227 CTAGCTTTAGCTTCTCA 1245
Db 2 CAACCTTTAGCTTCTCA 20

RESULT 479
LOCUS AX452909/c 20 bp DNA linear PAT 06-JUL-2002
DEFINITION Sequence 10 from Patent WO0242322.
ACCESSION AX452909
VERSION AX452909.1 GI:21712544
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Jackson, D., Casari, G. and Suckow, J.
TITLE Mammalian nuclear receptor cofactors c7 and c8 and methods of use
JOURNAL Patent: WO 0242322-A 10 30-MAY-2002;
LION Bioscience AG (DE)
LOCATION/Qualifiers
FEATURES
source
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer for amplifying CF8"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1520 AAAAAAAAAAAGTAAAG 1538
Db 20 ATAAAGAAAAAGTAAAG 2

RESULT 480
LOCUS AX462672/c 20 bp DNA linear PAT 15-JUL-2002
DEFINITION Sequence 416 from Patent EP1217079.
ACCESSION AX462672
VERSION AX462672.1 GI:21885885
KEYWORDS
SOURCE
ORGANISM
Aegilops tauschii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Aegilops.
REFERENCE
1
AUTHORS Bernard, M., Sourdil, P. and Guyomarch, H.
TITLE Microsatellite markers from Triticum tauschii
JOURNAL Patent: EP 1217079-A 416 26-JUN-2002;

RESULT 485
BD003450 20 bp DNA linear PAT 31-JAN-2002
LOCUS A gene related to migrate in man.
DEFINITION
ACCESSION BD003450
VERSION BD003450.1 GI:18631411
KEYWORDS JP 2001500743-A/19.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 20)
Frantz,R.R.I.E., Ferrarri,M.D., Terravinto,H.M. and Ogunofu,R.A.
A gene related to migrate in man
Patent: JP 2001500743-A 19 23-JAN-2001;
RYUKUS UNIVERSITY TO RAIDEN
OS Homo sapiens (human)
PN JP 2001500743-A/19
PD 23-JAN-2001
PF 26-SEP-1997 JP 1998515527
PR 27-SEP-1996 EP 96202707.4
PI RENE ROBERT ISAAC,ERIK FRANTZ,MICHEL DOMINIQUE FERRARI, PI
HISRA MARRY TERRAVINTO,RURU ANDRE OPUHOFU
PC C12N15/09,A01K67/027,C07K14/435,C07K16/18,C12N1/15,C12N1/19,
PC C12N1/21
PC C12N5/10,C12N1/02,C12N1/68,C12N15/00,C12N5/00 CC
FH Key Location/Qualifiers
FT primer bind (1). (20).
Location/Qualifiers
1..20
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1634 TCCCTACCCCTTTGAAAT 1652
Db 1 TCCCTACCCCTTTGATGAT 19

RESULT 486
BD056369 20 bp DNA linear PAT 27-AUG-2002
LOCUS Peptide having a function regulating transcription of gene.
DEFINITION BD056369
ACCESSION BD056369.1 GI:22601975
KEYWORDS JP 2001269176-A/3.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
1 (bases 1 to 20)
Takagi,M., Shinji,H. and Oca,K.
Peptide having a function regulating transcription of gene
Patent: JP 2001269176-A 3 02-OCT-2001;
AGENCY OF IND SCIENCE & TECHNOL
OS Artificial Sequence
PN JP 2001269176-A/3
PD 02-OCT-2001
PF 27-MAR-2000 JP 2000087536
PI MASARU TAKAGI,HIDEAKI SHINJI,KEN OTA
PC C12N15/09,C07K14/415,C12N1/15,C12N1/19,C12N1/21,C12N5/10// PC
C12P21/02.
PC (C12N15/09,C12R1:91),(C12N5/10,C12R1:91),C12N15/00,C12N5/00,
PC (C12N15/00,C12R1:91),(C12N5/00,C12R1:91)
CC Description of Artificial Sequence: Synthetic primer DNA FH
Key Location/Qualifiers
1..20
Location/Qualifiers

FEATURES
source 1..20
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1399 ATGAGTGTCAAAATPAGG 1417
Db 2 ATGCTGTCAAAATPAGG 20

RESULT 487
BD056371 20 bp DNA linear PAT 27-AUG-2002
LOCUS Peptide having a function regulating transcription of gene.
DEFINITION BD056371
ACCESSION BD056371.1 GI:22601977
VERSION BD056371.1 GI:22601977
KEYWORDS JP 2001269176-A/5.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
1 (bases 1 to 20)
Takagi,M., Shinji,H. and Oca,K.
Peptide having a function regulating transcription of gene
Patent: JP 2001269176-A 5 02-OCT-2001;
AGENCY OF IND SCIENCE & TECHNOL
OS Artificial Sequence
PN JP 2001269176-A/5
PD 02-OCT-2001
PF 27-MAR-2000 JP 2000087536
PI MASARU TAKAGI,HIDEAKI SHINJI,KEN OTA
PC C12N15/09,C07K14/415,C12N1/15,C12N1/19,C12N1/21,C12N5/10// PC
C12P21/02.
PC (C12N15/09,C12R1:91),(C12N5/10,C12R1:91),C12N15/00,C12N5/00,
PC (C12N15/00,C12R1:91),(C12N5/00,C12R1:91)
CC Description of Artificial Sequence: Synthetic primer DNA FH
Key Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1399 ATGAGTGTCAAAATPAGG 1417
Db 2 ATGCTGTCAAAATPAGG 20

RESULT 488
BD089539 20 bp DNA linear PAT 27-AUG-2002
LOCUS A method of arraying genome clone.
DEFINITION BD089539
ACCESSION BD089539.1 GI:22635149
VERSION BD089539.1 GI:22635149
KEYWORDS JP 2001321190-A/1783.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
1 (bases 1 to 20)
Soeda,E.
A method of arraying genome clone
Patent: JP 2001321190-A 1783 20-NOV-2001;
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
GENOTECHS
OS Artificial Sequence
PN JP 2001321190-A/1783
PD 20-NOV-2001

PF 12-MAR-2001 JP 2001068285
PI EITICHI SOEDA
PC C12N15/09, C12N15/09, C12M1/00, C12Q1/68, G01N3/53, G01N3/566, PC
C12N15/00,
PC C12N15/00
CC Description of Artificial Sequence: Synthetic DNA FH Key
Location/Qualifiers
FT source 1..20
/organism='Artificial Sequence'.
1..20
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1549 ATGTCACCCAGATGCCAG 1567
DB 19 ATGCCACTCAGATCCAG 1

RESULT 489
LOCUS BD161924 20 bp DNA linear PAT 17-JAN-2003
DEFINITION Method for carrying out thermal cycle of PCR using DNA-immobilized substrate.
ACCESSION BD161924 GI:27867682
VERSION BD161924.1
KEYWORDS JP 2002191369-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
1 (bases 1 to 20)
Tanga,N., Okamura,H. and Takahashi,K.
AUTHORS Method for carrying out thermal cycle of PCR using DNA-immobilized substrate
TITLE Patent: JP 2002191369-A 1 09-JUL-2002;
JOURNAL TOYO KOHAN CO LTD, KOJIRO TAKAHASHI
COMMENT OS JP 2002191369-A/1
PN JP 2002191369-A/1
PD 09-JUL-2002 JP 2000399573
PF 27-DEC-2000 JP 2000399573
PI MICHIYUKI TANGA, HIROSHI OKAMURA, KOJIRO TAKAHASHI PC
C12N15/09, C12N15/09, C12Q1/68, C12N15/00, C12N15/00 CC Method for carrying out thermal cycle of PCR using DNA- CC
immobilized
CC substrate
FH key
FT source 1..20
Location/Qualifiers
/organism='Artificial Sequence'.
1..20
Location/Qualifiers
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1300 AATCTATTTTATTTT 1318
DB 2 AATTTTATTTTATTTT 20

RESULT 490
LOCUS S4717684 20 bp DNA linear PRI 08-MAY-1993
DEFINITION lipoprotein lipase (introns 3, 6 and 8) [human, Genomic, 20 nt, segment 4 of 5].

ACCESSION S47179
VERSION S47179.1 GI:258898
KEYWORDS
SEGMENT 4 of 5
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Gotooda,T., Yamada,N., Murase,T., Shimano,H., Shinada,M., Harada,K., I (bases 1 to 20)
TITLE Detection of three separate DNA polymorphisms in the human lipoprotein lipase gene by gene amplification and restriction endonuclease digestion
JOURNAL J. Lipid Res. 33 (7), 1067-1072 (1992)
MEDLINE 93057100
PUBMED 1358995
REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gblseq 117241] from the original journal article.
COMMENTS Regions surrounding three polymorphic sites.
FEATURES
source
1..20
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'

Query Match 1.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1502 AGAAGATCTGTTATTA 1520
DB 20 AGAAGATCTGTTATTA 2

RESULT 491
LOCUS AB068086 20 bp DNA linear SYN 21-MAY-2003
DEFINITION Synthetic construct DNA, forward primer for human STS sts-H96854 at 1p36.
ACCESSION AB068086
VERSION AB068086
KEYWORDS AB068086.1 GI:15128890
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
AUTHORS Chen,Y.Z., Hayashi,Y., Wu,J.G., Takeoka,E., Maekawa,K., Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H., Morohashi,A., Onira,M., Nakagawara,A., Liu,S., Hoishi,M., Horii,A. and Soeda,E.
TITLE A BAC-based STS-content map spanning a 35-Mb region of human chromosome 1p35-p36
JOURNAL Genomics 74 (1), 55-70 (2001)
MEDLINE 21269192
PUBMED 11374902
REFERENCE 2 (bases 1 to 20)
AUTHORS Horii,A.
JOURNAL Direct Submission
TITLE Submitted (04-AUG-2001) Akira Horii, Tohoku University School of Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai, Miyagi 980-8575, Japan (E-mail: horii@mail.cc.tohoku.ac.jp, Tel:81-22-717-8042, Fax:81-22-717-8047)
FEATURES
source
1..20
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

misc_feature
1..20
/note='forward primer for human STS sts-H96854 at 1p36 sts-H96854 obtained from clones B293A18, B122B3, B91D18, Human BAC library RPCI-11'

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